

GenCore version 5.1.4.p5_4578
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OM protein - nucleic search, using frame_plus.p2n model

Run on: May 19, 2003, 22:09:49 ; Search time 1912 Seconds
(without alignments)
197.875 Million cell updates/sec

Title: US-09-768-840-1_COPY_254_266
Perfect score: 70
Sequence: 1 DLNKGCHLDGSEV 13

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
-O=/cpn2.1/USPTO.spool/US09768840/runat_14052003_095711_16644/app_query.fasta_1.199
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09768840.ecgn_1.1.2496.grunat_14052003_095711_16644 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_ov:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_mu:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_pl:*
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26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_fod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	70	100.0	1055	6	AR035969	AR035969 Sequence
2	70	100.0	1055	6	AR135029	AR135029 Sequence
3	70	100.0	1454	9	AF183423	AF183423 Homo sapi
4	70	100.0	1463	6	AR083085	AR083085 Sequence
5	70	100.0	1463	6	AR152960	AR152960 Sequence
6	70	100.0	1470	9	BC0113436	BC0113436 Homo sapi
7	70	100.0	1503	6	AX464230	AX464230 Sequence
8	70	100.0	1507	6	AX354366	AX354366 Sequence
9	70	100.0	1507	6	AX354369	AX354369 Sequence
10	70	100.0	179394	9	AC010619	AC010619 Homo sapi
11	62	88.6	1414	10	BC005487	BC005487 Mus muscu
12	62	88.6	1421	10	BC025602	BC025602 Mus muscu
13	62	88.6	110000	2	AC073763_0	AC073763 Mus muscu
14	62	88.6	186243	2	AC073740	AC073740 Mus muscu
15	62	88.6	191713	2	AC126256	AC126256 Mus muscu
16	51	72.9	184443	2	AC114853	AC114853 Rattus no
17	48	68.6	1454	9	BC010120	BC010120 Homo sapi
18	48	68.6	1637	6	AX460089	AX460089 Sequence
19	48	68.6	1832	6	AX480897	AX480897 Sequence
20	48	68.6	1929	6	AX338084	AX338084 Sequence
21	48	68.6	1998	10	MUSRCAL	DI3003 Mus musculu
22	48	68.6	2089	9	BC001656	BC001656 Homo sapi
23	48	68.6	2104	6	AX330466	AX330466 Sequence
24	48	68.6	2104	9	HUMRCN	D42073 Human mRNa
25	48	68.6	2416	9	AK094360	AK094360 Homo sapi
26	48	68.6	2557	10	MUSRET15	D43956 Mouse gene
27	48	68.6	2857	9	AK054901	AK054901 Homo sapi
28	48	68.6	3430	6	AX403585	AX403585 Sequence
29	48	68.6	44882	2	AC020850_4	Continuation (5 of
30	48	68.6	79018	9	AL627107	AL627107 Human DNA
31	48	68.6	86986	2	AC112629	AC112629 Rattus no
32	48	68.6	89311	2	AC097427	AC097427 Rattus no
33	48	68.6	94497	9	HSDJ65P5	AL078612 Human DNA
34	48	68.6	110000	2	AC020850_2	Continuation (3 of
35	48	68.6	134078	2	AC112459	AC112459 Rattus no
36	48	68.6	137393	2	AC120265	AC120265 Rattus no
37	48	68.6	149041	9	AC044782	AC044782 Homo sapi
38	48	68.6	151955	2	AC097101	AC097101 Rattus no
39	48	68.6	153448	2	AC112088	AC112088 Rattus no
40	48	68.6	153567	2	AC111970	AC111970 Rattus no
41	48	68.6	154241	2	AC128803	AC128803 Rattus no
42	48	68.6	157392	2	AC120934	AC120934 Rattus no
43	48	68.6	157639	2	AC131464	AC131464 Rattus no
44	48	68.6	176708	2	AC027548	AC027548 Homo sapi
45	48	68.6	179789	9	AC069543	AC069543 Homo sapi

ALIGNMENTS

RESULT 1

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AR035969
LOCUS AR035969 1055 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5871970.
ACCESSION AR035969
VERSION AR035969.1 GI:5952637
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Hillman,J.L. and Goli,S.K.
TITLE Calcium-binding protein
JOURNAL Patent: US 5871970-A 2 16-FEB-1999;
FEATURES
source
location/Qualifiers
1..1055
/organism="unknown"
BASE COUNT 225 a 300 c 375 g 151 t 4 others
ORIGIN
Alignment Scores: Length: 1055
Pred. No.: 0.0011 Matches: 13
Score: 70.00 Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 6 Gaps: 0
DB:

US-09-768-840-1_COPY_254_266 (1-13) x AR035969 (1-1055)
QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
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Db 793 GATCTGAACAGGATGGGCACCTGGATGGAGTGAGGTG 831

RESULT 2
AR135029
LOCUS AR135029 1055 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 2 from patent US 6194385.
ACCESSION AR135029
VERSION AR135029.1 GI:14123934
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Hillman,J.L. and Goli,S.K.
TITLE Calcium-binding protein
JOURNAL Patent: US 6194385-A 2 27-FEB-2001;
FEATURES
source
location/Qualifiers
1..1055
/organism="unknown"
BASE COUNT 225 a 300 c 375 g 151 t 4 others
ORIGIN
Alignment Scores: Length: 1055
Pred. No.: 0.0011 Matches: 13
Score: 70.00 Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 6 Gaps: 0
DB:

US-09-768-840-1_COPY_254_266 (1-13) x AR135029 (1-1055)
QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
|||||
Db 793 GATCTGAACAGGATGGGCACCTGGATGGAGTGAGGTG 831

RESULT 3
AF183423
LOCUS AF183423 1454 bp mRNA linear PRI 02-SEP-2000
DEFINITION Homo sapiens reticulocabin precursor mRNA, complete cds.
ACCESSION AF183423
VERSION AF183423.1 GI:9963784

```

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-09-768-840-1_COPY_254_266 (1-13) x AR035969 (1-1055)

QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13

|||||

Db 793 GATCTGAACAGGATGGGCACCTGGATGGAGTGAGGTG 831

RESULT 2

AR135029

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-09-768-840-1_COPY_254_266 (1-13) x AR135029 (1-1055)

QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13

|||||

Db 793 GATCTGAACAGGATGGGCACCTGGATGGAGTGAGGTG 831

RESULT 3

AF183423

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Homo sapiens.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1454)

Peng,Y., Gu,Y., Huang,C., Xu,S., Han,Z., Fu,G. and Chen,Z.

A novel gene expressed in human hypothalamus

Unpublished

2 (bases 1 to 1454)

Peng,Y., GU,W., Huang,C., Xu,S., Han,Z., Fu,G. and Chen,Z.

Direct Submission

Submitted (03-SEP-1999) Chinese National Human Genome Center at

Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong,

Shanghai 201203, P. R. China

Location/Qualifiers

1..1454

/organism="Homo sapiens"

/db_xref="taxon:9606"

/tissue_type="hypothalamus"

33..1019

/note="HRP-iso"

/codon_start=1

/evidence=not_experimental

/product="reticulocabin precursor"

/protein_id="AAG09692.1"

/db_xref="GI:9963785"

/translation="MMWRPVSLLLLLLHGAQGRKPSDAGPHGQGRVHQAAPLSDAP

HDDAHNGFOYDHEAFLEGRVAKFQDLTPESQARLGVIVDRMDRAGSDGVVSLAEL

RAWIAHTQORHTRDSVSAWMDVYDTRDGRVGVWELRNATYGHYAPGEFHVDEAET

YKMLARDERFRVADQDQSDMATREELTAFLHPEEPHMRDIVIAETLEDIDRKNKG

YVQVEYIADLYSAEPGEPAWQTEROQFRDRLNKDGLDGEVGHVWLPPLPAQD

QPLVEANHLHESDTRDKGRLSKAELTGNMNVGVSQATNYGEDLTRHDEL"

BASE COUNT 314 a 454 c 467 g 219 t

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-09-768-840-1_COPY_254_266 (1-13) x AF183423 (1-1454)

QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13

|||||

Db 792 GATCTGAACAGGATGGGCACCTGGATGGAGTGAGGTG 830

RESULT 4

AR083085

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.:

Score:

1463 bp DNA linear PAT 01-SEP-2000

Sequence 2 from patent US 5976801.

AR083085

AR083085

AR083085.1 GI:10009875

Unknown.

Unknown.

Unclassified.

1 (bases 1 to 1463)

Bandman,O., Hillman,J.L., Lal,P., Corley,N.C. and Shah,P.

Human reticulocabin isoforms

Patent: US 5976801-A 2 02-NOV-1999;

Location/Qualifiers

1..1463

/organism="unknown"

BASE COUNT 310 a 459 c 478 g 215 t 1 others

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Length: 1463
Matches: 13

Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 6
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AR083085 (1-1463)

QY 1 AspleuAsnLysAspGlyHisLeuAspGlySerGluVal 13
|||||
Db 808 GATCTGAACAGGATGGGACCTGGATGGAGTGAGGTG 846

RESULT 5
AR152960

LOCUS AR152960 1463 bp DNA linear PAT 08-AUG-2001

DEFINITION Sequence 2 from patent US 6235477.

ACCESSION AR152960

VERSION AR152960.1 GI:15120492

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1463)

AUTHORS Bandman,O., Hillman,J.L., Lal,P., Corley,N.C. and Shah,P.

TITLE Human reticulocalbin isoforms

JOURNAL Patent: US 6235477-A 2 22-MAY-2001;

FEATURES Location/Qualifiers

source 1..1463

BASE COUNT 310 a 459 c 478 g 215 t 1 others

ORIGIN /organism="unknown"

Alignment Scores:

Pred. No.: 0.00156 Length: 1463

Score: 70.00 Matches: 13

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AR152960 (1-1463)

QY 1 AspleuAsnLysAspGlyHisLeuAspGlySerGluVal 13

|||||

Db 808 GATCTGAACAGGATGGGACCTGGATGGAGTGAGGTG 846

RESULT 6

BC013436

LOCUS BC013436 1470 bp mRNA linear PRI 07-SEP-2001

DEFINITION Homo sapiens, hypothetical protein LOC57333, clone MGC:16899

IMAGE:3889718, mRNA, complete cds.

ACCESSION BC013436

VERSION BC013436.1 GI:15488584

KEYWORDS MGC.

SOURCE Homo sapiens.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1470)

Straussberg,R.

Submitted (04-SEP-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgaps-r@mail.nih.gov

Tissue Procurement: DCTD/PTP/Gazdar

cDNA Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-shgc.stanford.edu>

Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 14 Row: d Column: 12
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9963784.

FEATURES

Location/Qualifiers

source 1..1470

/organism="Homo sapiens"

/db_xref="LocusID:57333"

/db_xref="taxon:9606"

/clone="MGC:16899 IMAGE:3889718"

/tissue_type="Lung, carcinoma, large cell

undifferentiated"

/clone_lib="NIH_MGC_69"

/lab_host="DH10B"

/note="Vector: pCMV-SPORT6"

31..1017

/codon_start=1

/product="hypothetical protein LOC57333"

/protein_id="AAH13436.1"

/db_xref="GI:15488584"

/translation="MMWRPSVLLLLLLRHGAQKPSDPAGPHGQGRVHQAAPLSADP

HDDAHGNGFYDHEAFGLGVEAKFDQLTPEESQARLGRIVDRMDRAGDGGWVSLAEL

RAWIAHQQRHIRDSVSAAMDYTDTRGVRGWEELRNATYGHVAPGEERHVDVDAET

YKMLARDERRRIVADODGSMATREELTAFLHPEEPHMRDVIATLELDLRNKG

YVOVEYIADLYSAEPGEEEPANVQTERQFRDRDLNKGDLGSEVGHVWLPAPAD

QPLVEANHLHSDTDKDKRAEILGNMNMVGSQATNYGDLTRHDEL"

BASE COUNT 332 a 454 c 470 g 214 t

ORIGIN

Alignment Scores:

Pred. No.: 0.00157 Length: 1470

Score: 70.00 Matches: 13

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x BC013436 (1-1470)

QY 1 AspleuAsnLysAspGlyHisLeuAspGlySerGluVal 13

|||||

Db 790 GATCTGAACAGGATGGGACCTGGATGGAGTGAGGTG 828

RESULT 7

AX464230

LOCUS AX464230 1503 bp DNA linear PAT 16-JUL-2002

DEFINITION Sequence 363 from Patent WO0140466.

ACCESSION AX464230

VERSION AX464230.1 GI:21899131

KEYWORDS human.

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1

Baker,K.P., Beresini,M., DeForge,L., Desnoyers,L., Filvaroff,E.,

Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L.,

Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K.,

Wood,W.L. and Zhang,Z.

Secreted and transmembrane polypeptides and nucleic acids encoding

same

Patent: WO 0140466-A 363 07-JUN-2001;

Genentech Inc. (US)

Location/Qualifiers

source 1..1503

/organism="Homo sapiens"

/db_xref="taxon:9606"

BASE COUNT 357 a 456 c 474 g 216 t

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ORIGIN
Alignment Scores:
Pred. No.: 0.0016 Length: 1503
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AX464230 (1-1503)
QY 1 AspleuAsnLysAspGlyHisLeuAspGlySerGluVal 13
Db 794 GATCTGACAAAGGATGGGCACCTGGATGGAGTGAGGTG 832

RESULT 8
AX354366
LOCUS AX354366 1507 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 12 from Patent WO0196523.
ACCESSION AX354366
VERSION AX354366.1 GI:18619208
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 Kennedy,G.C., Kang,S., Reinhard,C. and Jefferson,A.B.
AUTHORS Polynucleotides related to colon cancer
TITLE Patent: WO 0196523-A 12 20-DEC-2001;
JOURNAL CHIRON CORPORATION (US)
FEATURES
source
Location/Qualifiers
1..1507
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 350 a 456 c 479 g 213 t 9 others
ORIGIN
Alignment Scores:
Pred. No.: 0.0016 Length: 1507
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AX354366 (1-1507)
QY 1 AspleuAsnLysAspGlyHisLeuAspGlySerGluVal 13
Db 813 GATCTGACAAAGGATGGGCACCTGGATGGAGTGAGGTG 851

RESULT 9
AX354369
LOCUS AX354369 1507 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 15 from Patent WO0196523.
ACCESSION AX354369
VERSION AX354369.1 GI:18619211
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 Kennedy,G.C., Kang,S., Reinhard,C. and Jefferson,A.B.
AUTHORS Polynucleotides related to colon cancer
TITLE Patent: WO 0196523-A 15 20-DEC-2001;
JOURNAL CHIRON CORPORATION (US)
FEATURES
source
Location/Qualifiers
1..1507
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 350 a 456 c 479 g 213 t 9 others
ORIGIN
Alignment Scores:
Pred. No.: 0.0016 Length: 1507
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AX354366 (1-1507)
QY 1 AspleuAsnLysAspGlyHisLeuAspGlySerGluVal 13
Db 813 GATCTGACAAAGGATGGGCACCTGGATGGAGTGAGGTG 851

RESULT 10
AX354369
LOCUS AX354369 179394 bp DNA linear PRI 29-MAY-2002
DEFINITION Homo sapiens chromosome 19 clone CTD-3148I10, complete sequence.
ACCESSION AC010619
VERSION AC010619.7 GI:21240682
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 179394)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 179394)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (16-SEP-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 179394)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (29-MAY-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT On May 29, 2002 this sequence version replaced gi:15920094.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.7% of Sequence;
Estimated Total Number of Errors is 0.4.
FEATURES
source
Location/Qualifiers
1..179394
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
/clone="CTD-3148I10"
BASE COUNT 40992 a 48084 c 48579 g 41739 t
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Alignment Scores:
Pred. No.: 0.267 Length: 179394
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AC010619 (1-179394)
QY 1 AspleuAsnLysAspGlyHisLeuAspGlySerGluVal 13
Db 129804 GATCTGACAAAGGATGGGCACCTGGATGGAGTGAGGTG 129842

RESULT 11
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BC005487 1414 bp mRNA linear ROD 07-AUG-2002
LOCUS Mus musculus, similar to hypothetical protein LOC57333, clone
IMAGE:3486146, mRNA, partial cds.
BC005487
BC005487.1 GI:13529538
house mouse.
SOURCE
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1414)
Direct Submission
Submitted (27-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapsb-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www.shgc.stanford.edu>
Contact: (Dickson, Mark) mcdgapaxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 7 Row: h Column: 5
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis.

FEATURES
source
1. .1414
/organism="Mus musculus"
/db_xref="taxon:10090"
/map="C57BL/6J"
/clone="IMAGE:3486146"
/tissue_type="Mammary tumor. WAP-TGF alpha model. 7 months
old, gross tissue."
/clone_lib="NCI_CGAP_Mam5"
/lab_host="DH10B"
/notes="Vector: pCMV-SPORT6"
<1. .948
/codon_start=1
/product="Similar to hypothetical protein LOC57333"
/protein_id="AAH05487.1"
/db_xref="GI:13529539"
/translation="LRHWALGKPSDAGPHGQDRVHGTPLSEAPHDDAHGNFQYDHE
AFLGRDVAKEFKLSPESQARLGRIVDRMDLAGSDGWSLAELRAWIHTQORHRR
DSVSAAHYTDTRDGRGVGWEELRNATYGHYEPGEFHEDEATYKKMLARDERRR
VAQDGSMATREELTAFLHPEEPHMRDIAETLEDLNKDKGYQVVEYIADLYS
EPEGEPPAWQTERQOFREFRDLNKDQDGSVGYWVLPSPQDQPLVEANLLHES
DTRDKGRSLKAEILSNMFMVGSQATNYGDLTRRHDEL"
BASE COUNT 422 a 384 c 392 g 216 t
ORIGIN

Alignment Scores:
Pred. No.: 0.045 Length: 1414
Score: 62.00 Matches: 12
Percent Similarity: 92.31% Conservative: 0
Best Local Similarity: 92.31% Mismatches: 1
Query Match: 88.57% Indels: 0
DB: 10 Gaps: 0

US-09-768-840-1_copy_254_266 (1-13) x BC005487 (1-1414)

Qy 1 AspLeuAnLysAspGlyHisLeuAspGlySerGluVal 13

Db 721 GATCTGAACAAGCAGCGCAACTGGATGGACAGTGAAGTC 759

RESULT 12
BC025602
LOCUS Mus musculus, similar to hypothetical protein LOC57333, clone
IMAGE:5250505, mRNA, complete cds.
BC025602
BC025602.1 GI:19343897
house mouse.
SOURCE
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1421)
Direct Submission
Submitted (06-MAR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapsb-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nih.gov
Akter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Hachighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastriopop, S., Thomas, P.J., Touchman, J.W.,
McDowell, J., Pearson, R., Stantripop, S., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Tsurgon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 56 Row: b Column: 12
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, GenomeScan gene prediction, Similarity but not identity
to protein.

FEATURES
source
1. .1421
/organism="Mus musculus"
/db_xref="taxon:10090"
/map="C57BL/6J"
/clone="MGC:36253 IMAGE:5250505"
/tissue_type="Mammary tumor. WAP-TGF alpha model. 7 months
old, gross tissue."
/clone_lib="NCI_CGAP_Mam5"
/lab_host="DH10B"
/notes="Vector: pCMV-SPORT6"
76. .1062
/codon_start=1
/product="Similar to hypothetical protein LOC57333"
/protein_id="AAH25602.1"
/db_xref="GI:19343898"
/translation="MMWRWSFLLLLLRHWALGKPSDAGPHGQDRVHGTPLSEAP
HDDAHGNFQYDHEAFLGRDVAKEFKLSPESQARLGRIVDRMDLAGSDGWSLAEL
RAWIAHTQORHRRDSVSAAHYTDTRDGRGVGWEELRNATYGHYEPGEFHEDEAT
YKKMLARDERRRVAQDGSMATREELTAFLHPEEPHMRDIAETLEDLNKDKGYQVVEYIADLYS
EPEGEPPAWQTERQOFREFRDLNKDQDGSVGYWVLPSPQDQPLVEANLLHESDTRDKGRSLKAEILSNMFMVGSQATNYGDLTRRHDEL"
BASE COUNT 335 a 414 c 427 g 245 t
ORIGIN

Alignment Scores:	0.0452	Length:	1421
Score:	62.00	Matches:	12
Percent Similarity:	92.31%	Conservative:	0
Best Local Similarity:	92.31%	Mismatches:	1
Query Match:	88.57%	Indels:	0
DB:	10	Gaps:	0
US-09-768-840-1_COPY_254_266 (1-13) x BC0255602 (1-1421)			
QY	1	AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal	13
DB	835	GATCTGAACAAGGACGGCACTGGATGGATGCAAGTC	873
RESULT 13			
AC073763_0			
WPCOMMENT			
Sequence split into 4 fragments LOCUS AC073763 Accession AC073763			
Fragment Name	Begin	End	
AC073763_0	1	110000	
AC073763_1	100001	210000	
AC073763_2	200001	310000	
AC073763_3	300001	409770	
LOCUS AC073763	409770 bp	DNA	linear HTG 29-JUN-2000
DEFINITION	Mus musculus clone RP23-343P5, WORKING DRAFT SEQUENCE, 63 unordered pieces.		
ACCESSION	AC073763		
VERSION	AC073763.1	GI:8810380	
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.		
SOURCE	Mus musculus		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
TITLE	DOE Joint Genome Institute.		
JOURNAL	1 (bases 1 to 409770)		
REFERENCE	2 (bases 1 to 409770)		
AUTHORS	DOE Joint Genome Institute.		
TITLE	Direct Submission		
JOURNAL	Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint		
COMMENT	Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA		
Center:	Joint Genome Institute		
Center Code:	JGI		
Web site:	http://www.jgi.doe.gov		
Project Information			
Center Project Name:	1868949		
Center clone name:	RPCI-23_343P5		
Summary Statistics			
Consensus quality:	353352 bases at least Q40		
Consensus quality:	382147 bases at least Q30		
Consensus quality:	388243 bases at least Q20		
Estimated insert size:	217190; agarose-fp estimation		
Estimated insert size:	403570; sum-of-contigs estimation		
Quality coverage:	8.5 in Q20 bases; agarose-fp estimation		
Quality coverage:	4.57 in Q20 bases; sum-of-contigs estimation.		
* NOTE:	This is a 'working draft' sequence. It currently		
* consists of 63 contigs.	The true order of the pieces		
* is not known and their order in this sequence record is			
* arbitrary. Gaps between the contigs are represented as			
* runs of N, but the exact sizes of the gaps are unknown.			
* This record will be updated with the finished sequence			
* as soon as it is available and the accession number will			
* be preserved.			
* 1	1003: contig of 1003 bp in length		
* 1004	1103: gap of unknown length		
* 1104	2382: contig of 1279 bp in length		
* 2383	2482: gap of unknown length		
* 2483	3614: contig of 1132 bp in length		

```

* 88224 93473: contig of 5250 bp in length
* 93474 93573: gap of unknown length
* 93574 98533: contig of 5080 bp in length
* 98534 98753: gap of unknown length
* 98754 103469: contig of 4716 bp in length
* 103470 103569: gap of unknown length
* 103570 109147: contig of 5578 bp in length
* 109148 109247: gap of unknown length
* 109248 116537: contig of 7290 bp in length
* 116538 116537: gap of unknown length
* 116538 124186: contig of 7549 bp in length
* 124187 124287: gap of unknown length
* 124288 132204: contig of 7918 bp in length
* 132205 132304: gap of unknown length
* 132305 140886: contig of 8582 bp in length
* 140887 140986: gap of unknown length
* 140987 151061: contig of 10075 bp in length
* 151062 151161: gap of unknown length
* 151162 159241: contig of 8080 bp in length
* 159242 159341: gap of unknown length
* 159342 167120: contig of 7779 bp in length
* 167121 167220: gap of unknown length
* 167221 178631: contig of 11411 bp in length
* 178632 178731: gap of unknown length
* 178732 180111: contig of 11380 bp in length
* 180112 190211: gap of unknown length
* 190212 201488: contig of 11277 bp in length
* 201489 201588: gap of unknown length
* 201589 212958: contig of 11370 bp in length
* 212959 227047: contig of 13989 bp in length
* 227048 227147: gap of unknown length
* 227148 241205: contig of 14058 bp in length
* 241206 258822: contig of 17517 bp in length
* 258823 277262: gap of unknown length
* 277263 277362: contig of 18340 bp in length
* 277363 299258: contig of 21896 bp in length
* 299259 321207: contig of 21849 bp in length
* 321208 342521: contig of 21214 bp in length
* 342522 342621: gap of unknown length
* 342622 374406: contig of 31785 bp in length
* 374407 374506: gap of unknown length
* 374507 409770: contig of 35264 bp in length.

```

FEATURES

source

```

1..409770
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-343P5"
/clone_lib="RPCI mouse BAC library 23"

```

```

BASE COUNT 98446 a 106220 c 104553 g 94328 t 6223 others
ORIGIN

```

Alignment Scores:

```

Pred. No.: 4 73 Length: 110000
Score: 62.00 Matches: 12
Percent Similarity: 92.31% Conservative: 0
Best Local Similarity: 92.31% Mismatches: 1
Query Match: 88.57% Indels: 0
DB: 2 Gaps: 0

```

```

US-09-768-840-1_COPY_254_266 (1-13) x AC073763_0 (1-110000)

```

```

OY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13

```

```

DB 65874 GATCTGAACAGGACGGCGGCGACTGGATGGCAGTCAAGTC 65912
|||||

```

RESULT 14

AC073740

LOCUS

186243 bp

DNA

linear

HTG 18-JUL-2000

BASE COUNT

43755 a 47751 c 48436 g 45300 t 1001 others

DEFINITION

```

Mus musculus clone RP23-274I22, WORKING DRAFT SEQUENCE, 11 ordered
pieces.

```

ACCESSION

AC073740

VERSION

AC073740.2 GI:9256778

KEYWORDS

HTG; HTGS_PHASE2; HTGS_DRAFT.

SOURCE

Mus musculus.

. ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus; Mus.

1 (bases 1 to 186243)

DOE Joint Genome Institute.

Sequencing of Mouse

Unpublished

2 (bases 1 to 186243)

DOE Joint Genome Institute.

Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint

Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

On Jul 18, 2000 this sequence version replaced gi:8810357.

-----Genome Center

Center: Joint Genome Institute

Center Code: JGI

Web site: http://www.jgi.doe.gov

Project Information

Center Project Name: 1842302

Center clone name: RPCI-23-274I22

Summary Statistics

Consensus quality: 175948 bases at least Q40

Consensus quality: 182693 bases at least Q30

Consensus quality: 184188 bases at least Q20

Estimated insert size: 202290; agarose-fp estimation

Estimated insert size: 185793; sum-of-contigs estimation

Quality coverage: 6.58 in Q20 bases; agarose-fp estimation

Quality coverage: 7.17 in Q20 bases; sum-of-contigs estimation

NOTE: This is a 'working draft' sequence. It currently

consists of 11 contigs. Gaps between the contigs

are represented as runs of N. The order of the pieces

is believed to be correct as given, however the sizes

of the gaps between them are based on estimates that have

been provided by the submitter

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

1 439 438: contig of 438 bp in length

539 12616: contig of 12078 bp in length

12617 12716: gap of unknown length

12717 24949: contig of 12233 bp in length

24950 25049: gap of unknown length

25050 42617: contig of 17568 bp in length

42618 42717: gap of unknown length

42718 92550: contig of 49833 bp in length

92551 92650: gap of unknown length

92651 94922: contig of 2272 bp in length

94923 95022: gap of unknown length

95023 97020: contig of 1998 bp in length

97021 97120: gap of unknown length

97121 157072: contig of 59952 bp in length

157073 157172: gap of unknown length

157173 174862: contig of 17690 bp in length

174863 174962: gap of unknown length

174963 178440: contig of 3478 bp in length

178441 186540: gap of unknown length

186541 186243: contig of 7703 bp in length.

Location/Qualifiers

1..186243

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="RP23-274I22"

/clone_lib="RPCI mouse BAC library 23"

Tue May 20 14:43:29 2003

us-09-768-840-1_copy_254_266.p2n.rge

ORIGIN

Alignment Scores: 8.3 Length: 186243
Pred. No.: 62.00 Matches: 12
Score: 92.31% Conservative: 0
Percent Similarity: 92.31% Mismatches: 1
Best Local Similarity: 92.31% Indels: 0
Query Match: 88.57% Gaps: 0
DB: 2

US-09-768-840-1_COPY_254_266 (1-13) x AC073740 (1-186243)

Qy 1 AspleuAsnlyAspGlyHisLeuAspGlySerGluVal 13
|||||
Db 123065 GATCTGACACAGGACGGCGGACCTGGATGGCAGTGAAGTC 123103

RESULT 15

AC126256 191713 bp DNA linear HTG 05-JUL-2002
LOCUS
DEFINITION Mus musculus chromosome UNK clone RP24-235B15, WORKING DRAFT

ACCESSION AC126256.2 GI:21699708
VERSION HTG; HTGS_P1ASE1; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS house mouse.
SOURCE Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS McPherson,J.D. and Waterston,R.H.

TITLE The sequence of Mus musculus clone

JOURNAL Unpublished

2 (bases 1 to 191713)

McPherson,J.D. and Waterston,R.H.

Direct Submission

Submitted (04-JUL-2002) Genome Sequencing Center, 4444 Forest Park

Parkway, St. Louis, MO 63108, USA

3 (bases 1 to 191713)

McPherson,J.D. and Waterston,R.H.

Direct Submission

Submitted (05-JUL-2002) Genome Sequencing Center, 4444 Forest Park

Parkway, St. Louis, MO 63108, USA

On Jul 5, 2002 this sequence version replaced gi:21693961.

COMMENT

----- Genome Center -----

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc/index.shtml>

Contact: submissions@watson.wustl.edu

----- Project Information -----

Center project name: M_BB0235B15

----- Summary Statistics -----

Sequencing vector: M13; 0%

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 189879 bases at least Q40

Consensus quality: 190172 bases at least Q30

Consensus quality: 190337 bases at least Q20

* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 2693: contig of 2693 bp in length

* 2694 2793: gap of unknown length

* 2794 27767: contig of 24974 bp in length

* 27768 27867: gap of unknown length
* 27868 61313: contig of 33446 bp in length
* 61314 61413: gap of unknown length
* 61414 131828: contig of 70415 bp in length
* 131829 131928: gap of unknown length
* 131929 191713: contig of 59785 bp in length.

FEATURES

source

1..191713

/organism="Mus musculus"

/db_xref="taxon:10090"

/chromosome="UNK"

/clone="RP24-235B15"

1..2693

/note="assembly_name:Contig32"

misc_feature

2794..27767

/note="assembly_name:Contig33"

misc_feature

27868..61313

/note="assembly_name:Contig34"

misc_feature

61414..131828

/note="assembly_name:Contig35"

misc_feature

131929..191713

/note="assembly_name:Contig36"

BASE COUNT 46194 a 49474 c 49482 g 46163 t 400 others

ORIGIN

Alignment Scores:

Pred. No.: 8.56 Length: 191713

Score: 62.00 Matches: 12

Percent Similarity: 92.31% Conservative: 0

Best Local Similarity: 92.31% Mismatches: 1

Query Match: 88.57% Indels: 0

DB: 2 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AC126256 (1-191713)

Qy 1 AspleuAsnlyAspGlyHisLeuAspGlySerGluVal 13

|||||

Db 161430 GATCTGACACAGGACGGCGGACCTGGATGGCAGTGAAGTC 161468

Search completed: May 20, 2003, 07:03:46

Job time : 1995 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: May 19, 2003, 12:24:06 ; Search time 233 seconds
(without alignments)
125.648 Million cell updates/sec

Title: US-09-768-840-1_COPY_254_266

Perfect score: 70

Sequence: 1 DLNKGCHLDGSEV I3

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
-Q/cgn2_1/USPTO.spool/US09768840/runat_14052003_095710_16637/app_query.fasta_1.199
-DB=N.Geneseq_101002 -Qfmt=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09768840 -CGN_1_1_263 @runat_14052003_095710_16637 -NCFU=6 -ICPU=3
-NO_XLPHY -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N.Geneseq_101002.*
1: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	70	100.0	1055	19	AAV57600	Human calcium-bind
2	70	100.0	1055	22	AAH48279	Human calcium bind
3	70	100.0	1463	20	AAH47229	Human reticulocalb
4	70	100.0	1480	22	AAI63890	Human polynucleoti
5	70	100.0	1480	22	AAS31631	CDNA encoding nove
6	70	100.0	1480	23	ABK43732	DNA encoding novel
7	70	100.0	1487	22	AAH34992	Human colon cancer
8	70	100.0	1503	20	AAH52253	Protein PRO272 cDN
9	70	100.0	1503	21	AAC58589	Human PRO272 prote
10	70	100.0	1503	22	AAS21425	Human CDNA sequenc
11	70	100.0	1503	22	AAF72411	Human PRO272 CDNA
12	70	100.0	1503	22	AAC97455	Human anglogenesis
13	70	100.0	1507	20	AAK00656	Human secreted pro
14	70	100.0	1507	24	AAH41601	Human colon cancer
15	70	100.0	1507	24	AAH41603	Human colon cancer
16	70	100.0	1542	21	AAZ36246	CDNA encoding a bo
17	48	68.6	236	22	ABA64623	Human breast cell
18	48	68.6	236	22	ABA64600	Human foetal liver
19	48	68.6	236	22	ABA31726	Probe #10192 for g
20	48	68.6	236	22	AAK13040	Human brain expres
21	48	68.6	236	22	AAK38771	Human bone marrow
22	48	68.6	236	22	AAI19577	Probe #9510 for ge
23	48	68.6	236	22	AAI44770	Probe #13456 used
24	48	68.6	236	22	AAI05297	Probe #5288 used t
25	48	68.6	236	24	ABS12846	Human genome-deriv
26	48	68.6	236	22	ABA51941	Human foetal liver
27	48	68.6	476	22	ABA21756	Probe #222 for gen
28	48	68.6	476	22	AAK00229	Human brain expres
29	48	68.6	476	22	AAK25672	Human bone marrow
30	48	68.6	476	22	AAI10299	Probe #232 for gen
31	48	68.6	476	22	AAI13549	Probe #235 used to
32	48	68.6	476	22	AAI00235	Probe #226 used to
33	48	68.6	476	24	ABS00245	Human genome-deriv
34	48	68.6	686	24	ABK44106	CDNA #46 encoding
35	48	68.6	1386	22	AAI66981	Human membrane tra
36	48	68.6	1616	23	AAS86824	DNA encoding novel
37	48	68.6	1637	24	AAI72316	Human transporter
38	48	68.6	1929	22	AAI66980	Human membrane tra
39	48	68.6	2055	24	ABQ35036	Human ovarian anti
40	48	68.6	2104	24	ABK64404	Human benign prost
41	48	68.6	2104	24	ABL62638	Colon adenocarcino
42	48	68.6	2358	22	AAH72801	Human cervical can
43	48	68.6	2625	22	AAS44597	Human full-length
44	48	68.6	2644	22	AAS44769	Human contig polyn
45	48	68.6	3430	24	AAD36323	Human transporter

ALIGNMENTS

RESULT 1
AAV57600
ID AAV57600 standard; cDNA; 1055 BP.
XX AAV57600;
XX AC
XX AAV57600;
XX 15-DEC-1998 (first entry)
XX Human calcium-binding protein encoding cDNA.
XX Human; calcium-binding protein; reticulocalbin; sickle cell anaemia;
KW HCBP; beta thalassaemia; cell proliferation; cancer; adenocarcinoma;
KW leukemia; lymphoma; melanoma; sarcoma; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX 34..1020
XX CDS

FT /*tag= a
FT /product= "calcium-binding protein"
XX
PN WO9844114-A1.
XX
XX 08-OCT-1998.
XX
XX 30-MAR-1998; 98WO-US06233.
XX
XX 31-MAR-1997; 97US-0828242.
XX
XX (INCY-) INCYTE PHARM INC.
XX
XX Goli SK, Hillman JL;
XX
XX WPI; 1998-542704/46.
XX
XX P-PSDB; AAW80746.
XX
XX A new human calcium binding protein - useful for treating or
XX preventing disorders associated with the expression of HCBP
XX
XX Claim 5; Page 43; 60pp; English.

XX The present sequence encodes a new human calcium binding protein (HCBP).
XX A pharmaceutical composition which includes the HCBP protein is claimed
XX and can be added directly to cells in vivo to promote regeneration or
XX differentiation of cells. HCBP can also be added to cells, cell lines,
XX tissue or organ culture to stimulate cell proliferation for heterologous
XX and autologous transplantation. The cells can be selected for their
XX ability to inhibit development of an infection or to correct a genetic
XX defect such as sickle cell anaemia, beta thalassaemia. An antagonist of
XX HCBP can be administered to a subject to treat or prevent a disorder
XX associated with cell proliferation e.g. many cancers including
XX adenocarcinoma, leukemia, lymphoma, melanoma, sarcoma and particularly
XX cancers of bladder, bone, brain, heart, kidney, liver. Antibodies
XX specific for HCBP may be used directly as an antagonist or indirectly as
XX a targeting or delivery mechanism for delivering pharmaceutical agents
XX to cell or tissue which express protein HCBP. A method is claimed for
XX treating or preventing a disorder associated with cell proliferation
XX which involves adding pharmaceutical composition of antagonist of HCBP.
XX
XX Sequence 1055 BP; 225 A; 300 C; 375 G; 151 T; 4 other;

Alignment Scores:
Pred. No.: 0.00127 Length: 1055
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 19 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AAV57600 (1-1055)

Qy 1 AspleuasnLysAspGlyHisLeuAspGlySerGluVal 13
Db 793 GATCTGAACAAGAGTGGGCACCTGGAGTGGAGTG 831

RESULT 2

ID AAH48279
XX AAH48279 standard; DNA; 1055 BP.

XX AC AAH48279;

XX 21-SEP-2001 (first entry)

XX Human calcium binding protein coding sequence.

XX Human; calcium binding protein; HCBP; cell proliferation disorder;
XX cancer; ds.

XX OS Homo sapiens.

XX Key Location/Qualifiers

CDS 34..1020
FT /*tag= a
FT /product= "HCBP"

XX US2001012831-A1.

XX 09-AUG-2001.

XX 23-JAN-2001; 2001US-0768840.

XX 21-MAR-1997; 97US-0828212.

XX 07-DEC-1998; 98US-0206499.

XX (INCY-) INCYTE PHARM INC.

XX Hillman JL, Goli SK;

XX WPI; 2001-464391/50.

XX P-PSDB; AAG64865.

XX Human calcium-binding protein, useful in the diagnosis, prevention, and
XX treatment of disorders associated with cell proliferation, e.g.
XX adenocarcinoma, leukemia, lymphoma, melanoma, sarcoma, or
XX teratocarcinoma.

XX Claim 16; Fig 1; 30pp; English.

XX The present invention provides the protein and coding sequences of human
XX calcium binding protein (HCBP). The sequences can be used in the
XX diagnosis, prevention and treatment of cell proliferation disorders, such
XX as cancer. The present sequence is the coding sequence of the invention.

XX Sequence 1055 BP; 225 A; 300 C; 375 G; 151 T; 4 other;

Alignment Scores:
Pred. No.: 0.00127 Length: 1055
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AAH48279 (1-1055)

Qy 1 AspleuasnLysAspGlyHisLeuAspGlySerGluVal 13
Db 793 GATCTGAACAAGAGTGGGCACCTGGAGTGGAGTG 831

RESULT 3

AAX27229

ID AAX27229 standard; DNA; 1463 BP.

XX AC AAX27229;

XX 28-MAY-1999 (first entry)

XX Human reticulocalbin gamma coding sequence.

XX Human; reticulocalbin gamma; RCNgamma; reticulocalbin delta; RCNdelta;
XX developmental disorder; neoplastic disorder; immunological disorder;
XX infection; ss.

XX OS Homo sapiens.

XX WO9907849-A2.

XX 18-FEB-1999.

XX 05-AUG-1998; 98WO-US16259.

XX 08-AUG-1997; 97US-0910927.

XX (INCY-) INCYTE PHARM INC.

XX Bandman O, Corley NC, Hillman JL, Lal P, Shah P;
 PI WPI; 1999-180492/15.
 XX DR P-PSDB; AAY00916.
 XX
 PT New human reticulocalbin isoforms - useful to diagnose, prevent,
 PT and treat infectious, developmental, neoplastic, and immunological
 PT disorders
 XX
 PS Claim 7; Fig 1; 82pp; English.
 XX
 CC This sequence encodes the human reticulocalbin gamma (RCNgamma) of the
 CC invention. RCNgamma and RCNdelt are used to treat an infectious or
 CC developmental disorder, and antagonists of them are used to treat a
 CC neoplastic or immunological disorder. Infectious disorders include e.g.
 CC pneumonia, lymphocytic choriomeningitis, Hantavirus, chronic bronchitis,
 CC hepatitis, herpesviruses, yellow fever, influenza, cancer, measles,
 CC mumps, HIV, rabies, poliovirus, coxsackie-virus, smallpox, Colorado tick
 CC fever, HIV, rabies, gastroenteritis, and rubella, encephalitis, and
 CC bacterial, fungal, parasitic, protozoal, or helminthic infections.
 CC Development disorders include e.g. renal tubular acidosis, anaemia,
 CC Cushing's syndrome, achondroplastic dwarfism, epilepsy, gonadal
 CC dysgenesis, hereditary neuropathies such as Charcot-Marie-Tooth disease,
 CC and neurofibromatosis, hypothyroidism, hydrocephalus, seizure disorders
 CC such as Sydenham's chorea and cerebral palsy, spinal bifida, and
 CC congenital glaucoma, cataract, or sensorineural hearing loss. Neoplastic
 CC disorders include e.g. adenocarcinoma, leukaemia, lymphoma, melanoma,
 CC myeloma, sarcoma and teratocarcinoma. Overexpression of reticulocalbin
 CC mRNA has been associated with increased metastatic invasive properties of
 CC three human breast cancer lines.
 XX
 SQ Sequence 1463 BP; 310 A; 459 C; 478 G; 215 T; 1 other;

Alignment Scores:
 Pred. No.: 0.00186 Length: 1463
 Score: 70.00 Matches: 13
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 20 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AAX27229 (1-1463)

Oy 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
 |||||
 Db 808 GATCTGACACAGGATGGGCACCTGGATGGAGTGAGGTG 846

RESULT 4
 AAI63890
 ID AAI63890 standard; cDNA: 1480 BP.
 AC AAI63890;
 XX
 XX 22-OCT-2001 (first entry)
 XX
 XX Human polynucleotide SEQ ID NO 98.
 XX
 KW Human: antiarthritic; antirheumatic; antiproliferative; vasotropic;
 KW cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;
 KW fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
 KW neuroprotective; antiallergic; hepatotropic; antidiabetic;
 KW antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial;
 KW antiparasitic; cardiant; gene therapy; cancer; immune disorder;
 KW cardiovascular disorder; neurological disease; infection; human; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200155308-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US01309.

XX 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
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 PR 11-JUL-2000; 2000US-0217487.
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 PR 06-SEP-2000; 2000US-0230437.
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 PR 08-SEP-2000; 2000US-0232080.
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 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
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 PR 14-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
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 PR 25-SEP-2000; 2000US-0234997.
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PR 02-OCT-2000; 2000US-0236802.
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PR 02-OCT-2000; 2000US-0237040.
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PR 20-OCT-2000; 2000US-0240960.
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PR 20-OCT-2000; 2000US-0241809.
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PR 01-NOV-2000; 2000US-0244617.
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PR 17-NOV-2000; 2000US-0249218.
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PR 17-NOV-2000; 2000US-0249264.
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PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
PR (HUMA-) HUMAN GENOME SCI INC.
XX PI Rosen CA, Barash SC, Ruben SM;
XX DR WPI; 2001-488781/53.
XX DR P-PSDB; AAM43584.
XX PR New isolated nucleic acids and polypeptides, useful for diagnosing,

PT treating and/or preventing human diseases and disorders -
XX Claim 1; SEQ ID NO 98; 664pp + Sequence Listing; English.
XX
XX The invention relates to human polynucleotides (AAI63803-AAI64012) and
CC the encoded proteins (AAM434497-AAM43660) useful for preventing, treating
CC or ameliorating medical conditions e.g. by protein or gene therapy. The
CC genes were isolated from a range of human tissues disclosed in the
CC specification. The nucleic acids, proteins, antibodies and (ant)agonists
CC are useful in the diagnosis, treatment and prevention of: (a) cancer,
CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,
CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,
CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
CC colitis; (d) neurological disorders e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 1480 BP; 329 A; 458 C; 479 G; 214 T; 0 other;

Alignment Scores:
Pred. No.: 0.00188 Length: 1480
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AAI63890 (1-1480)

QY 1 AspleuasnllyaspGlyHisLeuAspGlySerGluVal 13
|||
DB 806 GATCTGAACAAGATGGGCACCTGGACGGAGTGAGGTG 844

RESULT 5
AAS31631
ID AAS31631 standard; cDNA; 1480 BP.
XX AC AAS31631;
XX DT 04-DEC-2001 (first entry)
XX DE cDNA encoding novel human calcium-binding protein #55.
XX Human; calcium-binding protein; calcium flux; neurological disease;
KW Immune dysfunction; digestive disorder; neoplastic disease;
KW blood disorder; infectious disease; gene therapy; immunosuppressive;
KW antiarthritic; cytostatic; vasotropic; antibacterial; nootropic;
KW virucide; ss.
XX OS Homo sapiens.
XX PN WO200155304-A2.
XX PD 02-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US01302.
XX PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
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PR 11-JUL-2000; 2000US-0217487.
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PR 26-JUL-2000; 2000US-0220964.
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PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
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PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
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PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
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PR 05-SEP-2000; 2000US-0229509.
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PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
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PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
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PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 13-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 20-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
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PR 20-OCT-2000; 2000US-0241786.
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PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0244674.
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PR 08-NOV-2000; 2000US-0246524.
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PR 08-NOV-2000; 2000US-0246532.
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PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0256719.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 05-JAN-2001; 2001US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
XX WPI; 2001-465568/50.
DR P-PSDB; AAU19946.
XX
XX Isolated nucleic acid molecule encoding a calcium-binding protein is used in preventing, treating or ameliorating a medical condition -
PT
XX Claim 4; SEQ ID No 65; 542pp; English.
PS
XX The present invention relates to the isolation of novel human
CC calcium-binding proteins (AAU19892-AAU19969), and cDNA and genomic
CC sequences encoding for these proteins. The sequences of the invention
CC are useful in the diagnosis, prevention and/or prognosis of diseases
CC associated with aberrant calcium flux. Such disorders include
CC neurological diseases (e.g. amyotrophic lateral sclerosis, ALS),
CC immune dysfunction (e.g. severe combined immunodeficiency, SCID),

CC digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic
 CC disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or
 CC infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The
 CC novel calcium-binding proteins are also useful as screening tools to
 CC identify antagonists and/or agonists that may enhance or inhibit
 CC activities mediated by calcium-binding proteins. The polynucleotides of
 CC the invention are also useful in gene therapy. AAS31577-AAS31654
 CC represent cDNA sequences encoding for the novel human calcium-binding
 CC proteins.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 1480 BP; 329 A; 458 C; 479 G; 214 T; 0 other;

Alignment Scores:
 Pred. No.: 0.00188 Length: 1480
 Score: 70.00 Matches: 13
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AAS31631 (1-1480)

QY 1 AspleuAsnLysAspGlyHisLeuAspGlySerGluVal 13
 |||||
 DB 806 GAICTGAAACAGATGGCGACCTGGACGGAGTGAGGTG 844

RESULT 6

ABK43732
 ID ABK43732 standard; cDNA; 1480 BP.

AC ABK43732;

XX 05-JUN-2002 (first entry)

XX DNA encoding novel central nervous system protein #312.

XX Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
 KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
 KW cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;
 KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
 KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
 KW adenocarcinoma; reproductive system disorder; testicular feminisation;
 KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
 KW respiratory disorder; renal disorder; kidney failure; blood disorder;
 KW myocardial infarction; wound healing; cell proliferation; skin aging;
 KW food additive; food preservative; gene therapy; gene; ss.

XX Homo sapiens.

XX WO200155318-A2.

XX 03-AUG-2001.

XX 17-JAN-2001; 2001WO-US01332.

XX 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180828.

PR 24-FEB-2000; 2000US-0184564.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.

PR 07-JUL-2000; 2000US-0216880.

PR 11-JUL-2000; 2000US-0217487.

PR 11-JUL-2000; 2000US-0217496.

PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0225213.
 PR 14-AUG-2000; 2000US-0225214.
 PR 14-AUG-2000; 2000US-0225266.
 PR 14-AUG-2000; 2000US-0225267.
 PR 14-AUG-2000; 2000US-0225268.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
 PR 18-AUG-2000; 2000US-0226279.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226868.
 PR 22-AUG-2000; 2000US-0227182.
 PR 23-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 05-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 06-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 14-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 13-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.

CC Additionally, N may be used to produce the colon cancer-associated Ps,
 CC by inserting the nucleic acids into a host cell and culturing the cell
 CC to express the proteins. N and P can be used in the prevention, diagnosis
 CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
 CC and AAB77789 represent sequences used in the exemplification of the
 CC present invention.
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
 CC missing at time of publication, meaning no sequences are present for
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.
 XX
 SQ Sequence 1487 BP; 344 A; 452 C; 464 G; 221 T; 6 other;

Alignment Scores:

Pred. No.:	0.00189	Length:	1487
Score:	70.00	Matches:	13
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-09-768-840-1_COPY_254_266 (1-13) x AAH34992 (1-1487)

QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13

Db 793 GATCTGACACAGGATGGGCACCTGGATGGAGTGAGGTG 831

RESULT 8

AAH52253

ID AAX52253 standard; DNA; 1503 BP.

XX AC AAX52253;

XX AC AAX52253;

XX DT 25-JUN-1999 (first entry)

XX DE Protein PRO272 cDNA clone DNA40620-1183.

XX KW Secreted protein; transmembrane protein; human; enterocolitis;
 KW Zollinger-Ellison syndrome; gastrointestinal ulceration;
 KW congenital microvillus atrophy; skin disease; cell growth;
 KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
 KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy;
 KW fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;
 KW anti-thrombotic; wound healing; tissue repair; ss.

OS Homo sapiens.

XX WO9914328-A2.

XX PD 25-MAR-1999.

XX PF 16-SEP-1998;

XX PR 25-NOV-1997;

XX PR 17-SEP-1997;

XX PR 17-SEP-1997;

XX PR 17-SEP-1997;

XX PR 17-SEP-1997;

XX PR 17-SEP-1997;

XX PR 17-SEP-1997;

XX PR 17-SEP-1997;

XX PR 17-SEP-1997;

XX PR 17-SEP-1997;

XX PR 17-SEP-1997;

XX PR 17-SEP-1997;

XX PR 17-SEP-1997;

XX PR 17-SEP-1997;

XX PR 17-SEP-1997;

XX PR 17-SEP-1997;

XX PR 17-SEP-1997;

XX PR 17-SEP-1997;

XX PR 17-SEP-1997;

XX PR 17-SEP-1997;

XX PR 17-SEP-1997;

XX PR 17-SEP-1997;

XX PR 17-SEP-1997;

XX PR 17-SEP-1997;

XX PR 17-SEP-1997;

XX PR 17-SEP-1997;

XX PR 17-SEP-1997;

XX PR 17-SEP-1997;

PR 27-OCT-1997; 97US-0063329.
 PR 27-OCT-1997; 97US-0063327.
 PR 28-OCT-1997; 97US-0063541.
 PR 28-OCT-1997; 97US-0063542.
 PR 28-OCT-1997; 97US-0063544.
 PR 28-OCT-1997; 97US-0063549.
 PR 28-OCT-1997; 97US-0063550.
 PR 28-OCT-1997; 97US-0063564.
 PR 29-OCT-1997; 97US-0063435.
 PR 29-OCT-1997; 97US-0063704.
 PR 29-OCT-1997; 97US-0063732.
 PR 29-OCT-1997; 97US-0063738.
 PR 29-OCT-1997; 97US-0063734.
 PR 29-OCT-1997; 97US-0064215.
 PR 31-OCT-1997; 97US-0063735.
 PR 31-OCT-1997; 97US-0063870.
 PR 31-OCT-1997; 97US-0064103.
 PR 03-NOV-1997; 97US-0064248.
 PR 07-NOV-1997; 97US-0064809.
 PR 12-NOV-1997; 97US-0065186.
 PR 17-NOV-1997; 97US-0065846.
 PR 18-NOV-1997; 97US-0065693.
 PR 21-NOV-1997; 97US-0066120.
 PR 21-NOV-1997; 97US-0066364.
 PR 24-NOV-1997; 97US-0066772.
 PR 24-NOV-1997; 97US-0066466.
 PR 24-NOV-1997; 97US-0066770.
 PR 24-NOV-1997; 97US-0066511.
 PR 24-NOV-1997; 97US-0066453.
 XX
 PA (GETH) GENENTECH INC.

Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;

WPI; 1999-229533/19.
 P-PSDB; AAY13382.

New isolated human genes and polypeptides used in, e.g. treatment of
 gastrointestinal ulceration
 Claim 2; Fig 79; 320pp; English.

AAH52213-74 encode secreted and transmembrane human proteins, and are
 obtained from cDNA libraries, prepared from fetal lung, fetal kidney,
 fetal brain, fetal liver and fetal retina. The encoded polypeptides
 have specific uses based on their homology to known polypeptides,
 e.g. PRO211 and PRO217 can be used for disorders associated with the
 preservation and maintenance of gastrointestinal mucosa and the repair
 of acute and chronic mucosal lesions (e.g. enterocolitis,
 Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital
 microvillus atrophy), skin diseases associated with abnormal
 keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as
 lung squamous cell carcinoma of the vulva and gliomas), potent effects on
 cell growth and development, diseases related to growth or survival of
 nerve cells including Parkinson's disease, Alzheimer's disease, ALS,
 neuropathies or cancer. PRO265 can be used as a target for anti-tumor
 reducing dermal scarring. PRO264 can be used as a target for anti-tumor
 drugs. PRO533 may be used in the treatment of Usher Syndrome or Atrophia
 areata. PRO269 can be used as an anti-thrombotic agent; PRO287
 polypeptides and portions may have therapeutic applications in wound
 healing and tissue repair; PRO317 can be used for treating problems of
 the kidney, uterus, endometrium, blood vessels, or related tissue, e.g.
 in the heart of genital tract.

SQ Sequence 1503 BP; 357 A; 456 C; 474 G; 216 T; 0 other;

Alignment Scores:

Pred. No.:	0.00192	Length:	1503
Score:	70.00	Matches:	13
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	20	Gaps:	0

US-09-768-840-1_COPY_254_266 (1-13) x AAX52253 (1-1503)

QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
|||||
Db 794 GATCTGACACAGGATGGGCACCTGGATGGAGTGAGGTG 832

RESULT 9

AAC58589

ID AAC58589 standard; cDNA; 1503 BP.

XX AAC58589;

XX 29-JAN-2001 (first entry)

XX Human PRO272 protein UNQ239 encoding cDNA SEQ ID NO:50.

XX Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW antianemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW antilasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW osteoarthritis; spondyloarthritis; systemic sclerosis; sarcoidosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW autoimmune thrombocytopenia; immune-mediated renal disease;
KW demyelinating disease; hepatobiliary disease; Whipple's disease;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW autoimmune disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW graft rejection; graft-versus-host-disease; ss.

XX Homo sapiens.

XX OS

XX PN WO200053758-A2.

XX PD 14-SEP-2000.

XX PF

XX 02-MAR-2000; 2000WO-US05841.

XX 08-MAR-1999; 99WO-US05028.

PR 10-MAR-1999; 99US-0123618.

PR 12-MAR-1999; 99US-0123957.

PR 23-MAR-1999; 99US-0125775.

PR 12-APR-1999; 99US-0128849.

PR 20-APR-1999; 99WO-US08615.

PR 28-APR-1999; 99US-0131445.

PR 04-MAY-1999; 99US-0132371.

PR 14-MAY-1999; 99US-0134287.

PR 02-JUN-1999; 99WO-US12252.

PR 23-JUN-1999; 99US-0141037.

PR 20-JUL-1999; 99US-0144758.

PR 26-JUL-1999; 99US-0145698.

PR 28-JUL-1999; 99US-0146222.

PR 01-SEP-1999; 99WO-US20111.

PR 08-SEP-1999; 99WO-US20594.

PR 13-SEP-1999; 99WO-US20944.

PR 15-SEP-1999; 99WO-US21090.

PR 15-SEP-1999; 99WO-US21547.

PR 05-OCT-1999; 99WO-US23089.

PR 29-OCT-1999; 99US-0162506.

PR 29-NOV-1999; 99WO-US28214.

PR 30-NOV-1999; 99WO-US28313.

PR 30-NOV-1999; 99WO-US28409.

PR 01-DEC-1999; 99WO-US28301.

PR 01-DEC-1999; 99WO-US28634.

PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28564.

PR 02-DEC-1999; 99WO-US28565.

PR 16-DEC-1999; 99WO-US30095.

PR 20-DEC-1999; 99WO-US30999.

PR 30-DEC-1999; 99WO-US31274.

PR 05-JAN-2000; 2000WO-US00219.

PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.

XX (GETH) GENENTECH INC.

XX PA

XX PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;

PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;

PI Stewart TA, Tamas D, Watanabe CK, Wood WI, Yan M;

XX WPI: 2000-572271/53.

DR P-PSDB; AAB33424.

XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of

PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid

PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus .

PS Claim 23; Fig 21; 309pp; English.

XX The present invention describes sixty four human PRO proteins which can

CC be used in the treatment of immune related diseases. The human PRO

CC proteins, anti-PRO antibodies, agonists and antagonists are useful for

CC treating and diagnosing immune related disorders. The disorders are

CC selected from systemic lupus erythematosus, rheumatoid arthritis,

CC osteoarthritis, juvenile chronic arthritis, spondyloarthritis,

CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's

CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic

CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,

CC immune-mediated renal disease, demyelinating diseases of the central

CC and peripheral nervous systems, hepatobiliary diseases, inflammatory

CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,

CC autoimmune or immune-mediated skin diseases, allergic diseases,

CC immunological diseases of the lung, and transplantation associated

CC diseases including graft rejection and graft-versus-host-disease.

CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used

CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and

CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein

CC sequences given in the exemplification of the present invention.

XX SQ Sequence 1503 BP; 357 A; 456 C; 474 G; 216 T; 0 other;

Alignment Scores:

Pred. No.:	0.00192	Length:	1503
Score:	70.00	Matches:	13
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	21	Gaps:	0

US-09-768-840-1_COPY_254_266 (1-13) x AAC58589 (1-1503)

QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13

|||||

Db 794 GATCTGACACAGGATGGGCACCTGGATGGAGTGAGGTG 832

RESULT 10

AAS21425

ID AAS21425 standard; cDNA; 1503 BP.

XX AC AAS21425;

XX 24-OCT-2001 (first entry)

XX Human cDNA sequence encoding for PRO272 polypeptide.

XX Human secretory and transmembrane; PRO; mammalian; cancer; lung;

KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;

KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;

KW adipocyte; A-peptide; factor VIIA; gene therapy; ss.

XX

OS Homo sapiens.
XX WO20010466-A2.
XX
XX
XX 07-JUN-2001.
XX
XX 01-DEC-2000; 2000WO-US32678.
XX 01-DEC-1999; 99WO-US28301.
XX 01-DEC-1999; 99WO-US28634.
XX 02-DEC-1999; 99WO-US28551.
XX 02-DEC-1999; 99WO-US28564.
XX 02-DEC-1999; 99WO-US28565.
XX 09-DEC-1999; 99US-0170262.
XX 16-DEC-1999; 99WO-US30095.
XX 20-DEC-1999; 99WO-US30911.
XX 20-DEC-1999; 99WO-US30999.
XX 30-DEC-1999; 99WO-US31243.
XX 06-JAN-2000; 2000WO-US00277.
XX 06-JAN-2000; 2000WO-US00376.
XX 11-FEB-2000; 2000WO-US03565.
XX 18-FEB-2000; 2000WO-US04341.
XX 18-FEB-2000; 2000WO-US04342.
XX 22-FEB-2000; 2000WO-US04414.
XX 24-FEB-2000; 2000WO-US04914.
XX 24-FEB-2000; 2000WO-US05004.
XX 01-MAR-2000; 2000WO-US05601.
XX 21-MAR-2000; 2000WO-US07377.
XX 21-MAR-2000; 2000WO-US07532.
XX 30-MAR-2000; 2000WO-US08439.
XX 17-MAY-2000; 2000WO-US13705.
XX 22-MAY-2000; 2000WO-US14042.
XX 30-MAY-2000; 2000WO-US14941.
XX 02-JUN-2000; 2000WO-US15264.
XX 10-NOV-2000; 2000WO-US30873.

(GETH) GENENTECH INC.

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
WPI; 2001-408281/43.
P-PSDB; AAU12353.

Isolated, secretory and transmembrane PRO polypeptide used to detect
other PRO polypeptides, link bioactive molecules to cells expressing
PRO polypeptides, and detect the presence of mammalian tumours e.g.
lung, breast, prostate, cervical

Claim 3; Fig 363; 813pp; English.

AA521244-AA521518 encode for novel human secretory and transmembrane
PRO polypeptides. The PRO polypeptides are useful to detect other
PRO polypeptides, to link bioactive molecules to cells expressing
PRO polypeptides, to modulate biological activities of cells expressing
PRO polypeptides, and to detect the presence of mammalian lung, colon,
breast, prostate, rectal, cervical or liver tumours by comparing PRO
polypeptide expression in a cell sample to that in a control sample.
Some of the 275 sequences are also useful to stimulate the release of
tumour necrosis factor-alpha (TNF-alpha) from human blood, the
proliferation or differentiation of chondrocytes, the proliferation or
gene expression in pericyte cells, the release of proteoglycans from
cartilage, the proliferation of inner ear utricular supporting cells or
of T-lymphocytes, the release of a cytokine from peripheral blood
monocytes (PBMCs), or the proliferation of endothelial cells. Some of
the PRO polypeptides may modulate glucose or free fatty acid uptake by
skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
to factor VIIA. The PRO polypeptides can be used in assays to identify
molecules involved in binding interactions. The polynucleotides encoding
PRO polypeptides can be used to generate probes, antisense RNA/DNA,
transgenic or knock out animals and can be used in gene therapy.

SQ Sequence 1503 BP; 357 A; 456 C; 474 G; 216 T; 0 other;
Alignment Scores:
Pred. No.: 0.00192 Length: 1503
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AAS21425 (1-1503)

QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
|||||
Db 794 GATCTGAACAAGGATGGGCACCTGGATGGAGTGAGGTG 832

RESULT 11

AAF72411

ID AAF72411 standard; cDNA; 1503 BP.

XX AAF72411;

XX 24-APR-2001 (first entry)

DE Human PRO272 cDNA.

XX Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;

XX antiparkinsonian nootropic; neuroprotective; vulnerary; cardiac;

XX antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;

XX antiarthritic; antinfertility; antidiabetic; antiviral; diabetes;

XX ophthalmological; gene therapy; skin disease; gastrointestinal disorder;

XX ischaemia; inflammation; ss.

XX Homo sapiens.

XX WO200104311-A1.

XX 18-JAN-2001.

XX 22-FEB-2000; 2000WO-US04414.

XX 07-JUL-1999; 99US-0143048.

XX 26-JUL-1999; 99US-0145698.

XX 28-JUL-1999; 99US-0146222.

XX 08-SEP-1999; 99WO-US20594.

XX 13-SEP-1999; 99WO-US20944.

XX 15-SEP-1999; 99WO-US21090.

XX 15-SEP-1999; 99WO-US21547.

XX 05-OCT-1999; 99WO-US23089.

XX 29-NOV-1999; 99WO-US28214.

XX 30-NOV-1999; 99WO-US28313.

XX 16-DEC-1999; 99WO-US30095.

XX 20-DEC-1999; 99WO-US30911.

XX 20-DEC-1999; 99WO-US30999.

XX 05-JAN-2000; 99WO-US00219.

(GETH) GENENTECH INC.

XX Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
XX Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
XX Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;
XX Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
XX Williams PM, Wood WI;
XX WPI; 2001-081051/09.
XX P-PSDB; AAB80250.

Sixty one nucleic acids encoding PRO polypeptides which are useful in
the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung
squamous cell carcinoma) and neurodegenerative diseases (e.g.
Alzheimer's disease) -
Claim 2; Fig 79; 393pp; English.

XX The present sequence is one of sixty one nucleic acids encoding novel
 CC secreted and transmembrane PRO polypeptides. The PRO polypeptides are
 CC useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung
 CC squamous cell carcinoma), gastrointestinal disorders (e.g.
 CC enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,
 CC Parkinson's disease), wound repair, cardiovascular disorders (e.g.
 CC endometrial bleeding angiogenesis, ischaemias such as coronary
 CC ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma,
 CC rheumatoid arthritis, multiple sclerosis), infertility, AIDS and
 CC diabetes and retinal disorders such as retinitis pigmentosum.
 CC The PRO nucleic acids have applications in molecular biology, including
 CC use as hybridization probes, and in chromosome and gene mapping.
 XX
 SQ Sequence 1503 BP; 357 A; 456 C; 474 G; 216 T; 0 other;

Alignment Scores:
 Pred. No.: 0.00192 Length: 1503
 Score: 70.00 Matches: 13
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AAF72411 (1-1503)

QY 1 AspleuAsnLysAspGlyHisLeuAspGlySerGluVal 13
 |||||
 Db 794 GATCTGAACAAGGATGGCCACCTGGATGGAGTGAGGTG 832

RESULT 12
 AAC97455
 ID AAC97455 standard; cDNA; 1503 BP.
 AC AAC97455;
 XX
 XX 28-FEB-2001 (first entry)
 DT
 XX
 DE Human angiogenesis-associated protein PRO272 cDNA, SEQ ID NO:112.
 XX
 KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;
 KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
 KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
 KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
 KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;
 KW Alzheimer's disease; Huntington's disease; stroke; drug screening;
 KW gene therapy; transgenic animal; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200053753-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 05-JAN-2000; 2000WO-US00219.
 XX
 PR 08-MAR-1999; 99WO-US05028.
 PR 12-MAR-1999; 99US-0123957.
 PR 14-MAY-1999; 99US-0134287.
 PR 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 15-SEP-1999; 99WO-US21090.
 PR 05-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 30-NOV-1999; 99WO-US28313.
 PR 02-DEC-1999; 99WO-US28409.
 PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.

(GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;
 PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;

XX WPI: 2001-090793/10.
 DR P-FSDB; AAB53085.

XX New isolated nucleic acid for producing a PRO polypeptide, analyzing
 PT genetic disorders and treating cardiovascular, endothelial or
 PT angiogenic disorders, such as atherosclerosis, wounds or cancer -
 XX Claim 58; Fig 43; 293pp; English.

XX The invention relates to novel human angiogenesis-associated proteins
 CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding
 CC PRO proteins. The invention also relates to vectors and host cells
 CC comprising a PRO nucleic acid, the recombinant production of a PRO
 CC protein, PRO antibodies specific for a PRO protein, fusion proteins
 CC comprising a PRO protein, agonists or antagonists of a PRO protein, and
 CC compounds which inhibit the expression of a PRO gene. The invention
 CC additionally encompasses methods of identifying modulators of PRO
 CC expression or activity; diagnosing a cardiovascular, endothelial or
 CC angiogenic disorder, or a susceptibility to such a disorder by detecting
 CC mutations in a PRO gene, or the expression level of a PRO gene within a
 CC particular tissue; treating a cardiovascular, endothelial or angiogenic
 CC disorder via the administration of a PRO protein, PRO nucleic acid, or
 CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a
 CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial
 CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the
 CC administration of a PRO protein, or an agonist or antagonist thereof.
 CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO
 CC agonists and PRO antagonists may be used as therapeutic agents to treat
 CC cardiovascular, endothelial or angiogenic disorders, such as
 CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,
 CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,
 CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's
 CC disease, or stroke. PRO nucleic acids are additionally useful in the
 CC recombinant production of PRO proteins, as hybridisation probes to
 CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,
 CC to map genes encoding PRO proteins, to analyse genetic disorders, and in
 CC gene therapy. PRO nucleic acids can also be used to produce transgenic
 CC animals useful for the development and screening of potential
 CC therapeutic agents. The present sequence represents a cDNA encoding a PRO
 CC protein of the invention.

XX Sequence 1503 BP; 357 A; 456 C; 474 G; 216 T; 0 other;

Alignment Scores:

Pred. No.: 0.00192 Length: 1503
 Score: 70.00 Matches: 13
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AAC97455 (1-1503)

QY 1 AspleuAsnLysAspGlyHisLeuAspGlySerGluVal 13
 |||||
 Db 794 GATCTGAACAAGGATGGCCACCTGGATGGAGTGAGGTG 832

RESULT 13

AAX00656

ID AAX00656 standard; DNA; 1507 BP.

XX AAX00656;

AC AAX00656;

XX 25-MAR-1999 (first entry)

DT 25-MAR-1999 (first entry)

XX Human secreted protein gene 46 clone HSJBQ79.

DE Human secreted protein gene 46 clone HSJBQ79.

XX

KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
OS
XX Homo sapiens.
XX
XX WO9842738-A1.
XX
XX 01-OCT-1998.
XX
XX
XX 19-MAR-1998; 98WO-US05311.
XX
XX 30-MAY-1997; 97US-0050937.
XX 21-MAR-1997; 97US-0041276.
XX 21-MAR-1997; 97US-0041277.
XX 21-MAR-1997; 97US-0041281.
XX 21-MAR-1997; 97US-0042344.
XX 30-MAY-1997; 97US-0048069.
XX 30-MAY-1997; 97US-0048094.
XX 30-MAY-1997; 97US-0048095.
XX 30-MAY-1997; 97US-0048096.
XX 30-MAY-1997; 97US-0048099.
XX 30-MAY-1997; 97US-0048131.
XX 30-MAY-1997; 97US-0048135.
XX 30-MAY-1997; 97US-0048154.
XX 30-MAY-1997; 97US-0048160.
XX 30-MAY-1997; 97US-0048186.
XX 30-MAY-1997; 97US-0048187.
XX 30-MAY-1997; 97US-0048188.
XX 30-MAY-1997; 97US-0048350.
XX 30-MAY-1997; 97US-0048351.
XX 30-MAY-1997; 97US-0048352.
XX 30-MAY-1997; 97US-0048355.
XX 05-AUG-1997; 97US-0054804.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX
XX Brewer LA, Duan R, Ebner R, Ferrie AM, Florence KA;
XX Greene JM, Hu JS, Lafleur DM, Moore PA, Ni J, Olsen HS;
XX Rosen CA, Ruben SM, Shi Y, Young P;
XX
XX WPI; 1999-070066/06.
XX P-PSDB; AAW67852.
XX
XX New isolated human genes and the secreted polypeptides they encode -
XX useful for diagnosis and treatment of e.g. cancers, neurological
XX disorders, immune diseases, inflammation or blood disorders
XX
XX Claim 1; Page 209-210; 385pp; English.

XX This sequence represents a nucleic acid molecule which encodes a
XX secreted human protein. The gene number, and the clone it is derived
XX from, are detailed in the descriptor line. The gene can be used to
XX generate fusion proteins by linking to the gene to a human immunoglobulin
XX Fc portion (e.g. AAX00602) for increasing the stability of the fused
XX protein as compared to the human protein only.
XX The invention relates to 87 novel genes and their fragments (nucleic
XX acid sequences: AAX00611-X00724; amino acid sequences AAW67807-W68004)
XX which are useful for preventing, treating or ameliorating medical
XX conditions e.g. by protein or gene therapy. Also, pathological
XX conditions can be diagnosed by determining the amount of the new
XX polypeptides in a sample or by determining the presence of mutations in
XX the new polynucleotides. Specific uses are described for each of the 87
XX polynucleotides, based on which tissues they are most highly expressed in
XX (see AAX00611 for described uses).

XX Sequence 1507 BP; 350 A; 456 C; 479 G; 213 T; 9 other;

Alignment Scores:

Pred. No.: 0.00192 Length: 1507
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AAX00656 (1-1507)

QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13

|||||
DB 813 GATCTGAACAGGATGGGCACCTGGATGGAGTGAGGTG 851

RESULT 14

AAL41601

ID AAL41601 standard; cDNA; 1507 BP.

XX AC AAL41601;

XX DT 19-APR-2002 (first entry)

XX DE Human colon cancer related coding sequence SEQ ID NO: 12.
XX Human; colon cancer; cytostatic; drug design; adenomatous polyp;
XX colorectal carcinoma; high metastatic potential colon tumour;
XX metastatic colon cancer; gene; ss.
XX Homo sapiens.
XX WO200196523-A2.
XX 20-DEC-2001.
XX 15-JUN-2001; 2001WO-US19313.
XX 15-JUN-2000; 2000US-211835P.
XX (CHIR) CHIRON CORP.
XX Kennedy GC, Kang S, Reinhard C, Jefferson AB;
XX WPI; 2002-164362/21.

XX Detecting a cancerous colon cell, useful for diagnosing colon cancer
XX and for rational drug and therapy design, comprises detecting at least
XX one differentially expressed gene product -
XX
XX Claim 42; Page 105-106; 135pp; English.

XX The present invention relates to methods for detecting a cancerous colon
XX cell involving detecting at least one differentially expressed gene such
XX as those given in AAL41595-AAL41611. This is useful for diagnosing colon
XX cancer, in rational drug and therapy design, and for identifying
XX additional genes linked to the development or inhibition of development
XX of colon cancer. Examples of colon cancer which can be detected include
XX adenomatous polyp, colorectal carcinoma, high metastatic potential colon
XX tumours and metastatic colon cancer. The present sequence is a colon
XX cancer associated protein coding sequence.

XX Sequence 1507 BP; 350 A; 456 C; 479 G; 213 T; 9 other;

Alignment Scores:

Pred. No.: 0.00192 Length: 1507
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AAL41601 (1-1507)

QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13

Db 813 GATCTGAACAGGATGGGCACCTGGATGGAGGTG 851

RESULT 15

AA41603
ID AAL41603 standard; cDNA; 1507 BP.

XX AC AAL41603;

XX DT 19-APR-2002 (first entry)

XX DE Human colon cancer related coding sequence SEQ ID NO: 15.

XX KW Human: colon cancer; cytostatic; drug design; adenomatous polyp;
KW colorectal carcinoma; high metastatic potential colon tumour;
KW metastatic colon cancer; gene; ss.

XX OS Homo sapiens.

XX PN WO200196523-A2.

XX PD 20-DEC-2001.

XX PF 15-JUN-2001; 2001WO-US19313.

XX PR 15-JUN-2000; 2000US-211835P.

XX PA (CHIR) CHIRON CORP.

XX PI Kennedy GC, Kang S, Reinhard C, Jefferson AB;

XX DR WPI; 2002-164362/21.

XX PT Detecting a cancerous colon cell, useful for diagnosing colon cancer
PT and for rational drug and therapy design, comprises detecting at least
PT one differentially expressed gene product

XX PS Claim 42; Page 107; 135pp; English.

CC The present invention relates to methods for detecting a cancerous colon
CC cell involving detecting at least one differentially expressed gene such
CC as those given in AAL41595-AAL41611. This is useful for diagnosing colon
CC cancer, in rational drug and therapy design, and for identifying
CC additional genes linked to the development or inhibition of development
CC of colon cancer. Examples of colon cancer which can be detected include
CC adenomatous polyp, colorectal carcinoma, high metastatic potential colon
CC tumours and metastatic colon cancer. The present sequence is a colon
CC cancer associated protein coding sequence.

XX SQ Sequence 1507 BP; 350 A; 456 C; 479 G; 213 T; 9 other;

Alignment Scores:

Pred. No.:	0.00192	Length:	1507
Score:	70.00	Matches:	13
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-09-768-840-1_COPY_254_266 (1-13) x AAL41603 (1-1507)

QY 1 AspLeuAsnIysAspGlyHisLeuAspGlySerGluVal 13

Db 813 GATCTGAACAGGATGGGCACCTGGATGGAGGTG 851

Search completed: May 19, 2003, 13:58:04
Job time.: 237 secs

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GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 19, 2003, 22:09:51 ; Search time 1746 Seconds
(without alignments)
120.585 Million cell updates/sec

Title: US-09-768-840-1_COPY_254_266
Perfect score: 70
Sequence: 1 DLNKGHLDGSEV 13

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09768840.@cgn2_1.1906 -runat_14052003_095712_16653 -NCPU=6 -ICPU=3
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST : *
1: em_estba : *
2: em_esthum : *
3: em_estin : *
4: em_estmu : *
5: em_estov : *
6: em_estpl : *
7: em_estro : *
8: em_hic : *
9: gb_est1 : *
10: gb_est2 : *
11: gb_est3 : *
12: gb_est4 : *
13: gb_est5 : *
14: gb_est6 : *
15: em_estfun : *
16: em_estom : *
17: gb_gss : *
18: em_gss_hum : *
19: em_gss_inv : *
20: em_gss_pin : *
21: em_gss_vrt : *
22: em_gss_vrt : *
23: em_gss_fun : *
24: em_gss_mam : *
25: em_gss_mus : *
26: em_gss_pro : *
27: em_gss_rod : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	70	100.0	515	9	AA456267
2	70	100.0	554	12	BG742111
3	70	100.0	588	9	AI751749
4	70	100.0	624	14	BM716710
5	70	100.0	824	13	BI820206
6	70	100.0	900	9	AL569912
7	70	100.0	909	9	AL520512
8	70	100.0	931	12	BE880649
9	70	100.0	954	9	AL573989
10	70	100.0	1092	9	AL544155
11	66	94.3	601	14	BM695756
12	64	91.4	324	14	H74164
13	64	91.4	664	14	BQ374092
14	64	91.4	1005	9	AA520513
15	62	88.6	341	9	AA239568
16	62	88.6	401	14	W64383
17	62	88.6	532	12	BG347022
18	62	88.6	578	14	BQ564168
19	62	88.6	582	12	BF118990
20	62	88.6	583	10	AW550048
21	62	88.6	618	10	AW558437
22	62	88.6	676	10	BB398523
23	62	88.6	678	10	BB041431
24	62	88.6	693	14	BQ209584
25	62	88.6	694	14	BQ192961
26	62	88.6	696	14	BM934252
27	62	88.6	867	13	BI903868
28	62	88.6	1009	9	AL570372
29	62	88.6	1112	11	AK003918
30	61	87.1	395	10	BE015071
31	61	87.1	465	10	AW353288
32	61	87.1	478	10	AW653432
33	61	87.1	481	9	AI341112
34	61	87.1	574	13	BI344949
35	61	87.1	596	13	BI337575
36	61	87.1	852	9	AL543274
37	60	85.7	660	14	BQ182243
38	60	85.7	660	14	BQ773463
39	58	82.9	362	14	W54172
40	57	81.4	662	10	AW578296
41	57	81.4	1070	14	BM903507
42	54	77.1	658	14	BQ044993
43	53	75.7	558	14	BM900368
44	53	75.7	629	13	BM138832
45	52	74.3	438	12	BF988162

ALIGNMENTS

RESULT 1
AA456267
LOCUS
DEFINITION
515 bp mRNA linear EST 06-JUN-1997
zx99f04.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:811903 5', similar to SW:RCAL_MOUSE Q05186 RETICULOCALBIN PRECURSOR. ; , mRNA sequence.
AA456267
ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 515)
AUTHORS
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Gelsel, G., Jost, S.,

Tue May 20 14:43:31 2003

Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, K., and Wilson, R.
WashU-Merck EST Project 1997
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

TITLE JOURNAL COMMENT

Email: est@wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
High quality sequence stop: 464.

FEATURES source

1. 515
/organism="Homo sapiens"
/db_xref="GDB:6042814"
/db_xref="taxon:9606"
/clone="IMAGE:811903"
/clone_lib="Soares.NhMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NBHM, pregnant uterus NbHPU, and fetal heart NbH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
115 a 142 c 180 g 78 t

BASE COUNT ORIGIN

Alignment Scores:
Pred. No.: 0.018 Length: 515
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AA456267 (1-515)

QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
|||||
Db 259 GATCTGAACAAGGATGGCACCCTGGATGGAGTGAGGTG 297

RESULT 2 LOCUS

BG742111 554 bp mRNA linear EST 15-MAY-2001
602633581F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4778420 5',
mRNA sequence.

ACCESSION BG742111.1 GI:14052764

VERSION BG742111

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 554)

NIH-MGC http://mgs.nci.nih.gov/.

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: James Cleaver, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA

Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAMI0634 row: b column: 21

High quality sequence start: 3

High quality sequence stop: 554.

FEATURES source

1. 554
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4778420"
/clone_lib="NCI_CGAP_Skn3"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: skin; Vector: pCMV-Sport6; Site 1: Not 1; Site 2: SalI; Cloned unidirectionally. Primer: oligo dT.
Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library."
Technologies. Note: this is a NCI_CGAP Library."
131 a 146 c 194 g 83 t

BASE COUNT ORIGIN

Alignment Scores:
Pred. No.: 0.02 Length: 554
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x BG742111 (1-554)

QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
|||||

Db 274 GATCTGAACAAGGATGGCACCCTGGATGGAGTGAGGTG 312

RESULT 3

LOCUS AI751749

DEFINITION cnl1f11.x1 Normal Human Trabecular Bone Cells Homo sapiens CDNA

clone NHTBC_cnl1f11 random, mRNA sequence.

ACCESSION AI751749

VERSION AI751749.1 GI:5130013

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 588)

Jia, L.B., Young, M.F., Touchman, J.W., Bouffard, G.G.,
Beckstrom-Sternberg, S.M., Green, E.D., Powell, J.I., Yang, L.M., Robey
P.G., Hotchkiss, R.N. and Francomano, C.A.

SGAP: The Skeletal Genome Anatomy Project

Unpublished (1997)

Contact: Libin Jia

Medical Genetics Branch

National Human Genome Research Institute

10/10C101, 9000 Rockville Pike, Bethesda, MD 20892-1267, USA

Tel: 301-402-4877

Fax: 301-496-7157

Email: libin@helix.nih.gov

DNA Sequencing and analyses by National Institutes of Health

Intramural Sequencing Center (NISC).

Plate: 11 row: f column: 11

Seq primer: -21M13 forward primer (ABI).

FEATURES source

1. 588
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NHTBC_cnl1f11"
/clone_lib="Normal Human Trabecular Bone Cells"
/sex="Female"
/tissue_type="Bone"
/cell_type="Trabecular Bone Cells"

```

/lab_host="SURE"
/notes="Organ: Hip; Vector: pbluescript; Site_1: EcoRI;
Library constructed by Dr. Marian Young and Dr. Pamela
Gehron Robey (NIDCR)." 98 t 3 others

BASE COUNT 127 a 165 c 195 g 98 t 3 others
ORIGIN

Alignment Scores:
Pred. No.: 0.0218 Length: 588
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AT751749 (1-588)

QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
|||||
Db 167 GATCTGAACAAGGATGGGACCTGGATGGAGTGAGGTG 205

RESULT 4
BM716710 624 bp mRNA linear EST 28-FEB-2002
LOCUS
DEFINITION
UI-E-EJ0-ahg-p-08-0-UI-r2 UI-E-EJ0 Homo sapiens cDNA clone
UI-E-EJ0-ahg-p-08-0-UI 5', mRNA sequence.
ACCESSION
BM716710
VERSION
BM716710.1 GI:19029968
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 624)
AUTHORS
Bonaldo, M.F., Lennon, G. and Soares, M.B.
TITLE
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL
Genome Res. 6 (9), 791-806 (1996)
MEDLINE
9704477
COMMENT
Contact: Soares, MB
Program for Ret Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr Gregg Hageman
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.
FEATURES
Location/Qualifiers
1..624
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-EJ0-ahg-p-08-0-UI"
/clone_lib="UI-E-EJ0"
/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
Choroid"
/dev_stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/notes="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoRI; Site_2: Not I;
UI-E-EJ0 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoRI adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of

```

first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment, AATGCCCAT; optic nerve, CCATTAAAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).*

```

BASE COUNT 142 a 174 c 215 g 93 t
ORIGIN

Alignment Scores:
Pred. No.: 0.0237 Length: 624
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x BM716710 (1-624)

QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
|||||
Db 349 GATCTGAACAAGGATGGGACCTGGGACGAGTGAGGTG 387

RESULT 5
BI820206 824 bp mRNA linear EST 04-OCT-2001
LOCUS
DEFINITION
603037040F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5178104 5',
mRNA sequence.
ACCESSION
BI820206
VERSION
BI820206.1 GI:15931756
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 824)
AUTHORS
NIH-MGC http://mgi.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM11443 row: p column: 09
High quality sequence stop: 801.
FEATURES
Location/Qualifiers
1..824
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5178104"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
/notes="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
BASE COUNT 180 a 227 c 298 g 119 t
ORIGIN

Alignment Scores:

```

Pred. No.: 0.0354 Length: 824
 Score: 70.00 Matches: 13
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x B1820206 (1-824),

QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
 |||||
 Db 638 GATCTGAACAGGATGGCCACCTGGATGGAGTGAGTG 676

RESULT 6

AL569912/c AL569912 900 bp mRNA linear EST 16-FEB-2001
 LOCUS AL569912 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODI001YH07 3
 DEFINITION prime, mRNA sequence.

ACCESSION AL569912

VERSION AL569912.1 GI:12925723

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 900)

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT

Contact: Genoscope

Genoscope - Centre National de Sequencage

Bp 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

source

1..900

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CSODI001YH07"

/clone_lib="LTI_NFL006_PL2"

/tissue_type="placenta"

/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-stranded cDNA was digested with NotI and

cloned into the NotI and Eco RV sites of the pCMVSPORT 6

vector. Library was normalized. Library was constructed by

Life Technologies. Contact : Feng Liang Life Technologies,

a division of Invitrogen 9800 Medical Center Drive

Rockville, Maryland 20850, USA Fax : (1) 301 610 8371

Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com"

BASE COUNT 143 a 270 c 285 g 195 t 7 others

ORIGIN

Alignment Scores:

Pred. No.: 0.0401 Length: 900

Score: 70.00 Matches: 13

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AL569912 (1-900)

Qy 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13

|||||

Db 582 GATCTGAACAGGATGGCCACCTGGATGGAGTGAGTG 544

RESULT 7

AL520512/c AL520512 909 bp mRNA linear EST 13-FEB-2001

LOCUS AL520512 LTI_NFL004_NBC2 Homo sapiens cDNA clone CSODB006YC08 3

DEFINITION prime, mRNA sequence.

ACCESSION AL520512

VERSION AL520512.1 GI:12784005

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 909)

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT

Contact: Genoscope

Genoscope - Centre National de Sequencage

Bp 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

source

1..909

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CSODB006YC08"

/clone_lib="LTI_NFL004_NBC2"

/sex="male"

/tissue_type="neuroblastoma cells"

/lab_host="DH10B"

/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-stranded cDNA was digested with NotI and

cloned into the NotI and Eco RV sites of the pCMVSPORT 6

vector. Library was normalized. Library was constructed

by Life Technologies. Contact : Feng Liang Life

Technologies, a division of Invitrogen 9800 Medical Center

Drive Rockville, Maryland 20850, USA Fax : (1) 301 610

8371 Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com"

BASE COUNT 142 a 278 c 291 g 197 t 1 others

ORIGIN

Alignment Scores:

Pred. No.: 0.0407 Length: 909

Score: 70.00 Matches: 13

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AL520512 (1-909)

Qy 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13

|||||

Db 586 GATCTGAACAGGATGGCCACCTGGATGGAGTGAGTG 548

RESULT 8

BE880649

LOCUS BE880649

DEFINITION

601491556F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893989 5',

mRNA sequence.

ACCESSION BE880649

VERSION BE880649.1 GI:10329425

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 931)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTG/Gazdar

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LIAW682 row: 0 column: 14
 High quality sequence stop: 683.

FEATURES

source
 1. .931
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3893989"
 /clone_lib="NIH_MGC_69"
 /tissue_type="large cell carcinoma, undifferentiated"
 /lab_host="PH10B (phage-resistant)"
 /notes="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.1 kb. Library constructed by Life
 Technologies." 218 a 272 c 292 g 149 t

BASE COUNT 218 a 272 c 292 g 149 t
 ORIGIN

Alignment Scores:

Pred. No.: 0.0421 Length: 931
 Score: 70.00 Matches: 13
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x BE880649 (1-931)

QY 1 AspleuAnLysAspGlyHisLeuAspGlySerGluVal 13
 |||||
 Db 212 GATCTGAACAAGGATGGCACCCTGGATGGAGTGAGGTG 250

RESULT 9

AL573989/c 954 bp mRNA linear EST 16-FEB-2001
 LOCUS AL573989 LTI_NFL006_PL2 Homo sapiens CDNA clone CSODI053YN17 3
 DEFINITION prime, mRNA sequence.

ACCESSION AL573989
 VERSION AL573989.1 GI:12933759
 KEYWORDS EST.

SOURCE

ORGANISM human.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 954)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

source
 1. .954
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CSODI053YN17"
 /clone_lib="LTI_NFL006_PL2"
 /tissue_type="placenta"
 /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed by
 Life Technologies. Contact: Feng Liang Life Technologies,
 a division of Invitrogen 9800 Medical Center Drive
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com"

BASE COUNT 150 a 293 c 304 g 204 t 3 others
 ORIGIN

Alignment Scores:

Pred. No.: 0.0437 Length: 954
 Score: 70.00 Matches: 13
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AL573989 (1-954)

QY 1 AspleuAnLysAspGlyHisLeuAspGlySerGluVal 13
 |||||
 Db 595 GATCTGAACAAGGATGGCACCCTGGATGGAGTGAGGTG 557

RESULT 10

AL544155 1092 bp mRNA linear EST 16-FEB-2001
 LOCUS AL544155 LTI_NFL006_PL2 Homo sapiens CDNA clone CSODI020C22 5
 DEFINITION prime, mRNA sequence.

ACCESSION AL544155
 VERSION AL544155.1 GI:12876634
 KEYWORDS EST.

SOURCE

ORGANISM human.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1092)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

source
 1. .1092
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CSODI020C22"
 /clone_lib="LTI_NFL006_PL2"
 /tissue_type="placenta"
 /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed by
 Life Technologies. Contact : Feng Liang Life Technologies,
 a division of Invitrogen 9800 Medical Center Drive
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com"

BASE COUNT

231 a 313 c 389 g 156 t 3 others
 ORIGIN

Alignment Scores:

Pred. No.: 0.053 Length: 1092
 Score: 70.00 Matches: 13
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AL544155 (1-1092)

QY 1 AspleuAnLysAspGlyHisLeuAspGlySerGluVal 13
 |||||
 Db 796 GATCTGAACAAGGATGGCACCCTGGATGGAGTGAGGTG 834

RESULT 11

BM695756 601 bp mRNA linear EST 28-FEB-2002
 LOCUS BM695756 UI-E-CQ1-aew-p-23-0-UI.r1 UI-E-CQ1 Homo sapiens CDNA clone
 DEFINITION UI-E-CQ1-aew-p-23-0-UI 5', mRNA sequence.

UI-H-E20-bay-e-18-0-UI 3', mRNA sequence.

ACCESSION
BQ574092
VERSION
BQ574092.1
KEYWORDS
EST.
SOURCE

ORGANISM
Homo sapiens
human.

REFERENCE

1 (bases 1 to 664)
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of
Orthopedics

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD

POLYA-Yes.

FEATURES

source

Location/Qualifiers

1..664

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="UI-H-E20-bay-e-18-0-UI"

/clone_lib="NCI_CGAP_Ch1"

/tissue_type="Chondrosarcoma Grade II"

/dev_stage="Adult"

/lab_host="PH108 (Life Technologies)"

/note="Organ: Left Pelvis; Vector: pT73-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_Ch1 is a cDNA library containing the following
tissue(s): Chondrosarcoma Grade II. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT73-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
TGATCAGCT.

TAG_LIB=UI-H-E20

TAG_TISSUE=grade-2-chondrosarcoma

TAG_SEQ=ATCTAATG

BASE COUNT 103 a 183 c 226 g 152 t

ORIGIN

Alignment Scores:

Pred. No.: 0.292 Length: 664

Score: 64.00 Matches: 12

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 91.43% Indels: 0

DB: 14 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x BQ574092 (1-664)

QY 2 LeuAnLyAspGlyHisLeuAspGlySerGluVal 13

|||||

Db 662 CTGAACAAGGATGGGACCTGGGATGGGAGTG 627

RESULT 14

AL520513

LOCUS

DEFINITION

AL520513 LTI_NFL004_NBC2 Homo sapiens cDNA clone CS0DB006YC08 5

prime, mRNA sequence.

ACCESSION

AL520513

VERSION

AL520513.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 1005)

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

JOURNAL

COMMENT

Contact: Genoscope

Genoscope - Centre National de Sequencage

Bp 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

source

Location/Qualifiers

1..1005

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CS0DB006YC08"

/clone_lib="LTI_NFL004_NBC2"

/sex="male"

/tissue_type="neuroblastoma cells"

/lab_host="DH10B"

/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
9371 Email : fliang@lifetech.com.URL :
<http://fulllength.invitrogen.com>"

BASE COUNT 221 a 250 c 359 g 150 t

ORIGIN

Alignment Scores:

Pred. No.: 0.53 Length: 1005

Score: 64.00 Matches: 12

Percent Similarity: 92.31% Conservative: 0

Best Local Similarity: 92.31% Mismatches: 1

Query Match: 91.43% Indels: 0

DB: 9 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x AL520513 (1-1005)

QY 1 AspLeuAnLyAspGlyHisLeuAspGlySerGluVal 13

|||||

Db 784 GATCTGAACAGGATGGGACCTGGGATGGGAGTG 822

RESULT 15

AA239568

LOCUS

DEFINITION

AA239568 mv22b09.r1 GuayWoodford Beiler mouse kidney day 0 Mus musculus cDNA

clone IMAGE:65769 5' similar to gb:D13003 Mus musculus

reticulocalbin mRNA, complete cds (MOUSE);, mRNA sequence.

ACCESSION

AA239568

KEYWORDS

EST.

SOURCE

house mouse.

ORGANISM

Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Willie, T., Lennon, G., Soares, B., Wilson, R. and

Waterston, R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

JOURNAL

COMMENT

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:401617
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 260.
Location/Qualifiers
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-5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' Library provided
Lisa Guay-Woodford."

BASE COUNT 79 a 96 c 109 g 57 t
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Db 64 GATCTGAACAAGGACGGCGGCGACTGGATGGCAGTGAAGTC 102

Search completed: May 20, 2003, 07:32:14
Job time : 1764 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003. CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 19, 2003, 22:09:51 ; Search time 55 Seconds
(without alignments)
72.487 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

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Maximum Match 100%
Listing first 45 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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and is derived by analysis of the total score distribution.

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4	70	100.0	1463	4	US-09-270-270-2
5	70	100.0	1490	4	US-09-484-970B-53
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7	43	61.4	531	4	US-09-404-879A-5
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9	43	61.4	1613	4	US-09-061-154-3
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c 16	40	57.1	1308	3	US-09-023-339-6	Sequence 6, Appl1
c 17	40	57.1	1463	4	US-09-399-913-1	Sequence 1, Appl1
c 18	40	57.1	1463	4	US-09-298-731-1	Sequence 1, Appl1
c 19	40	57.1	1534	4	US-09-399-913-7	Sequence 7, Appl1
c 20	40	57.1	1534	4	US-09-298-731-7	Sequence 7, Appl1
c 21	40	57.1	1540	4	US-09-399-913-9	Sequence 9, Appl1
c 22	40	57.1	1540	4	US-09-298-731-9	Sequence 9, Appl1
c 23	40	57.1	1856	4	US-09-399-913-3	Sequence 3, Appl1
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c 30	40	57.1	14255	1	US-08-306-691B-55	Sequence 55, Appl1
c 31	40	57.1	14255	3	US-08-545-860D-1	Sequence 1, Appl1
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c 34	39	55.7	942	4	US-09-134-001C-1534	Sequence 1534, Ap
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c 37	39	55.7	1496	3	US-09-048-889-9	Sequence 9, Appl1
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c 43	39	55.7	2062	5	PCT-US95-13661-3	Sequence 3, Appl1
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ALIGNMENTS

RESULT 1
US-08-828-242-2
; Sequence 2, Application US/08828242
; Patent No. 5871970
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,242
; FILING DATE: Filed Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0261 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1055 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: CONTUT01
CLONE: 2509570
US-08-828-242-2

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

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Db 793 GATCTGAACAAGGATGGCCACCTGGATGGAGTGAGTG 831

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Sequence 2, Application US/09206499
Patent No. 6194385
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL CALCIUM-BINDING
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/206,499
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,242
FILING DATE: 03/31/1997
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0261 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1055 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: CONTUT01
CLONE: 2509570
US-09-206-499-2

Alignment Scores:
Pred. No.: 0.000118 Length: 1055
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Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

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US-09-768-840-1_COPY_254_266 (1-13) x US-09-206-499-2 (1-1055)

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RESULT 3
US-08-910-927B-2
Sequence 2, Application US/08910927B
Patent No. 5976801
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,927B
FILING DATE: Hereewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0358 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1463 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: RAYNOT02
CLONE: 922578
US-08-910-927B-2

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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RESULT 4
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; Sequence 2, Application US/09270270
; Patent No. 6235477
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/270,270
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/910,927
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0358 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1463 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: RATRNOT02
; CLONE: 922578
US-09-270-270-2

Alignment Scores:
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Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 4

US-09-768-840-1_COPY_254_266 (1-13) x US-09-270-270-2 (1-1463)
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RESULT 5
US-09-484-970B-53
; Sequence 53, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkmuth, Wayne
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484,970B
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PERL Program
; SEQ ID NO 53
; LENGTH: 1490
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6426186 016193.3
; NAME/KEY: unsure
; LOCATION: 25
; OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-53

Alignment Scores:
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 4

US-09-768-840-1_COPY_254_266 (1-13) x US-09-484-970B-53 (1-1490)
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RESULT 6
US-09-404-879A-60
; Sequence 60, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-404-879A-60

Alignment Scores:
Pred. No.: 7.3 Length: 480
Score: 43.00 Matches: 8
Percent Similarity: 75.00% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 3
Query Match: 61.43% Indels: 0
Gaps: 0
DB: 4

US-09-768-840-1_COPY_254_266 (1-13) x US-09-404-879A-60 (1-480)
Qy 1 AspleuAsnLysAspGlyHisLeuAspGlySerGlu 12
Db 209 GATCTGAACAAGGATGGGAAGATGGACCAAGAG 244

RESULT 7
US-09-404-879A-5
; Sequence 5, Application US/09404879A

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; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 531
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-404-879A-5

Alignment Scores:
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Score: 43.00 Matches: 8
Percent Similarity: 75.00% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 3
Query Match: 61.43% Indels: 0
DB: 4 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x US-09-404-879A-5 (1-531)
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RESULT 8
US-09-061-154-1/c
; Sequence 1, Application US/09061154
; Patent No. 6462188
; GENERAL INFORMATION:
; APPLICANT: Kirkness, E.
; TITLE OF INVENTION: NEW HUMAN 5-HT3 RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/061,154
; FILING DATE: 16-APR-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24366-20001.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1613 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 67...1389
; OTHER INFORMATION:
US-09-061-154-3

Alignment Scores:
Pred. No.: 30.4 Length: 1613
Score: 43.00 Matches: 7
Percent Similarity: 81.82% Conservative: 2
Best Local Similarity: 63.64% Mismatches: 2
Query Match: 61.43% Indels: 0
DB: 4 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x US-09-061-154-1 (1-1613)
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|||||
Db 1008 AACCAAGAGGCCATGCAGATGGTGAAGAAGTG 976

RESULT 9
US-09-061-154-3/c
; Sequence 3, Application US/09061154
; Patent No. 6462188
; GENERAL INFORMATION:
; APPLICANT: Kirkness, E.
; TITLE OF INVENTION: NEW HUMAN 5-HT3 RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/061,154
; FILING DATE: 16-APR-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24366-20001.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1613 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 67...1389
; OTHER INFORMATION:
US-09-061-154-3

Alignment Scores:
Pred. No.: 30.4 Length: 1613
Score: 43.00 Matches: 7
Percent Similarity: 81.82% Conservative: 2
Best Local Similarity: 63.64% Mismatches: 2
Query Match: 61.43% Indels: 0
DB: 4 Gaps: 0
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RESULT 13
US-09-023-339-3/c
; Sequence 3, Application US/09023339
; Patent No. 6127145
; GENERAL INFORMATION:
; APPLICANT: Sutliff, Thomas D.
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: Production of '1-Antitrypsin
; TITLE OF INVENTION: In Plants
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates

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;; STREET: P.O. Box 50850
;; CITY: Palo Alto
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94306
;;
;; COMPUTER READABLE FORM:
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSEQ for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/023,339
;; FILING DATE: 13-FEB-1998
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/037,991
;; FILING DATE: 13-FEB-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Petithory, Joanne R
;; REGISTRATION NUMBER: P42,995
;; REFERENCE/DOCKET NUMBER: 0665-0003.30
;; TELEPHONE: 650-324-0880
;; TELEFAX: 650-324-0960
;; INFORMATION FOR SEQ ID NO: 3:
;; LENGTH: 1185 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; CLONE: codon-optimized AAT coding sequence
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;; US-09-023-339-3
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;; Alignment Scores:
;; Pred. No.: 79.9 Length: 1185
;; Score: 40.00 Matches: 7
;; Percent Similarity: 80.00% Conservative: 1
;; Best Local Similarity: 70.00% Mismatches: 2
;; Query Match: 57.14% Indels: 0
;; DB: 3 Gaps: 0
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;; US-09-768-840-1_COPY_254_266 (1-13) x US-09-023-339-3 (1-1185)
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;; QY 1 AspleuAsnLysAspGlyHisLeuAspGly 10
;; ||||| ::||| |||||
;; Db 1092 GACCTCGGCGGATGGACATGGGGATGGC 1063
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;; RESULT 14
;; US-09-023-173-5/c
;; Sequence 5, Application US/09023173
;; Patent No. 6066781
;; GENERAL INFORMATION:
;; APPLICANT: Sutliff, Thomas D.
;; APPLICANT: Rodriguez, Raymond L.
;; TITLE OF INVENTION: Production of Mature Proteins
;; TITLE OF INVENTION: in Plants
;; NUMBER OF SEQUENCES: 23
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Dehlinger & Associates
;; STREET: 350 Cambridge Ave., Suite 250
;; CITY: Palo Alto
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94306
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSEQ for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/023,173
;; FILING DATE: 13-FEB-1998
;; CLASSIFICATION: 435
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;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/038,168
;; FILING DATE: 13-FEB-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Petithory, Joanne R
;; REGISTRATION NUMBER: P42995
;; REFERENCE/DOCKET NUMBER: 0665-0007.30
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650-324-0880
;; TELEFAX: 650-324-0960
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1260 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; CLONE: codon-optimized Ramy3D signal-mature AAT
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;; US-09-023-173-5
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;; Alignment Scores:
;; Pred. No.: 85.9 Length: 1260
;; Score: 40.00 Matches: 7
;; Percent Similarity: 80.00% Conservative: 1
;; Best Local Similarity: 70.00% Mismatches: 2
;; Query Match: 57.14% Indels: 0
;; DB: 3 Gaps: 0
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;; US-09-768-840-1_COPY_254_266 (1-13) x US-09-023-173-5 (1-1260)
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;; ||||| ::||| |||||
;; Db 1167 GACCTCGGCGGATGGACATGGGGATGGC 1138
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;; RESULT 15
;; US-09-023-173-10/c
;; Sequence 10, Application US/09023173
;; Patent No. 6066781
;; GENERAL INFORMATION:
;; APPLICANT: Sutliff, Thomas D.
;; APPLICANT: Rodriguez, Raymond L.
;; TITLE OF INVENTION: Production of Mature Proteins
;; TITLE OF INVENTION: in Plants
;; NUMBER OF SEQUENCES: 23
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Dehlinger & Associates
;; STREET: 350 Cambridge Ave., Suite 250
;; CITY: Palo Alto
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94306
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSEQ for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/023,173
;; FILING DATE: 13-FEB-1998
;; CLASSIFICATION: 435
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/038,168
;; FILING DATE: 13-FEB-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Petithory, Joanne R
;; REGISTRATION NUMBER: P42995
;; REFERENCE/DOCKET NUMBER: 0665-0007.30
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650-324-0880
;; TELEFAX: 650-324-0960
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1308 base pairs
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: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
US-09-023-173-10
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Pred. No.: 89.8 Length: 1308
Score: 40.00 Matches: 7
Percent Similarity: 80.00% Conservative: 1
Best Local Similarity: 70.00% Mismatches: 2
Query Match: 57.14% Indels: 0
DB: 3 Gaps: 0
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Qy 1 AspLeuAsnLysAspGlyHisLeuAspGly 10
Db 1208 GACCTCGGGCGGGATGGACATGGGATGGC 1179
Search completed: May 20, 2003, 07:33:30
Job time : 68 secs

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GenCore version 5.1.4.p5.4578
Copyright (C) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 19, 2003, 22:09:52 ; Search time 714 Seconds
(without alignments)
24.042 Million cell updates/sec

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Perfect score: 70
Sequence: 1 DLNKGHLDGSEV 13

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 828747 seqs, 660231138 residues

Total number of hits satisfying chosen parameters: 1657494

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=PublishedApplications_NA -OFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09768840 -CGN_1_1_130 -runat_14052003_095714_16679
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_NA:

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6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70	100.0	1055	10	US-09-768-840-2
2	70	100.0	1463	10	US-09-847-809A-2
3	70	100.0	1503	9	US-09-905-291A-220
4	70	100.0	1503	9	US-09-902-853-220
					Sequence 2, Appli
					Sequence 2, Appli
					Sequence 220, App
					Sequence 220, App

5	70	100.0	1503	9	US-09-907-824-220	Sequence 220, App
6	70	100.0	1503	9	US-09-907-841-220	Sequence 220, App
7	70	100.0	1503	9	US-09-904-011-220	Sequence 220, App
8	70	100.0	1503	9	US-10-028-072-363	Sequence 363, App
9	70	100.0	1503	9	US-09-906-742-220	Sequence 220, App
10	70	100.0	1503	9	US-10-121-049-363	Sequence 363, App
11	70	100.0	1503	9	US-10-123-904-363	Sequence 363, App
12	70	100.0	1503	9	US-10-140-470-363	Sequence 363, App
13	70	100.0	1503	9	US-09-906-838-220	Sequence 220, App
14	70	100.0	1503	9	US-09-907-613-220	Sequence 220, App
15	70	100.0	1503	9	US-09-907-942-220	Sequence 220, App
16	70	100.0	1503	9	US-10-175-748-363	Sequence 363, App
17	70	100.0	1503	9	US-10-176-918-363	Sequence 363, App
18	70	100.0	1503	9	US-10-176-921-363	Sequence 363, App
19	70	100.0	1503	9	US-10-137-863-363	Sequence 363, App
20	70	100.0	1503	9	US-10-140-474-363	Sequence 363, App
21	70	100.0	1503	9	US-09-904-820-220	Sequence 220, App
22	70	100.0	1503	9	US-09-904-859-220	Sequence 220, App
23	70	100.0	1503	9	US-09-909-204-220	Sequence 220, App
24	70	100.0	1503	9	US-10-142-431-363	Sequence 363, App
25	70	100.0	1503	9	US-10-143-114-363	Sequence 363, App
26	70	100.0	1503	9	US-09-904-786-220	Sequence 220, App
27	70	100.0	1503	9	US-09-906-646-220	Sequence 220, App
28	70	100.0	1503	9	US-09-906-700-220	Sequence 220, App
29	70	100.0	1503	9	US-10-140-002-363	Sequence 363, App
30	70	100.0	1503	9	US-09-902-903-220	Sequence 220, App
31	70	100.0	1503	9	US-09-903-749A-220	Sequence 220, App
32	70	100.0	1503	9	US-09-903-786-220	Sequence 220, App
33	70	100.0	1503	9	US-10-142-419-363	Sequence 363, App
34	70	100.0	1503	9	US-09-902-736-220	Sequence 220, App
35	70	100.0	1503	9	US-09-904-119-220	Sequence 220, App
36	70	100.0	1503	9	US-09-904-956-220	Sequence 220, App
37	70	100.0	1503	9	US-09-907-794-220	Sequence 220, App
38	70	100.0	1503	9	US-10-123-262-363	Sequence 363, App
39	70	100.0	1503	9	US-10-142-423-363	Sequence 363, App
40	70	100.0	1503	9	US-09-903-692-220	Sequence 220, App
41	70	100.0	1503	9	US-09-903-520-220	Sequence 220, App
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43	70	100.0	1503	9	US-09-904-462-220	Sequence 220, App
44	70	100.0	1503	9	US-09-905-056-220	Sequence 220, App
45	70	100.0	1503	9	US-09-907-925-220	Sequence 220, App

ALIGNMENTS

RESULT 1
US-09-768-840-2
; Sequence 2, Application US/09768840
; Patent No. US20010012831A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09768,840
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/206,499

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; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
;   NAME: Billings, Lucy J.
;   REGISTRATION NUMBER: 36,749
;   REFERENCE/DOCKET NUMBER: PF-0261 US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-855-0555
;   TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1055 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; IMMEDIATE SOURCE:
;   LIBRARY: CONTU01
;   CLONE: 2509570
; US-09-768-840-2
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; Alignment Scores:
; Pred. No.: 0.000101 Length: 1055
; Score: 70.00 Matches: 13
; Percent Similarity: 100.00% Conservative: 0
; Best Local Similarity: 100.00% Mismatches: 0
; Query Match: 100.00% Indels: 0
; DB: 10 Gaps: 0
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; Db 793 GATCTGAACAAGGATGGCCACCTGGATGGAGTGAGGTG 831
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; RESULT 2
; US-09-847-809A-2
; Sequence 2, Application US/09847809A
; Patent No. US20020081604A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Hillman, Jennifer L.
; Lal, Preeti
; Corley, Neil C.
; Shah, Purvi
;
; TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 01-May-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/270,270
; FILING DATE: 1999-03-16
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0358 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1463 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; IMMEDIATE SOURCE:
;   LIBRARY: RATNOT02
;   CLONE: 922578
; US-09-847-809A-2
;
; Alignment Scores:
; Pred. No.: 0.000147 Length: 1463
; Score: 70.00 Matches: 13
; Percent Similarity: 100.00% Conservative: 0
; Best Local Similarity: 100.00% Mismatches: 0
; Query Match: 100.00% Indels: 0
; DB: 10 Gaps: 0
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; US-09-768-840-1_COPY_254_266 (1-13) x US-09-847-809A-2 (1-1463)
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; Db 808 GATCTGAACAAGGATGGCCACCTGGATGGAGTGAGGTG 846
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; RESULT 3
; US-09-905-291A-220
; Sequence 220, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; FILE REFERENCE: Acids Encoding the Same
; CURRENT APPLICATION NUMBER: US/09/905,291A
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2001-07-12
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
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;; TITLE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: 10466-14
;; CURRENT APPLICATION NUMBER: US/09/902,853
;; PRIOR FILING DATE: 2001-07-10
;; PRIOR APPLICATION NUMBER: US/09/665,350
;; PRIOR FILING DATE: 2000-09-18
;; PRIOR APPLICATION NUMBER: US 60/143,048
;; PRIOR FILING DATE: 1999-07-07
;; PRIOR APPLICATION NUMBER: US 60/145,698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: US 60/146,222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/20944
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 220
;; LENGTH: 1503
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-905-291A-220

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Pred. No.: 0.000151 Length: 1503
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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Db 794 GATCTGACAGAGTGGGCACCTGGATGGAGTGAGGTG 832

RESULT 4

US-09-902-853-220
; Sequence 220, Application US/0902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

;; TITLE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: 10466-14
;; CURRENT APPLICATION NUMBER: US/09/902,853
;; PRIOR FILING DATE: 2001-07-10
;; PRIOR APPLICATION NUMBER: US/09/665,350
;; PRIOR FILING DATE: 2000-09-18
;; PRIOR APPLICATION NUMBER: US 60/143,048
;; PRIOR FILING DATE: 1999-07-07
;; PRIOR APPLICATION NUMBER: US 60/145,698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: US 60/146,222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/20944
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 220
;; LENGTH: 1503
;; TYPE: DNA
;; ORGANISM: Homo Sapien
US-09-902-853-220

Alignment Scores:
Pred. No.: 0.000151 Length: 1503
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-768-840-1_copy_254_266 (1-13) x US-09-902-853-220 (1-1503)

Oy 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
|||||
Db 794 GATCTGAACAAGGATGGGCACCTGGATGGAGTGAGGTG 832

RESULT 5

US-09-907-824-220
; Sequence 220, Application US/09907824
; Publication No. US20020197671A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,824
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 220
LENGTH: 1503
TYPE: DNA
ORGANISM: Homo Sapien
US-09-907-824-220

Alignment Scores:
Pred. No.: 0.000151 Length: 1503
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x US-09-907-824-220 (1-1503)

QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
|||||
Db 794 GATCTCAACAAGGATGGCACCTGGATGGAGTGGAGTG 832

RESULT 6
US-09-907-841-220
; Sequence 220, Application US/09907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,841
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 220
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-841-220

Alignment Scores:
Pred. No.: 0.000151 Length: 1503
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0


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Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-768-840-1_COPY_254_266 (1-13) x US-09-907-841-220 (1-1503)
Qy 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
Db 794 GATCTGAACAAGGATGGGCACCTGGATGGAGTGAGGTG 832
RESULT 7
US-09-904-011-220
; Sequence 220, Application US/09904011
; Publication No. US20030003530A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,011
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
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; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 220
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-904-011-220
Alignment Scores:
Pred. No.: 0.000151 Length: 1503
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-768-840-1_COPY_254_266 (1-13) x US-09-904-011-220 (1-1503)
Qy 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
Db 794 GATCTGAACAAGGATGGGCACCTGGATGGAGTGAGGTG 832
RESULT 8
US-10-028-072-363
; Sequence 363, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/028,072
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
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PRIOR APPLICATION NUMBER: 60/079294	PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079663	PRIOR FILING DATE: 1998-02-27
PRIOR APPLICATION NUMBER: 60/079728	PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/080165	PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/081203	PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229	PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081695	PRIOR FILING DATE: 1998-04-14
PRIOR APPLICATION NUMBER: 60/081817	PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081818	PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082999	PRIOR FILING DATE: 1998-04-24
PRIOR APPLICATION NUMBER: 60/083322	PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083545	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/084600	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084637	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085149	PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/085323	PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338	PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085339	PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085579	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086414	PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/086430	PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087106	PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/088026	PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088730	PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088741	PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810	PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858	PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089532	PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599	PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089907	PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947	PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090349	PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429	PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445	

;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090538
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07

Alignment Scores:
Pred. No.: 0.000151 Length: 1503
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x US-10-028-072-363 (1-1503)

QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13

Db 794 GATCTGAACAGGATGGGCACCTGGATGGAGTGAGGTG 832

RESULT 9

US-09-906-742-220
;; Sequence 220, Application US/09906742
;; Publication No. US20030023054A1
;; GENERAL INFORMATION:

;; APPLICANT: Genentech, Inc.
;; APPLICANT: Ashkenazi, Avi
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, A.
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, Christopher J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth, J.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Mather, Jennie P.
;; APPLICANT: Pan, James
;; APPLICANT: Paonl, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William, I.

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; TITLE OF INVENTION: Acids Encoding the Same

;; FILE REFERENCE: 10466-14

;; CURRENT APPLICATION NUMBER: US/09/906,742

;; PRIOR FILING DATE: 2001-07-16

;; PRIOR APPLICATION NUMBER: 09/665,350

;; PRIOR FILING DATE: 2000-09-18

;; PRIOR APPLICATION NUMBER: PCT/US00/04414

;; PRIOR FILING DATE: 2000-07-22

;; PRIOR APPLICATION NUMBER: US 60/143,048

;; PRIOR FILING DATE: 1999-07-07

;; PRIOR APPLICATION NUMBER: US 60/145,698

;; PRIOR FILING DATE: 1999-07-26

;; PRIOR APPLICATION NUMBER: US 60/146,222

;; PRIOR FILING DATE: 1999-07-28

;; PRIOR APPLICATION NUMBER: PCT/US99/20594

;; PRIOR FILING DATE: 1999-09-08

;; PRIOR APPLICATION NUMBER: PCT/US99/20944
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 220
;; LENGTH: 1503
;; TYPE: DNA
;; ORGANISM: Homo Sapien
US-09-906-742-220

Alignment Scores:
Pred. No.: 0.000151 Length: 1503
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x US-09-906-742-220 (1-1503)

QY 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13

Db 794 GATCTGAACAGGATGGGCACCTGGATGGAGTGAGGTG 832

RESULT 10

US-10-121-049-363

;; Sequence 363, Application US/10121049

;; Publication No. US2003002239A1

;; GENERAL INFORMATION:

;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Beresini, Maureen
;; APPLICANT: Deforge, Laura
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Sherwood, Steven
;; APPLICANT: Smith, Victoria
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K
;; APPLICANT: Wood, William
;; APPLICANT: Zhang, Zemin

;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

;; TITLE OF INVENTION: ACIDS ENCODING THE SAME

;; FILE REFERENCE: P3330R1C17

;; CURRENT APPLICATION NUMBER: US/10/121,049

;; CURRENT FILING DATE: 2002-04-12

;; Prior Application removed - See File Wrapper or Palm


```

; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,838
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 220
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-906-838-220

Alignment Scores:
Pred. No.: 0.000151 Length: 1503
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-768-840-1_COPY_254_266 (1-13) x US-09-906-838-220 (1-1503)
Qy 1 AspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 13
Db 794 GATCTGAACAGGATGGCACCTGGATGGAGTGAGTG 832

RESULT 14
US-09-907-613-220
; Sequence 220, Application US/09907613
; GENERAL INFORMATION:
; Publication No. US20030027145A1
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David

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; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,613
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 220
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-613-220

Alignment Scores:
Pred. No.: 0.000151 Length: 1503
Score: 70.00 Matches: 13
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0

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Result No.	%			DB	ID	Description
	Score	Match	Length			
1	70	100.0	327	9	US-09-984-245-166	Sequence 166, App
2	70	100.0	327	9	US-09-966-262-166	Sequence 166, App
3	70	100.0	327	9	US-09-983-966-166	Sequence 166, App
4	70	100.0	328	9	US-10-143-090-166	Sequence 166, App
5	70	100.0	328	9	US-09-905-291A-321	Sequence 221, App
6	70	100.0	328	9	US-09-902-853-221	Sequence 221, App
7	70	100.0	328	9	US-09-907-824-221	Sequence 221, App
8	70	100.0	328	9	US-09-907-841-221	Sequence 221, App
9	70	100.0	328	9	US-09-904-011-221	Sequence 221, App
10	70	100.0	328	9	US-10-028-072-364	Sequence 364, App
11	70	100.0	328	9	US-09-906-742-221	Sequence 221, App
12	70	100.0	328	9	US-10-121-049-364	Sequence 364, App
13	70	100.0	328	9	US-10-123-904-364	Sequence 364, App
14	70	100.0	328	9	US-10-140-470-364	Sequence 364, App
15	70	100.0	328	9	US-09-906-838-221	Sequence 221, App
16	70	100.0	328	9	US-09-907-613-221	Sequence 221, App
17	70	100.0	328	9	US-09-907-942-221	Sequence 221, App
18	70	100.0	328	9	US-10-175-746-364	Sequence 364, App
19	70	100.0	328	9	US-10-176-918-364	Sequence 364, App

Tue May 20 14:43:32 2003

us-09-768-840-1_copy_254_266.rapb

; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 166
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (300)
; OTHER INFORMATION: Xaa equals any of the L-amino acids commonly found in naturally
; OTHER INFORMATION: proteins
US-09-984-245-166

Query Match 100.0%; Score 70; DB 9; Length 327;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLNKGHLDGSEV 13
Db 253 DLNKGHLDGSEV 265

RESULT 2
US-09-966-262-166
; Sequence 166, Application US/09966262
; Publication No. US20030050461A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/966,262
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: US 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937

; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,099
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 166
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (300)
; OTHER INFORMATION: Xaa equals any of the L-amino acids commonly found in naturally
; OTHER INFORMATION: proteins
US-09-966-262-166

Query Match 100.0%; Score 70; DB 9; Length 327;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLNKGHLDGSEV 13
Db 253 DLNKGHLDGSEV 265

RESULT 3
US-09-983-966-166
; Sequence 166, Application US/09983966
; Publication No. US20030060619A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/983,966
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21

;; PRIOR APPLICATION NUMBER: US 60/041,281
;; PRIOR FILING DATE: 1997-03-21
;; PRIOR APPLICATION NUMBER: US 60/048,094
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,350
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,188
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,135
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/050,937
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,187
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,099
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,352
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,186
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,069
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,095
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,131
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,096
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,355
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,160
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,351
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/048,154
;; PRIOR FILING DATE: 1997-05-30
;; PRIOR APPLICATION NUMBER: US 60/054,804
;; PRIOR FILING DATE: 1997-08-05
;; PRIOR APPLICATION NUMBER: US 60/056,370
;; PRIOR FILING DATE: 1997-08-19
;; PRIOR APPLICATION NUMBER: US 60/060,862
;; PRIOR FILING DATE: 1997-10-02
;; NUMBER OF SEQ ID NOS: 343
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 166
;; LENGTH: 327
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: MISC_FEATURE
;; LOCATION: (300)
;; OTHER INFORMATION: Xaa equals any of the L-amino acids commonly found in naturally
US-09-983-966-166

Query Match 100.0%; Score 70; DB 9; Length 327;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DLNKGHLGDSV 13
DB 253 DLNKGHLGDSV 265
|||||

RESULT 4
US-10-143-090-166
;; Sequence 166, Application US/10143090
;; Publication No. US20030069406A1
;; GENERAL INFORMATION:
;; APPLICANT: Young et al.
;; TITLE OF INVENTION: 87 Human Secreted Proteins
;; FILE REFERENCE: P2004P1
;; CURRENT APPLICATION NUMBER: US/10/143,090

;; CURRENT FILING DATE: 2002-05-13
;; PRIOR APPLICATION NUMBER: 09/154,707
;; PRIOR FILING DATE: 1998-09-17
;; NUMBER OF SEQ ID NOS: 343
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 166
;; LENGTH: 327
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: MISC_FEATURE
;; LOCATION: (300)
;; OTHER INFORMATION: Xaa equals any of the L-amino acids commonly found in naturally
US-10-143-090-166

Query Match 100.0%; Score 70; DB 9; Length 327;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DLNKGHLGDSV 13
DB 253 DLNKGHLGDSV 265
|||||

RESULT 5
US-09-905-291A-221
;; Sequence 221, Application US/09905291A
;; Patent No. US20020160374A1
;; GENERAL INFORMATION:
;; APPLICANT: Genentech, Inc.
;; APPLICANT: Ashkenazi, Avi
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, A.
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, Christopher J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth, J.
;; APPLICANT: Kijavlin, Ivar J.
;; APPLICANT: Mather, Jennie P.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William, I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: 10466-14
;; CURRENT APPLICATION NUMBER: US/09/905,291A
;; PRIOR FILING DATE: 2001-07-12
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: 2000-02-22
;; PRIOR APPLICATION NUMBER: US 60/143,048
;; PRIOR FILING DATE: 1999-07-07
;; PRIOR APPLICATION NUMBER: US 60/145,698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: US 60/146,222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/20944
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 221
LENGTH: 328
TYPE: PRT
ORGANISM: Homo sapiens
US-09-905-291A-221

Query Match 100.0%; Score 70; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGHLDGSEV 13
Db 254 DLNKGHLDGSEV 266

RESULT 6
US-09-902-853-221
Sequence 221, Application US/09502853
Publication No. US20020192659A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secured and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,853
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US/09/665,350
PRIOR FILING DATE: 2000-09-18

PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 221
LENGTH: 328
TYPE: PRT
ORGANISM: Homo Sapien
US-09-902-853-221

Query Match 100.0%; Score 70; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGHLDGSEV 13
Db 254 DLNKGHLDGSEV 266

RESULT 7
US-09-907-824-221
Sequence 221, Application US/09907824
Publication No. US20020197671A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,824
PRIOR FILING DATE: 2001-07-17
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 221
LENGTH: 328
TYPE: PRT
ORGANISM: Homo Sapien
US-09-907-824-221

Query Match 100.0%; Score 70; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGHLDGSEV 13
DB 254 DLNKGHLDGSEV 266

RESULT 8

US-09-907-841-221
Sequence 221, Application US/09907841
Publication No. US20020198366A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,841
PRIOR FILING DATE: 2001-11-20
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-29
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 221
LENGTH: 328
TYPE: PRT
ORGANISM: Homo sapiens
US-09-907-841-221

Query Match 100.0%; Score 70; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGHLDGSEV 13
DB 254 DLNKGHLDGSEV 266

RESULT 9

US-09-904-011-221
Sequence 221, Application US/09904011
Publication No. US20030003530A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen

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; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,011
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
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; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
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; PRIOR APPLICATION NUMBER: PCT/US99/28214
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; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 221
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-011-221

Query Match 100.0%; Score 70; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGHLDGSEV 13
DB 254 DLNKGHLDGSEV 266
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RESULT 10
US-10-028-072-364
; Sequence 364, Application US/10028072
; Publication NO. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/028,072
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
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; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
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; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
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; PRIOR APPLICATION NUMBER: 60/059836
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; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063327
; PRIOR FILING DATE: 1997-10-27
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; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: 60/063550
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063561
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;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/063704
;; PRIOR FILING DATE: 1997-10-29
;; PRIOR APPLICATION NUMBER: 60/063733
;; PRIOR FILING DATE: 1997-10-29
;; PRIOR APPLICATION NUMBER: 60/063735
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;; PRIOR APPLICATION NUMBER: 60/063738
;; PRIOR FILING DATE: 1997-10-29
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;; PRIOR APPLICATION NUMBER: 60/066770
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;; PRIOR APPLICATION NUMBER: 60/069694
;; PRIOR FILING DATE: 1997-12-16
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;; PRIOR APPLICATION NUMBER: 60/073612
;; PRIOR FILING DATE: 1998-02-04
;; PRIOR APPLICATION NUMBER: 60/074086
;; PRIOR FILING DATE: 1998-02-09
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;; PRIOR FILING DATE: 1998-02-09
;; PRIOR APPLICATION NUMBER: 60/077791
;; PRIOR FILING DATE: 1998-03-12
;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
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;; PRIOR APPLICATION NUMBER: 60/079728
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;; PRIOR APPLICATION NUMBER: 60/081229
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;; PRIOR APPLICATION NUMBER: 60/081695
;; PRIOR FILING DATE: 1998-04-14
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;; PRIOR APPLICATION NUMBER: 60/083322
;; PRIOR FILING DATE: 1998-04-28
;; PRIOR APPLICATION NUMBER: 60/083545
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/084600
;; PRIOR FILING DATE: 1998-05-07

;; PRIOR APPLICATION NUMBER: 60/084627
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084637
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/085149
;; PRIOR FILING DATE: 1998-05-12
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;; PRIOR APPLICATION NUMBER: 60/085339
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/086414
;; PRIOR FILING DATE: 1998-05-22
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;; PRIOR FILING DATE: 19/98-06-11
;; PRIOR APPLICATION NUMBER: 60/089532
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;; PRIOR APPLICATION NUMBER: 60/089599
;; PRIOR FILING DATE: 1998-06-17
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;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089947
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;; PRIOR APPLICATION NUMBER: 60/090429
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;; PRIOR APPLICATION NUMBER: 60/090538
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07

Query Match 100.0%; Score 70; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGHLGDSV 13
|||||
Db 254 DLNKGHLGDSV 266

RESULT 11
US-09-906-742-221
; Sequence 221, Application US/09906742
; Publication No. US2003023054A1
; GENERAL INFORMATION:

APPLICANT: Genentech, Inc.
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, A.
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth, J.
 APPLICANT: Kijavrin, Ivar J.
 APPLICANT: Mather, Jennie P.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William, I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: 10466-14
 CURRENT APPLICATION NUMBER: US/09/906,742
 CURRENT FILING DATE: 2001-07-16
 PRIOR APPLICATION NUMBER: 09/665,350
 PRIOR FILING DATE: 2000-09-18
 PRIOR APPLICATION NUMBER: PCT/US00/04414
 PRIOR FILING DATE: 2000-02-22
 PRIOR APPLICATION NUMBER: US 60/143,048
 PRIOR FILING DATE: 1999-07-07
 PRIOR APPLICATION NUMBER: US 60/145,698
 PRIOR FILING DATE: 1999-07-26
 PRIOR APPLICATION NUMBER: US 60/146,222
 PRIOR FILING DATE: 1999-07-28
 PRIOR APPLICATION NUMBER: PCT/US99/20594
 PRIOR FILING DATE: 1999-09-08
 PRIOR APPLICATION NUMBER: PCT/US99/20944
 PRIOR FILING DATE: 1999-09-13
 PRIOR APPLICATION NUMBER: PCT/US99/21090
 PRIOR FILING DATE: 1999-09-15
 PRIOR APPLICATION NUMBER: PCT/US99/21547
 PRIOR FILING DATE: 1999-09-15
 PRIOR APPLICATION NUMBER: PCT/US99/23089
 PRIOR FILING DATE: 1999-10-05
 PRIOR APPLICATION NUMBER: PCT/US99/28214
 PRIOR FILING DATE: 1999-11-29
 PRIOR APPLICATION NUMBER: PCT/US99/28313
 PRIOR FILING DATE: 1999-11-30
 PRIOR APPLICATION NUMBER: PCT/US99/28564
 PRIOR FILING DATE: 1999-12-02
 PRIOR APPLICATION NUMBER: PCT/US99/28565
 PRIOR FILING DATE: 1999-12-02
 PRIOR APPLICATION NUMBER: PCT/US99/30095
 PRIOR FILING DATE: 1999-12-16
 PRIOR APPLICATION NUMBER: PCT/US99/30911
 PRIOR FILING DATE: 1999-12-20
 PRIOR APPLICATION NUMBER: PCT/US99/30999
 PRIOR FILING DATE: 1999-12-20
 PRIOR APPLICATION NUMBER: PCT/US00/00219
 PRIOR FILING DATE: 2000-01-05
 NUMBER OF SEQ ID NOS: 423
 SEQ ID NO 221
 LENGTH: 328
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-09-906-742-221

Query Match 100.0%; Score 70; DB 9; Length 328;
 Best Local Similarity 100.0%; Pred. No. 0.00034;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLNKGHLDGSEV 13
 DB 254 DLNKGHLDGSEV 266
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 RESULT 12
 US-10-121-049-364
 ; Sequence 364, Application US/10121049
 ; Publication No. US20030022239A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: Deforge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3330R1C17
 ; CURRENT APPLICATION NUMBER: US/10/121,049
 ; CURRENT FILING DATE: 2002-04-12
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 364
 ; LENGTH: 328
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-121-049-364
 Query Match 100.0%; Score 70; DB 9; Length 328;
 Best Local Similarity 100.0%; Pred. No. 0.00034;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGHLDGSEV 13
 DB 254 DLNKGHLDGSEV 266
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 RESULT 13
 US-10-123-904-364
 ; Sequence 364, Application US/10123904
 ; Publication No. US20030022238A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: Deforge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K

```
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC34
; CURRENT APPLICATION NUMBER: US/10/123,904
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 364
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-904-364

Query Match      100.08; Score 70; DB 9; Length 328;
Best Local Similarity 100.08; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGHLDGSEV 13
Db 254 DLNKGHLDGSEV 266

RESULT 14
US-10-140-470-364
; Sequence 364, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC160
; CURRENT APPLICATION NUMBER: US/10/140,470
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 364
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-470-364

Query Match      100.08; Score 70; DB 9; Length 328;
Best Local Similarity 100.08; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGHLDGSEV 13
Db 254 DLNKGHLDGSEV 266

RESULT 15
US-09-906-838-221
; Sequence 221, Application US/09906838
; Publication No. US20030027143A1
; GENERAL INFORMATION:
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; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavir, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,838
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
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; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 221
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-838-221
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us-09-768-840-1_copy_254_266.rapb

Tue May 20 14:43:32 2003

Query Match 100.0%; Score 70; DB 9; Length 328;
 Best Local Similarity 100.0%; Pred. No. 0.00034;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLNKGHLDGSEV 13
 | | | | | | | | | | | | | | |
 Db 254 DLNKGHLDGSEV 266

Search completed: May 14, 2003, 10:47:54
 Job time : 1.25806 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 14, 2003, 10:40:07 ; Search time 4.1173 Seconds
(without alignments)
650.575 Million cell updates/sec

Title: us-09-768-840-1_copy_254_266

Perfect score: 70

Sequence: 1 DLNKGHLGSGEV 13

Scoring table:

BLOSUM62

Gap 10.0 , Gapext 0.5

Searched: 671580 seqs, 205047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70	100.0	328	4 Q9HBZ8	Q9hbz8 homo sapien
2	70	100.0	328	4 Q96D15	Q96d15 homo sapien
3	62	88.6	259	11 Q9CTD4	Q9ctd4 mus musculus
4	62	88.6	315	11 Q99K35	Q99k35 mus musculus
5	62	88.6	328	11 Q8R137	Q8r137 mus musculus
6	48	68.6	384	4 Q96NQ4	Q96nq4 homo sapien
7	48	68.6	482	4 Q9BVC2	Q9bvc2 homo sapien
8	47	67.1	599	11 Q91WH8	Q91wh8 mus musculus
9	47	67.1	864	4 Q3UBC2	Q3ubc2 homo sapien
10	47	67.1	907	11 Q60902	Q60902 mus musculus
11	46	65.7	127	5 Q22159	Q22159 caenorhabdi
12	45	64.3	289	16 Q9PM44	Q9pm44 campylobact
13	44	62.9	322	13 Q93434	Q93434 fugu rubrip
14	44	62.9	343	5 Q9U460	Q9u460 plasmodium
15	44	62.9	592	2 Q9RDT6	Q9rdt6 rhodospiril
16	44	62.9	737	2 Q9EYQ5	Q9eyq5 clostridium

17	43	61.4	163	13	012996	O12996 xenopus lae
18	43	61.4	163	13	012997	O12997 xenopus lae
19	43	61.4	236	5	076670	076670 caenorhabdi
20	43	61.4	666	10	Q8VZP8	Q8vzp8 arabidopsis
21	43	61.4	756	2	Q92NN6	Q92nn6 bacillus sp
22	43	61.4	1181	10	Q9X116	Q9x116 arabidopsis
23	42	60.0	142	10	064866	064866 arabidopsis
24	42	60.0	186	5	Q20796	Q20796 caenorhabdi
25	42	60.0	189	13	Q90WX4	Q90wx4 brachydanio
26	42	60.0	189	13	Q8UWA4	Q8uwa4 oryzias lat
27	42	60.0	189	13	Q8UUY1	Q8uyy1 brachydanio
28	42	60.0	189	13	Q8QFN1	Q8qfn1 fugu rubrip
29	42	60.0	192	5	Q9W0H8	Q9w0h8 drosophila
30	42	60.0	193	5	Q96051	Q96051 drosophila
31	42	60.0	329	5	Q8SZK6	Q8szk6 arabidopsis
32	42	60.0	493	10	Q9ASV9	Q9asv9 arabidopsis
33	42	60.0	574	10	Q9MAH9	Q9mah9 arabidopsis
34	42	60.0	1636	16	Q9PEL7	Q9pel7 xylella fas
35	42	60.0	1779	5	Q9VM49	Q9vm49 drosophila
36	41	58.6	169	5	Q966R1	Q966r1 dictyosteli
37	41	58.6	231	16	Q98N90	Q98n90 thizobium l
38	41	58.6	282	16	Q9PP67	Q9pp67 campylobact
39	41	58.6	322	5	Q93136	Q93136 bombyx mori
40	41	58.6	343	5	Q25793	Q25793 plasmodium
41	41	58.6	411	4	Q9P129	Q9p129 homo sapien
42	41	58.6	475	6	Q18757	Q18757 oryctolagus
43	41	58.6	571	5	Q966F0	Q966f0 caenorhabdi
44	41	58.6	576	5	Q9BIJ4	Q9bij4 caenorhabdi
45	41	58.6	589	5	Q9N5B9	Q9n5b9 caenorhabdi

ALIGNMENTS

RESULT 1

Q9HBZ8
ID Q9HBZ8 PRELIMINARY; PRT; 328 AA.
AC Q9HBZ8;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Reticulocabin.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HYPOPHALAMUS;
RA Peng Y., Gu Y., Huang C., Xu S., Han Z., Fu G., Chen Z.;
RT "A novel gene expressed in human hypothalamus.";
RL Submitted (SEP1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF183423; AAG09692.1; -
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000886; EF-hand.
DR Pfam; PF00036; ehand; 4.
DR SMART; SM00054; EFh; 3.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
DR PROSITE; PS00014; EF_TARGET; UNKNOWN_1.
SQ SEQUENCE 328 AA; 37424 MW; 9D23648795D3C670 CRC64;

Query Match 100.0%; Score 70; DB 4; Length 328;

Best Local Similarity 100.0%; Pred. No. 0.00085;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGHLGSGEV 13

Db 254 DLNKGHLGSGEV 266

RESULT 2

Q96D15

ID Q96D15 PRELIMINARY; PRT; 328 AA.

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AC Q96D15;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 37.5 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013436; AAH13436.1;
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 5.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 328 AA; 37493 MW; B64EDB28B9610B8D CRC64;

Query Match 100.0%; Score 70; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.00085;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGDLGSEV 13
DB 254 DLNKGDLGSEV 266
|||||
RESULT 3
O9CTD4 PRELIMINARY; PRT; 259 AA.
AC Q9CTD4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 6030455P07RIK.
GN 6030455P07RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RC MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Nikola I., Pesole G., Quackenbush J.,
RA Kiehl P., Lewis S., Matsuo S., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Stauble F., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann W., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK003918; BAB23076.1;
DR MGD; MGI:1915346; 6030455P07RIK.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000886; ER_target.

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Pfam; PF00036; ehand; 4.
DR SMART; SM00054; EPH; 3.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 259 AA; 31063 MW; 7910A9F0476260A1 CRC64;

Query Match 88.6%; Score 62; DB 11; Length 259;
Best Local Similarity 92.3%; Pred. No. 0.015;
Matches 12; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY 1 DLNKGDLGSEV 13
DB 185 DLNKGDLGSEV 197
|||||
RESULT 4
O99K35 PRELIMINARY; PRT; 315 AA.
AC O99K35;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to hypothetical protein LOC57333 (Fragment).
GN 6030455P07RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005487; AAH05487.1;
DR MGD; MGI:1915346; 6030455P07RIK.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00036; ehand; 4.
DR SMART; SM00054; EPH; 3.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 315 AA; 36269 MW; CECB4DAEE54D24E4 CRC64;

Query Match 88.6%; Score 62; DB 11; Length 315;
Best Local Similarity 92.3%; Pred. No. 0.018;
Matches 12; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY 1 DLNKGDLGSEV 13
DB 241 DLNKGDLGSEV 253
|||||
RESULT 5
O8R137 PRELIMINARY; PRT; 328 AA.
AC O8R137;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to hypothetical protein LOC57333.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025602; AAH25602.1;
KW Hypothetical protein.
SQ SEQUENCE 328 AA; 37973 MW; 913F5C6F0F88B316 CRC64;

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Query Match 88.6%; Score 62; DB 11; Length 328;
Best Local Similarity 92.3%; Pred. No. 0.019;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DLNKGHLDGSEV 13
DB 254 DLNKGHLDGSEV 266

RESULT 6

ID Q96NQ4 PRELIMINARY; PRT; 384 AA.
AC Q96NQ4;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE CDNA FLJ30339 fis, clone BRACE2007401, moderately similar to
DE Oryctolagus cuniculus peroxisomal Ca-dependent solute carrier
DE mRNA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CEREBELLUM;
RA Toshiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
RA Izogai T.;
RT "NEDO human cDNA sequencing project";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK054901; BAB70825.1;
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam; PF00036; efhand; 2.
DR Pfam; PF00153; mito_carr; 3.
DR ProDom; PD000012; EF-hand; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
SQ SEQUENCE 384 AA; 43018 MW; 33973A38D1F9BC5E CRC64;

Query Match 68.6%; Score 48; DB 4; Length 384;
Best Local Similarity 61.5%; Pred. No. 5.3;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 DLNKGHLDGSEV 13
DB 6 DRNQGHDVSEI 18

RESULT 7

ID Q9BV35 PRELIMINARY; PRT; 482 AA.
AC Q9BV35;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 54.0 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EYE;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC001656; AAH01656.1;

DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002087; Mit_carrier.
DR Pfam; PF00036; efhand; 3.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR ProDom; PD000012; EF-hand; 1.
DR SMART; SM00054; EPH; 3.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 482 AA; 54035 MW; 8917BEA2BC2FB42B CRC64;

Query Match 68.6%; Score 48; DB 4; Length 482;
Best Local Similarity 61.5%; Pred. No. 6.7;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 DLNKGHLDGSEV 13
DB 90 DRNQGHDVSEI 102

RESULT 8

ID Q91WH8 PRELIMINARY; PRT; 599 AA.
AC Q91WH8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Similar to epidermal growth factor receptor pathway substrate 15,
DE related sequence.
GN EPS15-RS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015259; AAH15259.1;
DR MGD; MGI:104582; Eps15-rs.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR000261; EPS15-repeat.
DR Pfam; PF00036; efhand; 4.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 599 AA; 66206 MW; B62762A063F21FA9 CRC64;

Query Match 67.1%; Score 47; DB 11; Length 599;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 DLNKGHLDGSE 12
DB 172 DIDKGDHLDRE 183

RESULT 9

ID Q9UBC2 PRELIMINARY; PRT; 864 AA.
AC Q9UBC2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Epidermal growth factor receptor substrate EPS15R.
GN EPS15R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE=BRAIN;
RA Nakashima S., Morinaka K., Ikeda M., Kishida S., Koyama S.,
RL Kikuchi A.;
RN Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Ueki N.;
RL "HRI NTT human fetal brain cDNA Project.";
RN Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN EMBL; AF110265; AAF21930.1;
DR EMBL; AB015346; BAA88118.1;
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000261; EPS15_repeat.
DR Pfam; PF00036; ehand; 4.
DR SMART; SM00054; EFh; 3.
DR SMART; SM00027; EH; 3.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 864 AA; 94254 MW; F4126069F6E00387 CRC64;

Query Match 67.1%; Score 47; DB 47; Length 864;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DLNKGHLDGSE 12
Db 172 DIDKDGHLDRDE 183

RESULT 10
Q60902 PRELIMINARY; PRT; 907 AA.
AC Q60902;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-2002 (TrEMBLrel. 20, Last annotation update)
DE Eps15R protein.
GN Eps15-RS OR EPS15R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE;
RX MEDLINE=96003812; PubMed=7568168;
RA Wong W.T., Schumacher C., Salscini A.E., Romano A., Castagnino P.,
RA Pellicci P.G., Di Fiore P.;
RT "A protein-binding domain, EH, identified in the receptor tyrosine
RT kinase substrate Eps15 and conserved in evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:9530-9534(1995).
DR EMBL; U29156; AAA87202.1;
DR MGD; MGI:104582; Eps15-rs.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000261; EPS15_repeat.
DR InterPro; IPR003903; UIM.
DR Pfam; PF00036; ehand; 4.
DR SMART; SM00054; EFh; 3.
DR SMART; SM00027; EH; 3.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
SQ SEQUENCE 907 AA; 99320 MW; 2FA79DFBAC834E1E CRC64;

Query Match 67.1%; Score 47; DB 11; Length 907;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DLNKGHLDGSE 12
Db 172 DIDKDGHLDRDE 183

RESULT 11

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```

Q22159 PRELIMINARY; PRT; 127 AA.
AC Q22159;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE T04F3.4 protein.
GN T04F3.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Kershaw J.K.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z72513; CAA96671.2;
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_2.
SQ SEQUENCE 127 AA; 14704 MW; 40CE9A863ADE694 CRC64;

Query Match 65.7%; Score 46; DB 5; Length 127;
Best Local Similarity 61.5%; Pred. No. 3.5;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DLNKGHLDGSEV 13
Db 62 DLNKNFIDGIEI 74

RESULT 12
Q9PM44 PRELIMINARY; PRT; 289 AA.
AC Q9PM44;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical protein Cj1631c.
GN Cj1631c.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 11168;
RX MEDLINE=20150912; PubMed=10688204;
RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
RA Jorgensen K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences.";
RL Nature 403:665-668(2000).
DR EMBL; AL139079; CAB73619.1;
DR InterPro; IPR02048; EF-hand.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 289 AA; 32539 MW; 98B618A0419F7BEC CRC64;

Query Match 64.3%; Score 45; DB 16; Length 289;
Best Local Similarity 61.5%; Pred. No. 12;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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QY 1 DLNRDGHLDGSEV 13
 Db 165 DVNRDGRVDDSDV 177

RESULT 13

ID 093434 PRELIMINARY; PRT; 322 AA.
 AC 093434;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Reticulocalbin.
 GN RCN1.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99007268; PubMed=9789042;
 RA Miles C., Elgar G., Coles E., Kleinjan D.J., Van Heyningen V.,
 RA Hastie N.;
 RT "Complete sequencing of the Fugu WAGR region from WT1 to PAX6:
 RT Dramatic compaction and conservation of synteny with human chromosome
 RT 11p13.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:13068-13072(1998).
 DR EMBL: AL015133; CAA16492.1; -;
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR000886; ER-target.
 DR SMART: PF00036; ehand; 6.
 DR SMART: SM00054; Efh; 2.
 DR PROSITE: PS00018; EF_HAND; UNKNOWN_4.
 DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
 SQ SEQUENCE 322 AA; 38207 MW; 85F99C053AC34C5C CRC64;

Query Match 62.9%; Score 44; DB 13; Length 322;
 Best Local Similarity 61.5%; Pred. No. 21;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLNRDGHLDGSEV 13
 Db 248 DLNRDGHLDGSEV 260

RESULT 14

ID 090460 PRELIMINARY; PRT; 343 AA.
 AC 090460;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Membrane-associated calcium-binding protein.
 GN PFS40.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FCCL/RN;
 RA Shan 2.X., Yu X.B., Li X.R., Ma C.L., Fang J.M.;
 RT "Construction of a prokaryotic expression plasmid and sequence
 RT analysis of the pfs40 gene of Plasmodium falciparum HAINAN isolate.";
 RL Chung-Kuo Jen Shou Kung Huan Ping Tsa Chih 17:21-25(2001).
 DR EMBL: AF202094; AAF14633.1; -;
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00036; ehand; 5.
 DR ProDom: PD000012; EF-hand; 1.
 DR SMART: SM00054; Efh; 5.
 DR PROSITE: PS00018; EF_HAND; UNKNOWN_5.
 SQ SEQUENCE 343 AA; 39421 MW; A0F59D86D070529E CRC64;

Query Match 62.9%; Score 44; DB 5; Length 343;
 Best Local Similarity 53.8%; Pred. No. 22;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLNRDGHLDGSEV 13
 Db 223 DTNRDGYDKKEI 235

RESULT 15

ID 090RT6 PRELIMINARY; PRT; 592 AA.
 AC 090RT6;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE PHA synthase.
 GN PHACRR.
 OS Rhodospirillum rubrum.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;
 OC Rhodospirillum.
 OX NCBI_TaxID=1085;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20261043; PubMed=10803898;
 RA Clemente T., Shah D., Tran M., Stark D., Padgett S., Dennis D.,
 RA Brueckner K., Steinbuechel A., Mitsky T.;
 RT "Sequence of PHA synthase gene from two strains of Rhodospirillum
 RT rubrum and in vivo substrate specificity of four PHA synthases across
 RT two heterologous expression systems.";
 RL Appl. Microbiol. Biotechnol. 53:420-429(2000).
 DR EMBL: AJ245888; CAB65395.1; -;
 SQ SEQUENCE 592 AA; 66428 MW; 87A254102DC5675F CRC64;

Query Match 62.9%; Score 44; DB 2; Length 592;
 Best Local Similarity 66.7%; Pred. No. 40;
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LNRDGHLDGSEV 13
 Db 388 MNKGVLDGSEM 399

Search completed: May 14, 2003, 10:45:31
 Job time : 6.1173 secs

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GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: May 14, 2003, 10:41:13 ; Search time 1.4868 Seconds
(without alignments)
257.262 Million cell updates/sec

Title: US-09-768-840-1_COPY_254_266

Perfect score: 70

Sequence: 1 DLNKGHLGSEV 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70	100.0	328	2	US-08-828-242-1
2	70	100.0	328	2	US-08-910-927B-1
3	70	100.0	328	4	US-09-206-493-1
4	70	100.0	328	4	US-09-270-270-1
5	48	68.6	325	2	US-08-828-242-4
6	48	68.6	325	4	US-09-206-499-4
7	48	68.6	331	2	US-08-828-242-3
8	48	68.6	331	2	US-08-910-927B-5
9	48	68.6	331	4	US-09-206-499-3
10	48	68.6	331	4	US-09-270-270-5
11	40	57.1	203	4	US-09-399-913-12
12	40	57.1	203	4	US-09-399-913-12
13	40	57.1	216	4	US-09-399-913-2
14	40	57.1	216	4	US-09-399-913-6
15	40	57.1	216	4	US-09-298-731-2
16	40	57.1	216	4	US-09-298-731-6
17	40	57.1	227	4	US-09-399-913-8
18	40	57.1	227	4	US-09-399-913-8
19	40	57.1	227	4	US-09-298-731-8
20	40	57.1	227	4	US-09-298-731-10
21	40	57.1	245	4	US-09-399-913-4
22	40	57.1	245	4	US-09-298-731-4
23	40	57.1	3969	4	US-08-061-376-5
24	39	55.7	105	2	US-08-918-727-6
25	39	55.7	105	3	US-09-205-680A-6
26	39	55.7	276	3	US-09-048-889-4
27	39	55.7	313	4	US-09-134-001C-4371

28	39	55.7	473	1	US-08-073-383-6	Sequence 6, Appli
29	39	55.7	473	5	PCT-US94-06365-6	Sequence 6, Appli
30	38	54.3	109	4	US-09-399-913-34	Sequence 34, Appli
31	38	54.3	109	4	US-09-298-731-34	Sequence 34, Appli
32	38	54.3	188	3	US-09-048-889-3	Sequence 3, Appli
33	38	54.3	200	4	US-09-298-731-32	Sequence 32, Appli
34	38	54.3	229	4	US-09-399-913-70	Sequence 70, Appli
35	38	54.3	233	4	US-09-399-913-49	Sequence 49, Appli
36	38	54.3	233	4	US-09-399-913-51	Sequence 51, Appli
37	38	54.3	246	1	US-08-271-354-9	Sequence 9, Appli
38	38	54.3	246	2	US-08-565-861-9	Sequence 9, Appli
39	38	54.3	246	5	PCT-US94-07638-9	Sequence 9, Appli
40	38	54.3	250	4	US-09-399-913-72	Sequence 72, Appli
41	38	54.3	256	4	US-09-399-913-32	Sequence 32, Appli
42	37	52.9	837	4	US-09-390-234-14	Sequence 14, Appli
43	36	51.4	12	5	PCT-US93-05701-11	Sequence 11, Appli
44	36	51.4	20	1	US-07-740-175B-5	Sequence 5, Appli
45	36	51.4	20	5	PCT-US92-06334A-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-828-242-1
; Sequence 1, Application US/08828242
; Patent No. 5871970
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,242
; FILING DATE: Filed Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0261 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: CONUTUT01
; CLONE: 2509570
US-08-828-242-1

Query Match 100.0%; Score 70; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGHLDGSEV 13
 Db 254 DLNKGHLDGSEV 266

RESULT 2
 US-08-910-927B-1
 ; Sequence 1, Application US/08910927B
 ; Patent No. 5976801
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Shah, Purvi
 ; TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/910,927B
 ; FILING DATE: Hereewith
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PP-0358 US
 ; TELEPHONE: 650-855-0555
 ; TELEFAX: 650-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 328 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: RATNOT02
 ; CLONE: 922578
 ; US-08-910-927B-1

Query Match 100.0%; Score 70; DB 2; Length 328;
 Best Local Similarity 100.0%; Pred. No. 0.00025;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGHLDGSEV 13
 Db 254 DLNKGHLDGSEV 266

RESULT 3
 US-09-206-499-1
 ; Sequence 1, Application US/09206499
 ; Patent No. 6194385
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Goli, Surya K.
 ; TITLE OF INVENTION: NOVEL CALCIUM-BINDING

; TITLE OF INVENTION: PROTEIN
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/206,499
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/828,242
 ; FILING DATE: 03/31/1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0261 US
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 328 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: CONUTUT01
 ; CLONE: 2509570
 ; US-09-206-499-1

Query Match 100.0%; Score 70; DB 4; Length 328;
 Best Local Similarity 100.0%; Pred. No. 0.00025;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGHLDGSEV 13
 Db 254 DLNKGHLDGSEV 266

RESULT 4
 US-09-270-270-1
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 ; Patent No. 6235477
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Shah, Purvi
 ; TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/270,270
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/910,927
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0358 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-845-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 328 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: RAYNOT02
CLONE: 922578
US-09-270-270-1

Query Match 100.0%; Score 70; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGHLGSEV 13
DB 254 DLNKGHLGSEV 266

RESULT 5

US-08-828-242-4
Sequence 4, Application US/08828242
Patent No. 5871970
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL CALCIUM-BINDING
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,242
FILING DATE: Filed Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0261 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 220582
US-08-828-242-4

Query Match 68.6%; Score 48; DB 2; Length 325;
Best Local Similarity 69.2%; Pred. No. 1.3;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLNKGHLGSEV 13
DB 251 DLNKGKLDKDEI 263

RESULT 6

US-09-206-499-4
Sequence 4, Application US/09206499
Patent No. 6194385
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL CALCIUM-BINDING
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/206,499
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,242
FILING DATE: 03/31/1997
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0261 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 220582
US-09-206-499-4

Query Match 68.6%; Score 48; DB 4; Length 325;
Best Local Similarity 69.2%; Pred. No. 1.3;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLNKGHLGSEV 13
DB 251 DLNKGKLDKDEI 263

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; Patent No. 5871970
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
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; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: Filed Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0261 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 331 amino acids
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; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1262329
US-08-828-242-3
Query Match 68.6%; Score 48; DB 2; Length 331;
Best Local Similarity 69.2%; Pred. No. 1.3;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 DLNKGHLGDSV 13
Db 257 DLNKGKLDKDEI 269
RESULT 8
US-08-910-927B-5
; Sequence 5, Application US/08910927B
; Patent No. 5976801
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
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; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
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; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
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; CURRENT APPLICATION DATA:
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0358 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 331 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1262329
US-08-910-927B-5
Query Match 68.6%; Score 48; DB 2; Length 331;
Best Local Similarity 69.2%; Pred. No. 1.3;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 DLNKGHLGDSV 13
Db 257 DLNKGKLDKDEI 269
RESULT 9
US-09-206-499-3
; Sequence 3, Application US/09206499
; Patent No. 6194385
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/206,499
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,242
; FILING DATE: 03/31/1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
```

REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0261 US
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 331 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1262329
US-09-206-499-3

Query Match 68.6%; Score 48; DB 4; Length 331;
Best Local Similarity 69.2%; Pred. No. 1.3;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLNKGHLGSEV 13
DB 257 DLNKGKLDKDEI 269

RESULT 10
US-09-270-270-5
Sequence 5, Application US/09270270
Patent No. 6235477
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,270
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/910,927
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0358 US
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 331 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1262329

US-09-270-270-5

Query Match 68.6%; Score 48; DB 4; Length 331;
Best Local Similarity 69.2%; Pred. No. 1.3;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLNKGHLGSEV 13
DB 257 DLNKGKLDKDEI 269

RESULT 11
US-09-399-913-12
Sequence 12, Application US/09399913
Patent No. 6361971
GENERAL INFORMATION:
APPLICANT: Rhodes, Kenneth
APPLICANT: Betty, Maria
APPLICANT: Ling, Huai-Ping
APPLICANT: An, Wenqian
TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR
FILE REFERENCE: MNI-070CP2
CURRENT APPLICATION NUMBER: US/09/399,913
CURRENT FILING DATE: 1999-09-21
EARLIER APPLICATION NUMBER: USSN 60/110,277
EARLIER FILING DATE: 1998-11-30
EARLIER APPLICATION NUMBER: USSN 60/110,033
EARLIER FILING DATE: 1998-11-25
EARLIER APPLICATION NUMBER: USSN 60/109,333
EARLIER FILING DATE: 1998-11-20
EARLIER APPLICATION NUMBER: USSN 09/298,731
EARLIER FILING DATE: 1999-04-23
EARLIER APPLICATION NUMBER: USSN 09/350,614
EARLIER FILING DATE: 1999-07-09
EARLIER APPLICATION NUMBER: USSN 09/350,874
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 203
TYPE: PRT
ORGANISM: Rattus sp.
US-09-399-913-12

Query Match 57.1%; Score 40; DB 4; Length 203;
Best Local Similarity 46.2%; Pred. No. 17;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DLNKGHLGSEV 13
DB 151 DINKGYNKEEM 163

RESULT 12
US-09-298-731-12
Sequence 12, Application US/09298731
Patent No. 6369197
GENERAL INFORMATION:
APPLICANT: KENNETH RHODES, MARIA BETTY, HUAI-PING LING, AND FRANK AN
TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR
FILE REFERENCE: MNI-070
CURRENT APPLICATION NUMBER: US/09/298,731
CURRENT FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 203
TYPE: PRT
ORGANISM: Rattus sp.
US-09-298-731-12

Query Match 57.1%; Score 40; DB 4; Length 203;
Best Local Similarity 46.2%; Pred. No. 17;

Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DLNKGHLDGSEV 13
|:||||::|:
Db 151 DINKDGYINKEEM 163

RESULT 13
US-09-399-913-2
; Sequence 2, Application US/09399913
; Patent No. 6361971
; GENERAL INFORMATION:
; APPLICANT: Rhodes, Kenneth
; APPLICANT: Betty, Maria
; APPLICANT: Ling, Huai-Ping
; APPLICANT: An, Wenqian
; TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR
; FILE REFERENCE: MNI-070CP2
; CURRENT APPLICATION NUMBER: US/09/399,913
; EARLIER FILING DATE: 1999-09-21
; EARLIER APPLICATION NUMBER: USSN 60/110,277
; EARLIER FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: USSN 60/110,033
; EARLIER FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: USSN 60/109,333
; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: USSN 09/298,731
; EARLIER FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: USSN 09/350,614
; EARLIER FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: USSN 09/350,874
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-399-913-2

Query Match 57.1%; Score 40; DB 4; Length 216;
Best Local Similarity 46.2%; Pred. No. 18;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DLNKGHLDGSEV 13
|:||||::|:
Db 135 DINKDGYINKEEM 147

RESULT 14
US-09-399-913-6
; Sequence 6, Application US/09399913
; Patent No. 6361971
; GENERAL INFORMATION:
; APPLICANT: Rhodes, Kenneth
; APPLICANT: Betty, Maria
; APPLICANT: Ling, Huai-Ping
; APPLICANT: An, Wenqian
; TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR
; FILE REFERENCE: MNI-070CP2
; CURRENT APPLICATION NUMBER: US/09/399,913
; EARLIER FILING DATE: 1999-09-21
; EARLIER APPLICATION NUMBER: USSN 60/110,277
; EARLIER FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: USSN 60/110,033
; EARLIER FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: USSN 60/109,333
; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: USSN 09/298,731
; EARLIER FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: USSN 09/350,614
; EARLIER FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: USSN 09/350,874

; EARLIER FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-399-913-6

Query Match 57.1%; Score 40; DB 4; Length 216;
Best Local Similarity 46.2%; Pred. No. 18;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DLNKGHLDGSEV 13
|:||||::|:
Db 135 DINKDGYINKEEM 147

RESULT 15
US-09-298-731-2
; Sequence 2, Application US/09298731
; Patent No. 636197
; GENERAL INFORMATION:
; APPLICANT: KENNETH RHODES, MARIA BETTY, HUAI-PING LING, AND FRANK AN
; FILE REFERENCE: MNI-070
; CURRENT APPLICATION NUMBER: US/09/298,731
; CURRENT FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-298-731-2

Query Match 57.1%; Score 40; DB 4; Length 216;
Best Local Similarity 46.2%; Pred. No. 18;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DLNKGHLDGSEV 13
|:||||::|:
Db 135 DINKDGYINKEEM 147

Search completed: May 14, 2003, 10:47:15
Job time : 2.4868 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 14, 2003, 10:34:02 ; Search time 4.1173 Seconds
(without alignments)
420.726 Million cell updates/sec

Title: US-09-768-840-1_copy_254_266
Perfect score: 70
Sequence: 1 DLNKGHLGSEV 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

No.	Score	Match	Length	ID	Description
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2:	70	100.0	328	19	AAW80746
3:	70	100.0	328	20	AAI13382
4:	70	100.0	328	20	AAI00916
5:	70	100.0	328	20	AAW67852
6:	70	100.0	328	21	AAW67852
7:	70	100.0	328	21	AAW33424
8:	70	100.0	328	21	AAI53640
9:	70	100.0	328	22	AAI12353
10:	70	100.0	328	22	AAW64865
11:	70	100.0	328	22	AAW80250
12:	70	100.0	328	22	AAW80250
13:	70	100.0	328	22	AAW80250
14:	70	100.0	328	22	AAW80250
15:	70	100.0	328	22	AAW80250
16:	70	100.0	328	22	AAW80250
17:	70	100.0	328	22	AAW80250
18:	70	100.0	328	22	AAW80250
19:	70	100.0	328	22	AAW80250
20:	70	100.0	328	22	AAW80250
21:	70	100.0	328	22	AAW80250
22:	70	100.0	328	22	AAW80250
23:	70	100.0	328	22	AAW80250

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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2	70	100.0	328	19	AAW80746
3	70	100.0	328	20	AAI13382
4	70	100.0	328	20	AAI00916
5	70	100.0	328	20	AAW67852
6	70	100.0	328	21	AAW67852
7	70	100.0	328	21	AAW33424
8	70	100.0	328	21	AAI53640
9	70	100.0	328	22	AAI12353
10	70	100.0	328	22	AAW64865
11	70	100.0	328	22	AAW80250

11	70	100.0	328	22	AAB53085	Human angiotensin
12	70	100.0	343	22	AAU87402	Novel central nerv
13	70	100.0	343	22	AAU43584	Human polypeptide
14	70	100.0	343	22	AAU19946	Novel human calciu
15	48	68.6	66	22	ABB27587	Human peptide #238
16	48	68.6	66	22	ABB27587	Human peptide #238
17	48	68.6	66	22	ABB27587	Human peptide #238
18	48	68.6	66	22	ABB27587	Human peptide #238
19	48	68.6	66	22	ABB27587	Human peptide #238
20	48	68.6	66	22	ABB27587	Human peptide #238
21	48	68.6	66	22	ABB27587	Human peptide #238
22	48	68.6	66	22	ABB27587	Human peptide #238
23	48	68.6	66	22	ABB27587	Human peptide #238
24	48	68.6	66	22	ABB27587	Human peptide #238
25	48	68.6	66	22	ABB27587	Human peptide #238
26	48	68.6	66	22	ABB27587	Human peptide #238
27	48	68.6	66	22	ABB27587	Human peptide #238
28	48	68.6	66	22	ABB27587	Human peptide #238
29	48	68.6	66	22	ABB27587	Human peptide #238
30	48	68.6	66	22	ABB27587	Human peptide #238
31	48	68.6	66	22	ABB27587	Human peptide #238
32	48	68.6	66	22	ABB27587	Human peptide #238
33	48	68.6	66	22	ABB27587	Human peptide #238
34	48	68.6	66	22	ABB27587	Human peptide #238
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37	48	68.6	66	22	ABB27587	Human peptide #238
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39	48	68.6	66	22	ABB27587	Human peptide #238
40	48	68.6	66	22	ABB27587	Human peptide #238
41	48	68.6	66	22	ABB27587	Human peptide #238
42	48	68.6	66	22	ABB27587	Human peptide #238
43	48	68.6	66	22	ABB27587	Human peptide #238
44	48	68.6	66	22	ABB27587	Human peptide #238
45	48	68.6	66	22	ABB27587	Human peptide #238

ALIGNMENTS

RESULT 1
AAG75587
ID AAG75587 standard; Protein; 240 AA.
XX
AC AAG75587;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen protein SEQ ID NO:6351.
XX
KW Human; colon cancer; colon cancer, antigen; diagnosis; detection;
KW colorectal carcinoma.
XX
OS Homo sapiens.
XX
PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US26524.
XX
PR 29-SEP-1999; 99US-0157137.
PR 03-NOV-1999; 99US-0163280.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
DR WPI; 2001-235357/24.
XX
PT N-PSDB; AAH34992.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX
PT useful for preventing, diagnosing and/or treating colorectal cancers -

PR 27-OCT-1997; 97US-0063329.
 PR 27-OCT-1997; 97US-0063327.
 PR 28-OCT-1997; 97US-0063541.
 PR 28-OCT-1997; 97US-0063542.
 PR 28-OCT-1997; 97US-0063544.
 PR 28-OCT-1997; 97US-0063549.
 PR 28-OCT-1997; 97US-0063550.
 PR 28-OCT-1997; 97US-0063564.
 PR 29-OCT-1997; 97US-0063435.
 PR 29-OCT-1997; 97US-0063704.
 PR 29-OCT-1997; 97US-0063732.
 PR 29-OCT-1997; 97US-0063738.
 PR 29-OCT-1997; 97US-0063734.
 PR 29-OCT-1997; 97US-0064215.
 PR 31-OCT-1997; 97US-0063735.
 PR 31-OCT-1997; 97US-0063870.
 PR 31-OCT-1997; 97US-0064103.
 PR 03-NOV-1997; 97US-0064248.
 PR 07-NOV-1997; 97US-0064809.
 PR 12-NOV-1997; 97US-0065186.
 PR 17-NOV-1997; 97US-0065846.
 PR 18-NOV-1997; 97US-0065693.
 PR 21-NOV-1997; 97US-0066120.
 PR 21-NOV-1997; 97US-0066364.
 PR 24-NOV-1997; 97US-0066772.
 PR 24-NOV-1997; 97US-0066466.
 PR 24-NOV-1997; 97US-0066770.
 PR 24-NOV-1997; 97US-0066511.
 PR 24-NOV-1997; 97US-0066453.
 PA (GETH) GENENTECH INC.
 XX
 XX
 PI Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;
 DR WPT; 1999-229533/19.
 DR N-PSDB; AAX52253.
 XX
 PT New isolated human genes and polypeptides used in, e.g. treatment of
 PT gastrointestinal ulceration
 XX
 XX Claim 12; Fig 80; 320pp; English.
 PS
 XX
 CC AAY13344-403 represent secreted and transmembrane human proteins.
 CC The cDNA sequences are obtained from cDNA libraries, prepared from
 CC fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.
 CC The encoded polypeptides have specific uses based on their homology to
 CC known polypeptides, e.g. PRO211 and PRO217 can be used for disorders
 CC associated with the preservation and maintenance of gastrointestinal
 CC mucosa and the repair of acute and chronic mucosal lesions
 CC (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal
 CC ulceration and congenital microvillus atrophy), skin diseases associated
 CC with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial
 CC cancers such as lung squamous cell carcinoma of the vulva and gliomas),
 CC potent effects on cell growth and development, diseases related to
 CC growth or survival of nerve cells including Parkinson's disease,
 CC Alzheimer's disease, AIDS, neuropathies or cancer. PRO265 can be used as
 CC for fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used
 CC as a target for anti-tumor drugs. PRO533 may be used in the treatment
 CC of Usher Syndrome or Atrophia areata. PRO269 can be used as an
 CC anti-thrombotic agent; PRO287 polypeptides and portions may have
 CC therapeutic applications in wound healing and tissue repair; PRO317 can
 CC be used for treating problems of the kidney, uterus, endometrium, blood
 CC vessels, or related tissue, e.g. in the heart of genital tract.
 XX
 SQ Sequence 328 AA;
 Query Match 100.0%; Score 70; DB 20; Length 328;
 Best Local Similarity 100.0%; Pred. No. 0.00056;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 DLNKGHLDGSEV 13
 Db 254 DLNKGHLDGSEV 266
 RESULT 5
 AAW67852
 ID AAW67852 standard; Protein; 328 AA.

RESULT 4
 AAY00916
 ID AAY00916 standard; Protein; 328 AA.
 XX
 AC AAY00916;
 XX
 DT 28-MAY-1999 (first entry)
 XX
 DE Human reticulocalbin gamma protein sequence.
 XX
 KW Human; reticulocalbin gamma; RCNgamma; reticulocalbin delta; RCNdelta;
 KW developmental disorder; neoplastic disorder; immunological disorder;
 XX infection.
 XX
 OS Homo sapiens.
 XX
 PN WO9907849-A2.
 XX
 PD 18-FEB-1999.
 XX
 PF 05-AUG-1998; 98WO-US16259.
 XX
 PR 08-AUG-1997; 97US-0910927.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Bandman O, Corley NC, Hillman JL, Lal P, Shah P;
 DR WPT; 1999-180492/15.
 DR N-PSDB; AAX27229.
 XX
 PT New human reticulocalbin isoforms - useful to diagnose, prevent,
 PT and treat infectious, developmental, neoplastic, and immunological
 PT disorders
 XX
 XX Claim 1; Fig 1; 82pp; English.
 PS
 XX
 CC This sequence is the human reticulocalbin gamma (RCNgamma) of the
 CC invention. RCNgamma and RCNdelta are used to treat an infectious or
 CC developmental disorder, and antagonists of them are used to treat a
 CC neoplastic or immunological disorder. Infectious disorders include e.g.
 CC pneumonia, lymphocytic choriomeningitis, Hantavirus, chronic bronchitis,
 CC hepatitis, herpesviruses, yellow fever, influenza, cancer, measles,
 CC mumps, rhinovirus, poliovirus, coxsackie-virus, smallpox, Colorado tick
 CC fever, HIV, rabies, gastroenteritis, and rubella, encephalitis, and
 CC bacterial, fungal, parasitic, protozoal, or helminthic infections.
 CC Developmental disorders include e.g. renal tubular acidosis, anaemia,
 CC Cushing's syndrome, achondroplastic dwarfism, epilepsy, gonadal
 CC dysgenesis, hereditary neuropathies such as Charcot-Marie-Tooth disease,
 CC and neurofibromatosis, hypothyroidism, hydrocephalus, seizure disorders,
 CC such as Sydenham's chorea and cerebral palsy, spinal bifida, and
 CC congenital glaucoma, cataract, or sensorineural hearing loss. Neoplastic
 CC disorders include e.g. adenocarcinoma, leukaemia, lymphoma, melanoma,
 CC myeloma, sarcoma and teratocarcinoma. Overexpression of reticulocalbin
 CC mRNA has been associated with increased metastasis of reticulocalbin
 CC three human breast cancer lines.
 XX
 SQ Sequence 328 AA;
 Query Match 100.0%; Score 70; DB 20; Length 328;
 Best Local Similarity 100.0%; Pred. No. 0.00056;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 DLNKGHLDGSEV 13
 Db 254 DLNKGHLDGSEV 266
 RESULT 5
 AAW67852
 ID AAW67852 standard; Protein; 328 AA.

CC The invention relates to 87 novel genes and their fragments (nucleic acid sequences: AAX00611-X00724; amino acid sequences: AAW67807-W68004) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 87 polynucleotides, based on which tissues they are most highly expressed in (see AAX00611 for described uses).

CC Query Match 100.0%; Score 70; DB 20; Length 328;
CC Best Local Similarity 100.0%; Pred. NO. 0.00056; Indels 0; Caps 0;
CC Matches 13; Conservative 0; Mismatches 0;

QY 1 DLNKGDLGSEV 13
DB 253 DLNKGDLGSEV 265

RESULT 6
AAB33424
ID AAB33424 standard; Protein; 328 AA.

XX AC. AAB33424;
XX DT 29-JAN-2001 (first entry)
XX DE Human PRO272 protein UNQ239 SEQ ID NO:51.

XX KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW osteoarthritis; spondyloarthritis; Sjogren's syndrome; thyroiditis;
KW idiopathic inflammatory myopathy; immune-mediated renal disease;
KW autoimmune thrombocytopenia; immune-mediated renal disease;
KW demyelinating disease; hepatobiliary disease; Whipple's disease;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW autoimmune disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW graft rejection; graft-versus-host-disease.

XX OS Homo sapiens.
XX PN WO200053758-A2.
XX PD 14-SEP-2000.
XX PF 02-MAR-2000; 2000WO-US05841.

XX PR 08-MAR-1999; 99WO-US05028.
XX PR 10-MAR-1999; 99US-0123618.
XX PR 12-MAR-1999; 99US-0123957.
XX PR 23-MAR-1999; 99US-0125775.
XX PR 12-APR-1999; 99US-0128849.
XX PR 20-APR-1999; 99WO-US08615.
XX PR 28-APR-1999; 99US-0131445.
XX PR 04-MAY-1999; 99US-0132371.
XX PR 14-MAY-1999; 99US-0134287.
XX PR 02-JUN-1999; 99WO-US12252.
XX PR 23-JUN-1999; 99US-0141037.
XX PR 20-JUL-1999; 99US-0144758.
XX PR 26-JUL-1999; 99US-0145698.
XX PR 28-JUL-1999; 99US-0146222.
XX PR 01-SEP-1999; 99WO-US20111.
XX PR 08-SEP-1999; 99WO-US20594.
XX PR 13-SEP-1999; 99WO-US20944.
XX PR 15-SEP-1999; 99WO-US21090.
XX PR 15-SEP-1999; 99WO-US21547.

XX AAW67852;
XX 25-MAR-1999 (first entry)
XX Human secreted protein encoded by gene 46 clone HSJBQ79.
XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
XX diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
XX developmental abnormality; foetal deficiency; blood; allergy; renal;
XX immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
XX inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
XX cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
XX osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
XX endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX OS Homo sapiens.

XX Key Location/Qualifiers
XX Misc-difference 300
XX /label= unknown
XX Misc-difference 328
XX /label= unknown

XX WO9842738-A1.
XX 01-OCT-1998.
XX 19-MAR-1998; 98WO-US05311.

XX PR 30-MAY-1997; 97US-0050937.
XX PR 21-MAR-1997; 97US-0041276.
XX PR 21-MAR-1997; 97US-0041277.
XX PR 21-MAR-1997; 97US-0041281.
XX PR 21-MAR-1997; 97US-0042344.
XX PR 30-MAY-1997; 97US-0048069.
XX PR 30-MAY-1997; 97US-0048094.
XX PR 30-MAY-1997; 97US-0048095.
XX PR 30-MAY-1997; 97US-0048096.
XX PR 30-MAY-1997; 97US-0048099.
XX PR 30-MAY-1997; 97US-0048131.
XX PR 30-MAY-1997; 97US-0048135.
XX PR 30-MAY-1997; 97US-0048154.
XX PR 30-MAY-1997; 97US-0048160.
XX PR 30-MAY-1997; 97US-0048186.
XX PR 30-MAY-1997; 97US-0048187.
XX PR 30-MAY-1997; 97US-0048188.
XX PR 30-MAY-1997; 97US-0048350.
XX PR 30-MAY-1997; 97US-0048351.
XX PR 30-MAY-1997; 97US-0048352.
XX PR 30-MAY-1997; 97US-0048355.
XX PR 05-AUG-1997; 97US-0054804.

XX (HUMA-) HUMAN GENOME SCI INC.
XX Brewer LA, Duan R, Ebner R, Ferrie AM, Florence KA;
XX Greene JM, Hu JS, Lafleur DW, Moore PA, Ni J, Olsen HS;
XX Rosen CA, Ruben SM, Shi Y, Young P;
XX WPI; 1999-070066/06.
XX N-PSDB; AAX00636.

XX New isolated human genes and the secreted polypeptides they encode -
XX useful for diagnosis and treatment of e.g. cancers, neurological
XX disorders, immune diseases, inflammation or blood disorders
XX Claim 11; Page 297-298; 385pp; English.

XX This sequence represents a secreted human protein encoded by the gene
XX clone detailed in the descriptor line. The gene can be used to generate
XX fusion proteins by linking to the gene to a human immunoglobulin Fc
XX portion (e.g. AAX00602) for increasing the stability of the fused
XX protein as compared to the human protein only.

PR 05-OCT-1999; 99WO-US23089.
 PR 29-OCT-1999; 99US-0162506.
 PR 29-NOV-1999; 99WO-US28214.
 PR 30-NOV-1999; 99WO-US28313.
 PR 30-NOV-1999; 99WO-US28409.
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30099.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 11-FEB-2000; 2000WO-US00376.
 PR 18-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PA (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
 PI Kabakoff RC, Lu Y, Fan J, Pennica D, Shelton DL, Smith V;
 PI Stewart TA, Tamas D, Watanabe CK, Wood WI, Yan M;
 XX WPI: 2000-572271/53.

DR N-PSDB; AAC58569.
 DR WPI: 2000-572271/53.

XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus .

XX Claim 33; Fig 22; 309pp; English.

XX The present invention describes sixty four human PRO proteins which can
 CC be used in the treatment of immune related diseases. The human PRO
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
 CC treating and diagnosing immune related disorders. The disorders are
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthritis,
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
 CC immune-mediated renal disease, demyelinating diseases of the central
 CC and peripheral nervous systems, hepatobiliary diseases, inflammatory
 CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,
 CC autoimmune or immune-mediated skin diseases, allergic diseases,
 CC immunological diseases of the lung, and transplantation associated
 CC diseases including graft rejection and graft-versus-host-disease.
 CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and
 CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.

XX Sequence 328 AA;

Query Match 100.0%; Score 70; DB 21; Length 328;
 Best Local Similarity 100.0%; Pred. No. 0.00056;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGDLGDSV 13

Db 254 DLNKGDLGDSV 266

RESULT 7

AAV53640

XX ID AAV53640 standard; Protein: 328 AA.

AC AAV53640;

XX

DT 22-FEB-2000 (first entry)
 XX A bone marrow secreted protein designated BMS37.
 DE
 XX
 XX Bone marrow secreted protein; bone marrow stromal cell; cytokine;
 KW cell proliferation; cell differentiation; hematopoiesis; anaemia;
 KW myeloid cell deficiency; lymphoid cell deficiency; myeloid cell;
 KW erythroid progenitor cell; colony stimulating factor; granulocyte;
 KW monocyte; macrophage; myelo-suppression; megakaryocyte; platelet;
 KW platelet disorder; thrombocytopenia; hematopoietic stem cell;
 KW stem cell disorder; aplastic anaemia; bone differentiation;
 KW paroxysmal nocturnal hemoglobinuria; bone growth; cartilage;
 KW ligament; nerve; wound healing; tissue repair; burn; incision; ulcer;
 KW bone fracture; cartilage damage; artificial joint.
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..20
 FT /note= "signal peptide"
 FT
 XX
 XX WO9933979-A2.
 PN
 XX
 XX 08-JUL-1999.
 PD
 XX
 XX 18-DEC-1998; 98WO-US27008.
 PF
 XX
 XX 30-DEC-1997; 97US-0068958.
 PR
 XX 24-SEP-1998; 98US-0101603.
 PR
 XX 30-SEP-1998; 98US-0102540.
 PR
 XX (CHIR) CHIRON CORP.
 PA
 XX
 XX Lin H, Cao L;
 PI
 XX
 XX WPI: 2000-038344/03.
 DR N-PSDB; AAZ36246.
 DR
 XX
 XX New isolated human polynucleotide and secreted proteins can induce
 PT production of other cytokines in certain cell populations .
 PT
 XX
 XX Claim 2; Page 113; 120pp; English.
 PS
 XX
 XX AAV53622-43 represent bone marrow secreted proteins of human bone marrow
 CC stromal cells. The proteins can exhibit cytokine, cell proliferation, or
 CC cell differentiation activity (either inducing or inhibiting). They can
 CC be used to support colony forming cells or factor-dependent cell lines,
 CC to regulate hematopoiesis, and to treat myeloid or lymphoid cell
 CC deficiencies. In addition, they may be used to support the growth and
 CC proliferation of erythroid progenitor cells, and to treat various
 CC anaemias. They can have colony stimulating factor (CSF) activity and can
 CC be used to support the growth and proliferation of myeloid cells such as
 CC granulocytes, monocytes or macrophages, to prevent or treat
 CC myelo-suppression, to support the growth and proliferation of
 CC megakaryocytes and platelets, thereby allowing prevention or treatment
 CC of platelet disorders such as thrombocytopenia, to support the growth
 CC and proliferation of hematopoietic stem cells, either in place of or in
 CC conjunction with platelet transfusions, to treat stem cell disorders,
 CC such as aplastic anaemia and paroxysmal nocturnal hemoglobinuria, or to
 CC repopulate the stem cell compartment after irradiation or chemotherapy.
 CC They can be used for growth or differentiation of bone, cartilage,
 CC tendon, ligament, or nerve tissue, as well as for wound healing and
 CC tissue repair and replacement, and in the treatment of burns, incisions
 CC and ulcers, to induce cartilage and/or bone growth in circumstances
 CC where bone is not normally formed and thus have an application in healing
 CC bone fractures and cartilage damage or defects, prophylactic use in
 CC fracture reduction and also in the improved fixation of artificial
 CC joints.
 XX
 XX Sequence 328 AA;

Query Match 100.0%; Score 70; DB 21; Length 328;
 Best Local Similarity 100.0%; Pred. No. 0.00056;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGHLDGSEV 13
Db 254 DLNKGHLDGSEV 266
IIIIIIIIIIIIIIIIIIII

RESULT 8
AAU12353
ID AAU12353 standard; Protein; 328 AA.
XX AAU12353;
AC
XX 24-OCT-2001 (first entry)
DT
XX Human PRO272 polypeptide sequence.
DE
XX Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW adipocyte; A-peptide; factor VIIA; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200140466-A2.
XX
XX 07-JUN-2001.
PD
XX 01-DEC-2000; 2000WO-US32678.
PF
XX 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28584.
PR 02-DEC-1999; 99WO-US28565.
PR 09-DEC-1999; 99US-0170262.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US31243.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04144.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 10-NOV-2000; 2000WO-US30873.
XX
XX (GETH) GENENTECH INC.
PA
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WL, Zhang Z;
XX
XX WPI: 2001-408281/43.
DR N-PSDB; AAS21425.
XX
XX Isolated, secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing
PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
PT lung, breast, prostate, cervical
XX
XX Claim 12; Fig 364; 813pp; English.

XX AAU12172-AAU12446 represent novel human secretory and transmembrane
CC PRO polypeptides. The PRO polypeptides are useful to detect other
CC PRO polypeptides, to link bioactive molecules to cells expressing
CC PRO polypeptides, to modulate biological activities of cells expressing
CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample.
CC Some of the 275 sequences are also useful to stimulate the release of
CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
CC proliferation or differentiation of chondrocytes, the proliferation or
CC gene expression in pericyte cells, the release of proteoglycans from
CC cartilage, the proliferation of inner ear utricular supporting cells or
CC of T-lymphocytes, the release of a cytokine from endothelial cells. Some of
CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
CC to factor VIIA. The PRO polypeptides can be used in assays to identify
CC molecules involved in binding interactions. The polynucleotides encoding
CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy.
XX
SQ Sequence 328 AA;
Query Match 100.0%; Score 70; DB 22; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGHLDGSEV 13
Db 254 DLNKGHLDGSEV 266
IIIIIIIIIIIIIIIIIIII

RESULT 9
AAG64865
ID AAG64865 standard; protein; 328 AA.
XX
AC AAG64865;
XX
XX 21-SEP-2001 (first entry)
DT
XX Human calcium binding protein.
DE
XX Human; calcium binding protein; HCBP; cell proliferation disorder;
KW cancer.
KW
XX Homo sapiens.
XX US2001012831-A1.
XX
XX 09-AUG-2001.
XX
XX 23-JAN-2001; 2001US-0768840.
XX
XX 21-MAR-1997; 97US-0828212.
XX 07-DEC-1998; 98US-0206499.
XX
XX (INCY-) INCYTE PHARM INC.
XX
XX Hillman JL, Goli SK;
XX WPI: 2001-464391/50.
XX N-PSDB; AAH48279.
XX
XX Human calcium-binding protein, useful in the diagnosis, prevention, and
PT treatment of disorders associated with cell proliferation, e.g.
PT adenocarcinoma, leukemia, lymphoma, melanoma, sarcoma, or
PT teratocarcinoma
XX
XX Claim 1; Fig 1; 30pp; English.
PS
XX The present invention provides the protein and coding sequences of human
XX calcium binding protein (HCBP). The sequences can be used in the

CC diagnosis, prevention and treatment of cell proliferation disorders, such
 CC as cancer. The present sequence is the protein of the invention.

XX Sequence 328 AA;

Query Match 100.0%; Score 70; DB 22; Length 328;

Best Local Similarity 100.0%; Pred. No. 0.00056;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGHLGSEV 13

IIIIIIIIIIIIIIIIIIII

Db 254 DLNKGHLGSEV 266

RESULT 10

AA80250

ID AAB80250 standard; Protein; 328 AA.

AC AAB80250;

XX 24-APR-2001 (first entry)

XX Human PRO272 protein.

DE Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;

KW antiparkinsonian nootropic; neuroprotective; vulnery; cardiant;

KW antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;

KW antiarthritic; antinfertility; antidiabetic; antiviral; diabetes;

KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;

KW ischaemia; inflammation.

XX Homo sapiens.

OS WO200104311-A1.

XX 18-JAN-2001.

XX 22-FEB-2000; 2000WO-US04414.

XX 07-JUL-1999; 99US-0143048.

XX 26-JUL-1999; 99US-0145698.

XX 28-JUL-1999; 99US-0146222.

XX 08-SEP-1999; 99WO-US20594.

XX 13-SEP-1999; 99WO-US20944.

XX 15-SEP-1999; 99WO-US21090.

XX 05-OCT-1999; 99WO-US23089.

XX 29-NOV-1999; 99WO-US28214.

XX 30-NOV-1999; 99WO-US28313.

XX 16-DEC-1999; 99WO-US30095.

XX 20-DEC-1999; 99WO-US30911.

XX 05-JAN-2000; 99WO-US30999.

XX 05-JAN-2000; 99WO-US00219.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;

PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;

PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;

PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;

PI Williams PM, Wood WI;

XX WPI: 2001-081051/09.

DR N-PSDB; AAF72411.

XX Sixty one nucleic acids encoding PRO polypeptides which are useful in

PT the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung

PT squamous cell carcinoma) and neurodegenerative diseases (e.g.

PT Alzheimer's disease)

XX Claim 1; Fig 80; 393pp; English.

PS The present sequence is one of sixty one novel secreted and

XX

CC transmembrane PRO polypeptides. The PRO polypeptides are
 CC useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung
 CC squamous cell carcinoma), gastrointestinal disorders (e.g.
 CC enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,
 CC Parkinson's disease), wound repair, cardiovascular disorders (e.g.
 CC endometrial bleeding angiogenesis), ischaemia such as coronary
 CC ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma,
 CC rheumatoid arthritis, multiple sclerosis), infertility, AIDS and
 CC diabetes and retinal disorders such as retinitis pigmentosa.
 CC The PRO nucleic acids have applications in molecular biology, including
 CC use as hybridization probes, and in chromosome and gene mapping.

XX Sequence 328 AA;

Query Match 100.0%; Score 70; DB 22; Length 328;

Best Local Similarity 100.0%; Pred. No. 0.00056;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGHLGSEV 13

IIIIIIIIIIIIIIIIIIII

Db 254 DLNKGHLGSEV 266

RESULT 11

AAB53085

ID AAB53085 standard; Protein; 328 AA.

XX AAB53085;

XX 28-FEB-2001 (first entry)

XX Human angiogenesis-associated protein PRO272, SEQ ID NO:113.

DE Human; angiogenesis-associated protein; PRO; endothelial cell growth;

XX cardiac hypertrophy; cardiovascular disorder; endothelial disorder;

KW myogenic disorder; atherosclerosis; osteoporosis; hypertension;

KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;

KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;

KW Alzheimer's disease; Huntington's disease; stroke; drug screening;

KW gene therapy; transgenic animal.

XX Homo sapiens.

XX WO200053753-A2.

XX 14-SEP-2000.

XX 05-JAN-2000; 2000WO-US00219.

XX 08-MAR-1999; 99WO-US05028.

XX 12-MAR-1999; 99US-0123957.

XX 14-MAY-1999; 99US-0134287.

XX 02-JUN-1999; 99WO-US12252.

XX 23-JUN-1999; 99US-0141037.

XX 20-JUL-1999; 99US-0144758.

XX 01-SEP-1999; 99WO-US20111.

XX 08-SEP-1999; 99WO-US20594.

XX 15-SEP-1999; 99WO-US21090.

XX 05-OCT-1999; 99WO-US21547.

XX 30-NOV-1999; 99WO-US28313.

XX 02-DEC-1999; 99WO-US28584.

XX 02-DEC-1999; 99WO-US28565.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;

PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;

PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;

XX WPI: 2001-090793/10.

DR N-PSDB; AAC97455.

XX New isolated nucleic acid for producing a PRO polypeptide, analyzing

PT genetic disorders and treating cardiovascular, endothelial or

PT angiogenic disorders, such as atherosclerosis, wounds or cancer -

XX

XX Claim 69; Fig 44; 293pp; English.

XX The invention relates to novel human angiogenesis-associated proteins

XX designated PRO proteins (AAH53064-B53097), and to nucleic acids encoding

CC PRO proteins. The invention also relates to vectors and host cells

CC comprising a PRO nucleic acid, the recombinant production of a PRO

CC protein, PRO antibodies specific for a PRO protein, fusion proteins

CC comprising a PRO protein, agonists or antagonists of a PRO protein, and

CC compounds which inhibit the expression of a PRO gene. The invention

CC additionally encompasses methods of identifying modulators of PRO

CC expression or activity; diagnosing a cardiovascular, endothelial or

CC angiogenic disorder, or a susceptibility to such a disorder by detecting

CC mutations in a PRO gene, or the expression level of a PRO gene within a

CC particular tissue; treating a cardiovascular, endothelial or angiogenic

CC disorder via the administration of a PRO protein, PRO nucleic acid, or

CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a

CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial

CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the

CC administration of a PRO protein, or an agonist or antagonist thereof.

CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO

CC agonists and PRO antagonists may be used as therapeutic agents to treat

CC cardiovascular, endothelial or angiogenic disorders, such as

CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,

CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,

CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's

CC disease, or stroke. PRO nucleic acids are additionally useful in the

CC recombinant production of PRO proteins, as hybridisation probes to

CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,

CC to map genes encoding PRO proteins, to analyse genetic disorders, and in

CC gene therapy. PRO nucleic acids can also be used to produce transgenic

CC animals useful for the development and screening of potential

CC therapeutic agents. The present sequence represents a PRO protein of the

XX invention.

XX

XX Sequence 328 AA;

XX

XX Query Match 100.0%; Score 70; DB 22; Length 328;

XX Best Local Similarity 100.0%; Pred. No. 0.00056;

XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLNKGHLGSEV 13

Db 254 DLNKGHLGSEV 266

RESULT 12

AAU87402

ID AAU87402 standard; Protein; 343 AA.

XX

XX AC AAU87402;

XX

XX 05-JUN-2002 (first entry)

DT

DE Novel central nervous system protein #312.

XX

XX Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;

KW hyperproliferative disorder; neoplasm; cardiovascular disorder;

KW cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;

KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;

KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;

KW adenocarcinoma; reproductive system disorder; testicular feminisation;

KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;

KW respiratory disorder; renal disorder; kidney failure; blood disorder;

KW myocardial infarction; wound healing; cell proliferation; skin aging;

KW food additive; food preservative; gene therapy.

XX

OS Homo sapiens.

XX

XX WO200155318-A2.

XX

XX 02-AUG-2001.

XX

XX 17-JAN-2001; 2001WO-US01332.

XX

XX 31-JAN-2000; 2000US-0179065.

XX

XX 04-FEB-2000; 2000US-0180628.

XX

XX 24-FEB-2000; 2000US-0184664.

XX

XX 02-MAR-2000; 2000US-0186350.

XX

XX 16-MAR-2000; 2000US-0189874.

XX

XX 17-MAR-2000; 2000US-0190076.

XX

XX 18-APR-2000; 2000US-0198123.

XX

XX 19-MAY-2000; 2000US-0205515.

XX

XX 07-JUN-2000; 2000US-0209467.

XX

XX 28-JUN-2000; 2000US-0214886.

XX

XX 30-JUN-2000; 2000US-0215135.

XX

XX 07-JUL-2000; 2000US-0216647.

XX

XX 07-JUL-2000; 2000US-0216880.

XX

XX 11-JUL-2000; 2000US-0217487.

XX

XX 11-JUL-2000; 2000US-0217496.

XX

XX 14-JUL-2000; 2000US-0218290.

XX

XX 26-JUL-2000; 2000US-0220964.

XX

XX 26-JUL-2000; 2000US-0224518.

XX

XX 14-AUG-2000; 2000US-0224519.

XX

XX 14-AUG-2000; 2000US-0225213.

XX

XX 14-AUG-2000; 2000US-0225214.

XX

XX 14-AUG-2000; 2000US-0225267.

XX

XX 14-AUG-2000; 2000US-0225268.

XX

XX 14-AUG-2000; 2000US-0225270.

XX

XX 14-AUG-2000; 2000US-0225447.

XX

XX 14-AUG-2000; 2000US-0225757.

XX

XX 14-AUG-2000; 2000US-0225758.

XX

XX 14-AUG-2000; 2000US-0225759.

XX

XX 18-AUG-2000; 2000US-0226279.

XX

XX 22-AUG-2000; 2000US-0226681.

XX

XX 22-AUG-2000; 2000US-0226868.

XX

XX 22-AUG-2000; 2000US-0227182.

XX

XX 23-AUG-2000; 2000US-0227009.

XX

XX 30-AUG-2000; 2000US-0228924.

XX

XX 01-SEP-2000; 2000US-0229287.

XX

XX 01-SEP-2000; 2000US-0229343.

XX

XX 01-SEP-2000; 2000US-0229344.

XX

XX 01-SEP-2000; 2000US-0229345.

XX

XX 05-SEP-2000; 2000US-0229509.

XX

XX 05-SEP-2000; 2000US-0229513.

XX

XX 06-SEP-2000; 2000US-0230437.

XX

XX 06-SEP-2000; 2000US-0230438.

XX

XX 08-SEP-2000; 2000US-0231242.

XX

XX 08-SEP-2000; 2000US-0231243.

XX

XX 08-SEP-2000; 2000US-0231244.

XX

XX 08-SEP-2000; 2000US-0231413.

XX

XX 08-SEP-2000; 2000US-0231414.

XX

XX 08-SEP-2000; 2000US-0232080.

XX

XX 08-SEP-2000; 2000US-0232081.

XX

XX 12-SEP-2000; 2000US-0232397.

XX

XX 14-SEP-2000; 2000US-0232398.

XX

XX 14-SEP-2000; 2000US-0232399.

XX

XX 14-SEP-2000; 2000US-0232400.

XX

XX 14-SEP-2000; 2000US-0232401.

XX

XX 14-SEP-2000; 2000US-0233063.

XX

XX 14-SEP-2000; 2000US-0233064.

XX

XX 14-SEP-2000; 2000US-0233065.

XX

XX 21-SEP-2000; 2000US-0234223.

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XX 21-SEP-2000; 2000US-0234274.

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XX 25-SEP-2000; 2000US-0234997.

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XX 25-SEP-2000; 2000US-0234998.

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XX 26-SEP-2000; 2000US-0235484.

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XX 27-SEP-2000; 2000US-0235834.

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 PR 05-JAN-2001; 2000US-0259678.
 (HUMA-) HUMAN GENOME SCI INC.
 XX
 PA

PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI: 2001-581633/65.
 DR N-PSDB; ABR43732.
 XX
 PT New isolated nucleic acid encoding a protein for diagnosing,
 PT preventing, treating or ameliorating medical conditions and used as
 PT food additives or preservatives -
 XX
 PS Claim 9; SEQ ID NO 920; 837pp; English.
 XX
 CC The invention describes an isolated nucleic acid molecule (I) encoding a
 CC novel central nervous system protein. (I) and polypeptides (III) encoded
 CC by (I), are used to treat a medical conditions and in diagnosis of a
 CC pathological condition. Disorders which are diagnosed or treated include
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
 CC angiotrophic lateral sclerosis, infections caused by bacteria, viruses
 CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
 CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,
 CC adenocarcinomas and irritable bowel syndrome, reproductive system
 CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
 CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.
 CC leukaemia, disorders involving neovascularisation e.g. malignancies,
 CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
 CC acute kidney failure and blood related disorders e.g. myocardial
 CC infarction. The polypeptides can also be used to aid wound healing and
 CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
 CC maintain organs before transplantation, for supporting cell culture of
 CC primary tissues, to regenerate tissues and in chemotaxis. The
 CC polypeptides can also be used as a food additive or preservative to
 CC increase or decrease storage capabilities, fat content, lipid, protein,
 CC
 Query Match 100.0%; Score 70; DB 22; Length 343;
 Best Local Similarity 100.0%; Pred. No. 0.00059;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DLNKGHLGSEV 13
 Db 269 DLNKGHLGSEV 281
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 ID AAM43584 standard; Protein; 343 AA.
 XX
 AC AAM43584;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 262.
 XX
 KW Human: antiarthritic; antirheumatic; antiproliferative; vasotropic;
 KW cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
 KW fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
 KW neuroprotective; antiallergic; hepatotropic; antidiabetic;
 KW antiinflammatory; antitumor; vulnary; anticonvulsant; antibacterial;
 KW antiparasitic; cardiant; gene therapy; cancer; immune disorder;
 KW cardiovascular disorder; neurological disease; infection; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200155308-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US01309.
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 PR 31-JAN-2000; 2000US-0179065.
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 PR 24-FEB-2000; 2000US-0184664.

PR	02-MAR-2000;	2000US-0186350
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PR	08-DEC-2000;	2000US-0251990;
PR	11-DEC-2000;	2000US-0254090;
PR	11-DEC-2000;	2000US-0254097;
PR	05-JAN-2001;	2001US-0259678;
XX		
XX		
PA	(HUMA-)	HUMAN GENOME SCI INC
XX		
PI	Rosen CA,	Barash SC, Ruben
XX		
DR	WPI;	2001-488781/53.
DR	N-PSD;	RAI63890.
XX		
XX		
PT	New isolated nucleic acids and	
XX	treating and/or preventing h	
XX		
PS	Claim 11;	SEQ ID NO 262; 664;
XX		
XX		

CC The invention relates to human polynucleotides (AAI63803-AAI64012) and
 CC the encoded proteins (AA434497-AA43660) useful for preventing, treating
 CC or ameliorating medical conditions e.g. by protein or gene therapy. The
 CC genes were isolated from a range of human tissues disclosed in the
 CC specification. The nucleic acids, proteins, antibodies and (ant)agonists
 CC are useful in the diagnosis, treatment and prevention of: (a) cancer,
 CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,
 CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
 CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,
 CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 343 AA;

Query Match 100.0%; Score 70; DB 22; Length 343;

Best Local Similarity 100.0%; Pred. No. 0.00059;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLNKGHLGDSGV 13

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DB 269 DLNKGHLGDSGV 281

RESULT 14

AAU19946

ID AAU19946 standard; Protein: 343 AA.

AC AAU19946;

DT 04-DEC-2001 (first entry)

DE Novel human calcium-binding protein #55.

XX Human; calcium-binding protein; calcium flux; neurological disease;
 KW immune dysfunction; digestive disorder; neoplastic disease;
 KW blood disorder; infectious disease; gene therapy; immunosuppressive;
 KW antithratic; cytostatic; vasotropic; antibacterial; nootropic;
 KW virucide.

XX Homo sapiens.

XX WO200155304-A2.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US01302.

XX 31-JAN-2000; 2000US-0179065.

XX 04-FEB-2000; 2000US-0180628.

XX 24-FEB-2000; 2000US-0184664.

XX 02-MAR-2000; 2000US-0186350.

XX 16-MAR-2000; 2000US-0189874.

XX 17-MAR-2000; 2000US-0190076.

XX 18-APR-2000; 2000US-0198123.

XX 19-MAY-2000; 2000US-0205515.

XX 07-JUN-2000; 2000US-0209467.

XX 28-JUN-2000; 2000US-0214886.

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XX 26-JUL-2000; 2000US-0220963.

XX 26-JUL-2000; 2000US-0220964.

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PR 08-NOV-2000; 2000US-0246478.
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PR 08-NOV-2000; 2000US-0246524.
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PR 01-DEC-2000; 2000US-0250391.
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PR 05-JAN-2001; 2001US-0259678.
PR (HUMA-) HUMAN GENOME SCI INC.
XX PA
XX PI
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-465568/50.
XX N-PSDB; AAS31631.
XX
XX Isolated nucleic acid molecule encoding a calcium-binding protein is
XX used in preventing, treating or ameliorating a medical condition -
XX
XX Claim 11; SEQ ID NO 143; 542pp; English.
XX
XX The present invention relates to the isolation of novel human
XX calcium-binding proteins, and cDNA (AAS31577-AAS31654) and genomic
XX sequences encoding for these proteins. The sequences of the invention
XX are useful in the diagnosis, prevention and/or prognosis of diseases
XX associated with aberrant calcium flux. Such disorders include
XX neurological diseases (e.g. amyotrophic lateral sclerosis, ALS),
XX immune dysfunction (e.g. severe combined immunodeficiency, SCID),
XX digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic
XX disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or
XX infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The
XX novel calcium-binding proteins are also useful as screening tools to
XX identify antagonists and/or agonists that may enhance or inhibit
XX activities mediated by calcium-binding proteins. The polynucleotides of
XX the invention are also useful in gene therapy. AAU19892-AAU19969
XX represent the novel human calcium-binding proteins.
XX Note: The sequence data for this patent did not form part of the printed
XX

CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ Sequence 343 AA;
XX
XX Query Match 100.0%; Score 70; DB 22; Length 343;
XX Best Local Similarity 100.0%; Pred. No. 0.00059; Indels 0; Gaps 0;
XX Matches 13; Conservative 0; Mismatches 0;
XX
XX QY 1 DLNKGHLDGSEV 13
XX |||||
XX Db 269 DLNKGHLDGSEV 281
XX
XX RESULT 15
XX ABB27587
XX ID ABB27587 standard; Peptide; 66 AA.
XX
XX AC ABB27587;
XX
XX DT 01-FEB-2002 (first entry)
XX
XX DE Human peptide #238 encoded by breast cell single exon nucleic acid probe.
XX
XX KW Human; microarray; single exon probe; gene expression; breast;
XX KW disease; cancer.
XX
XX OS Homo sapiens.
XX
XX PN WO200157271-A2.
XX
XX PD 09-AUG-2001.
XX
XX PF 30-JAN-2001; 2001WO-US00562.
XX
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-496933/54.
XX
XX PT New spatially-addressable set of single exon nucleic acid probes,
XX useful for measuring gene expression in sample derived from human
XX breast, comprises number of single exon nucleic acid probes -
XX
XX PS Claim 27; SEQ ID NO 10555; 327pp + sequence listing; English.
XX
XX CC The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human breast and BT 474 cells. The method involves contacting
XX the probes with a collection of detectably labelled nucleic acids
XX derived from mRNA of human breast, and then measuring the label
XX bound to each probe of the microarray. The probes are useful for
XX verifying the expression of regions of genomic DNA predicted to
XX encode proteins. They are useful for gene discovery, and for
XX determining predisposition and/or prognosing breast disease. Gene
XX expression analysis is useful for assessing the toxicity of chemical
XX agents on cells. The microarray of this invention presents a far greater
XX diversity of probes for measuring gene expression, with far less bias
XX than expressed sequence tag microarrays. The method is suitable for
XX rapid production of functional information from genomic sequence. The
XX present sequence is a peptide encoded by a single exon nucleic acid
XX probe of the invention.
XX Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX

CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 66 AA;

Query Match 58.68; Score 48; DB 22; Length 66;
Best Local Similarity 69.28; Pred. No. 0.56;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLNKDGHLDGSEV 13

DB 27 DLNKDGLDKDEI 39

Search completed: May 14, 2003, 10:42:57
Job time : 5.1173 secs

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 14, 2003, 10:34:02 ; Search time 103.883 Seconds
(without alignments)
420.726 Million cell updates/sec

Title: US-09-768-840-1

Perfect score: 1772

Sequence: 1 MWRRPSVLLLLLLRRHAQG.....FVGSQATNYGEDLTRHDEL 328

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
- 3: /SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
- 4: /SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
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- 10: /SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
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- 19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
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- 22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	1772	100.0	328	19 AAW80746	Human calcium-bind
2	1772	100.0	328	20 AAY13382	Amino acid sequenc
3	1772	100.0	328	20 AAY00916	Human reticulocalb
4	1772	100.0	328	21 AAB33424	Human PRO272 prote
5	1772	100.0	328	21 AAY53640	A bone marrow secr
6	1772	100.0	328	22 AAU12353	Human PRO272 polyp
7	1772	100.0	328	22 AAG64865	Human calcium bind
8	1772	100.0	328	22 AAB80250	Human PRO272 prote
9	1772	100.0	328	22 AAB53085	Human angiogenesis
10	1764	99.5	343	22 AAU87402	Novel central nerv

11	1764	99.5	343	22 AAM43584	Human polypeptide
12	1764	99.5	343	22 AAU19946	Novel human calciu
13	1761	99.4	328	20 AAW67852	Human secreted pro
14	978	55.2	240	22 AAG75587	Human colon cancer
15	967	54.6	184	20 AAW67906	Human secreted pro
16	956	54.0	311	23 ABP41959	Human ovarian anti
17	944	53.3	331	22 AAG64866	Human reticulocalb
18	944	53.3	331	22 AAO17363	Human reticulocalb
19	938	52.9	325	22 AAG64867	Murine reticulocal
20	857.5	48.4	315	22 AAB94090	Human protein sequ
21	857.5	48.4	315	23 AAU84387	Novel human secret
22	842.5	47.5	315	19 AAW37865	Human protein comp
23	842.5	47.5	315	20 AAY00917	Human reticulocalb
24	842.5	47.5	315	20 AAW67886	Human secreted pro
25	833.5	47.0	315	22 AAW93808	Human polypeptide,
26	482	27.2	96	20 AAY11533	Human 5' EST secre
27	457	25.8	342	22 ABB64246	Drosophila melanog
28	456.5	25.8	317	18 AAW21949	E6-binding protein
29	456.5	25.8	349	23 ABP41860	Human ovarian anti
30	449.5	25.4	317	23 AAG65817	Human reticulocalb
31	448.5	25.3	192	22 ABB57787	Drosophila melanog
32	362.5	20.5	219	17 AAK77660	HPV E6-binding pro
33	347	19.6	119	22 AAM93520	Human polypeptide,
34	266.5	15.0	362	18 AAW12373	Human stromal cell
35	260.5	14.7	361	18 AAW12372	Mouse stromal cell
36	230.5	13.0	259	22 AAB93731	Human protein sequ
37	220	12.4	450	18 AAW12375	Human stromal cell
38	205	11.6	94	20 AAY12347	Human 5' EST secre
39	196	11.1	66	22 ABB27587	Human peptide #238
40	196	11.1	66	22 ABB32751	Peptide #257 encod
41	196	11.1	66	22 ABB18233	Protein #232 encod
42	196	11.1	66	22 AAW53562	Human brain expres
43	196	11.1	66	22 AAW65945	Human bone marrow
44	196	11.1	66	22 AAM13812	Peptide #246 encod
45	196	11.1	66	22 AAM26213	Peptide #250 encod

ALIGNMENTS

RESULT 1

AAW80746

ID AAW80746 standard; Protein; 328 AA.

AC AAW80746;

XX

DT 15-DEC-1998 (first entry)

XX

DE Human calcium-binding protein.

XX

XX Human; calcium-binding protein; reticulocalbin; sickle cell anaemia;
KW HCBP; beta thalassaemia; cell proliferation; cancer; adenocarcinoma;
KW leukemia; lymphoma; melanoma; sarcoma.

XX Homo sapiens.

OS

XX WO9844114-A1.

PN

XX 08-OCT-1998.

PD

XX 30-MAR-1998; 98WO-US06233.

PF

XX 31-MAR-1997; 97US-0828242.

PR

XX (INCY-) INCYTE PHARM INC.

XX Goli SK, Hillman JL;

XX WPI; 1998-542704/46.

DR N-PSDB; AAV57600.

XX

PT A new human calcium binding protein - useful for treating or
preventing disorders associated with the expression of HCBP

XX Claim 1; Page 42-43; 60pp; English.

XX The present sequence is a new human calcium binding protein (HCBP).

CC A pharmaceutical composition which includes the HCBP protein is claimed

CC and can be added directly to cells in vivo to promote regeneration or

CC differentiation of cells. HCBP can also be added to cells, cell lines,

CC tissue or organ culture to stimulate cell proliferation for heterologous

CC and autologous transplantation. The cells can be selected for their

CC ability to inhibit development of an infection or to correct a genetic

CC defect such as sickle cell anemia, beta thalassemia. An antagonist of

CC HCBP can be administered to a subject to treat or prevent a disorder

CC associated with cell proliferation e.g. many cancers including

CC adenocarcinoma, leukemia, lymphoma, melanoma, sarcoma and particularly

CC cancers of bladder, bone, brain, heart, kidney, liver. Antibodies

CC specific for HCBP may be used directly as an antagonist or indirectly as

CC a targeting or delivery mechanism for delivering pharmaceutical agents

CC to cell or tissue which express protein HCBP. A method is claimed for

CC treating or preventing a disorder associated with cell proliferation

CC which involves adding pharmaceutical composition of antagonist of HCBP.

XX Sequence 328 AA;

SQ Query Match 100.0%; Score 1772; DB 19; Length 328;

Best Local Similarity 100.0%; Pred. No. 1.7e-155;

Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLRHGAQCKPSDAGPHGGRVHQAPLSDAPHDHAGNFQYDHEAFL 60

Db 1 MMWRPSVLLLLLRHGAQCKPSDAGPHGGRVHQAPLSDAPHDHAGNFQYDHEAFL 60

QY 61 GREVAKFQDLTPESQARLGRIVDRMDRAGDGDGWSLAELRAWIAHTQQRHIRDSVSA 120

Db 61 GREVAKFQDLTPESQARLGRIVDRMDRAGDGDGWSLAELRAWIAHTQQRHIRDSVSA 120

QY 121 AWDYTDRCRGVGEELRNATYGHYAPGEEFHDVEAEYKKMLARDFRFRVADQGD 180

Db 121 AWDYTDRCRGVGEELRNATYGHYAPGEEFHDVEAEYKKMLARDFRFRVADQGD 180

QY 181 SMATREELTAFLHPEEPHMDIVIAETLEDLRNKGQYVOVEYIADLYSAEPGEPEA 240

Db 181 SMATREELTAFLHPEEPHMDIVIAETLEDLRNKGQYVOVEYIADLYSAEPGEPEA 240

QY 241 WVQTERQQRFDRLNKDGLDSEVGHVWLPAPQDQPLVEANHLHESDTRDKDRLSKA 300

Db 241 WVQTERQQRFDRLNKDGLDSEVGHVWLPAPQDQPLVEANHLHESDTRDKDRLSKA 300

QY 301 EILGNWNMFVGSQATNYGEDLTRHDEL 328

Db 301 EILGNWNMFVGSQATNYGEDLTRHDEL 328

RESULT 2

AA13382

ID AA13382 standard; Protein; 328 AA.

XX

XX AA13382;

XX

XX 25-JUN-1999 (first entry)

XX Amino acid sequence of protein PRO272.

DE Secreted protein; transmembrane protein; human; enterocolitis;

XX Zollinger-Ellison syndrome; gastrointestinal ulceration;

XX congenital microvillus atrophy; skin disease; cell growth;

XX abnormal keratinocyte differentiation; psoriasis; epithelial cancer;

XX Parkinson's disease; Alzheimer's disease; ALS; neuropathy;

XX fibronectin; dermal scarring; Usher Syndrome; Atrophia areata;

XX anti-thrombotic; wound healing; tissue repair.

OS Homo sapiens.

XX

PN W09914328-A2.

XX 25-MAR-1999.

XX 16-SEP-1998; 98WO-US19330.

XX 25-NOV-1997; 97US-0066840.

XX 17-SEP-1997; 97US-0059113.

XX 17-SEP-1997; 97US-0059115.

XX 17-SEP-1997; 97US-0059117.

XX 17-SEP-1997; 97US-0059119.

XX 17-SEP-1997; 97US-0059121.

XX 17-SEP-1997; 97US-0059122.

XX 17-SEP-1997; 97US-0059184.

XX 18-SEP-1997; 97US-0059263.

XX 15-OCT-1997; 97US-0059266.

XX 15-OCT-1997; 97US-0062125.

XX 17-OCT-1997; 97US-0062285.

XX 17-OCT-1997; 97US-0062287.

XX 21-OCT-1997; 97US-0063486.

XX 24-OCT-1997; 97US-0062814.

XX 24-OCT-1997; 97US-0062816.

XX 24-OCT-1997; 97US-0063045.

XX 24-OCT-1997; 97US-0063120.

XX 24-OCT-1997; 97US-0063121.

XX 24-OCT-1997; 97US-0063127.

XX 24-OCT-1997; 97US-0063128.

XX 27-OCT-1997; 97US-0063329.

XX 27-OCT-1997; 97US-0063327.

XX 28-OCT-1997; 97US-0063541.

XX 28-OCT-1997; 97US-0063542.

XX 28-OCT-1997; 97US-0063544.

XX 28-OCT-1997; 97US-0063549.

XX 28-OCT-1997; 97US-0063550.

XX 28-OCT-1997; 97US-0063564.

XX 29-OCT-1997; 97US-0063435.

XX 29-OCT-1997; 97US-0063704.

XX 29-OCT-1997; 97US-0063732.

XX 29-OCT-1997; 97US-0063738.

XX 29-OCT-1997; 97US-0063734.

XX 29-OCT-1997; 97US-0064215.

XX 29-OCT-1997; 97US-0063735.

XX 31-OCT-1997; 97US-0063870.

XX 31-OCT-1997; 97US-0064103.

XX 03-NOV-1997; 97US-0064248.

XX 07-NOV-1997; 97US-0064809.

XX 12-NOV-1997; 97US-0065186.

XX 17-NOV-1997; 97US-0065846.

XX 18-NOV-1997; 97US-0065693.

XX 21-NOV-1997; 97US-0066120.

XX 21-NOV-1997; 97US-0066364.

XX 24-NOV-1997; 97US-0066772.

XX 24-NOV-1997; 97US-0066466.

XX 24-NOV-1997; 97US-0066770.

XX 24-NOV-1997; 97US-0066511.

XX 24-NOV-1997; 97US-0066453.

(GETH) GENENTECH INC.

Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;

WPI; 1999-229533/19.

DR N-PSDB; AAX52253.

XX New Isolated human genes and polypeptides used in, e.g. treatment of

XX gastrointestinal ulceration

XX Claim 12; Fig 80; 320pp; English.

XX AA13344-403 represent secreted and transmembrane human proteins.

CC The cDNA sequences are obtained from cDNA libraries, prepared from

CC fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.

CC The encoded polypeptides have specific uses based on their homology to

CC known polypeptides, e.g. PRO211 and PRO217 can be used for disorders

associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital microvillus atrophy), skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as lung squamous cell carcinoma of the vulva and gliomas), potent effects on cell growth and development, diseases related to growth or survival of nerve cells including Parkinson's disease, Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as a target for anti-tumor drugs. PRO533 may be used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can be used as an anti-thrombotic agent; PRO287 polypeptides and portions may have therapeutic applications in wound healing and tissue repair; PRO317 can be used for treating problems of the kidney, uterus, endometrium, blood vessels, or related tissue, e.g. in the heart of genital tract.

Sequence 328 AA;

Query Match 100.0%; Score 1772; DB 20; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.7e-155;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLLLRHGAQGGKSPDAGPHGQGRVHQAAAPLSDAPHDDAHGNFYDHEAFL 60
DB 1 MMWRPSVLLLLLLLRHGAQGGKSPDAGPHGQGRVHQAAAPLSDAPHDDAHGNFYDHEAFL 60

QY 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGGWVSLAEALRAWTAAHTQORHIRDSVSA 120
DB 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGGWVSLAEALRAWTAAHTQORHIRDSVSA 120

QY 121 AWDTYDTRDGRVGEELRNATYGHYAPGEEFHDVEDAETYYKKMLARDERRFRVADQGD 180
DB 121 AWDTYDTRDGRVGEELRNATYGHYAPGEEFHDVEDAETYYKKMLARDERRFRVADQGD 180

QY 181 SMATREELTAFLHPEEPFPHMRDVIATETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
DB 181 SMATREELTAFLHPEEPFPHMRDVIATETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240

QY 241 WVOTERQQFRDRLNKGDLGSEVGHVWLPAPQDQPLVEANHLHSDTKDGRLSKA 300
DB 241 WVOTERQQFRDRLNKGDLGSEVGHVWLPAPQDQPLVEANHLHSDTKDGRLSKA 300

QY 301 EILGNMNFVGSQATNYGEDLTRHDEL 328
DB 301 EILGNMNFVGSQATNYGEDLTRHDEL 328

RESULT 3
AAY00916
ID AAY00916 standard; Protein; 328 AA.

AC AAY00916;
XX AAY00916;
XX 28-MAY-1999 (first entry)

Human reticulocalbin gamma protein sequence.

Human; reticulocalbin gamma; RCNdelta; reticulocalbin delta; RCNdelta; developmental disorder; neoplastic disorder; immunological disorder; infection.

OS Homo sapiens.
XX WO9907849-A2.
XX 18-FEB-1999.
XX 05-AUG-1998; 98WO-US16259.
XX 08-AUG-1997; 97US-0910927.
XX (INCY-) INCYTE PHARM INC.

XX PI

Bandman O, Corley NC, Hillman JL, Lal P, Shah P;

WPI: 1999-180492/15.
N-PSDB: AAX27229.

New human reticulocalbin isoforms - useful to diagnose, prevent, and treat infectious, developmental, neoplastic, and immunological disorders

Claim 1; Fig 1; 82pp; English.

This sequence is the human reticulocalbin gamma (RCNgamma) of the invention. RCNgamma and RCNdelta are used to treat an infectious or developmental disorder, and antagonists of them are used to treat a neoplastic or immunological disorder. Infectious disorders include e.g. pneumonia, lymphocytic choriomeningitis, Hantavirus, chronic bronchitis, hepatitis, herpesviruses, yellow fever, influenza, cancer, measles, mumps, rhinovirus, poliovirus, coxsackie-virus, smallpox, Colorado tick fever, HIV, rabies, gastroenteritis, and rubella, encephalitis, and bacterial, fungal, parasitic, protozoal, or helminthic infections. Development disorders include e.g. renal tubular acidosis, anaemia, Cushing's syndrome, achondroplastic dwarfism, epilepsy, gonadal dysgenesis, hereditary neuropathies such as Charcot-Marie-Tooth disease, and neurofibromatosis, hypothyroidism, hydrocephalus, seizure disorders, congenital glaucoma, cataract, or sensorineural hearing loss. Neoplastic disorders include e.g. adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma and teratocarcinoma. Overexpression of reticulocalbin mRNA has been associated with increased matrix invasive properties of three human breast cancer lines.

Sequence 328 AA;

Query Match 100.0%; Score 1772; DB 20; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.7e-155;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLLLRHGAQGGKSPDAGPHGQGRVHQAAAPLSDAPHDDAHGNFYDHEAFL 60
DB 1 MMWRPSVLLLLLLLRHGAQGGKSPDAGPHGQGRVHQAAAPLSDAPHDDAHGNFYDHEAFL 60

QY 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGGWVSLAEALRAWTAAHTQORHIRDSVSA 120
DB 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGGWVSLAEALRAWTAAHTQORHIRDSVSA 120

QY 121 AWDTYDTRDGRVGEELRNATYGHYAPGEEFHDVEDAETYYKKMLARDERRFRVADQGD 180
DB 121 AWDTYDTRDGRVGEELRNATYGHYAPGEEFHDVEDAETYYKKMLARDERRFRVADQGD 180

QY 181 SMATREELTAFLHPEEPFPHMRDVIATETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
DB 181 SMATREELTAFLHPEEPFPHMRDVIATETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240

QY 241 WVOTERQQFRDRLNKGDLGSEVGHVWLPAPQDQPLVEANHLHSDTKDGRLSKA 300
DB 241 WVOTERQQFRDRLNKGDLGSEVGHVWLPAPQDQPLVEANHLHSDTKDGRLSKA 300

QY 301 EILGNMNFVGSQATNYGEDLTRHDEL 328
DB 301 EILGNMNFVGSQATNYGEDLTRHDEL 328

RESULT 4
AAB33424
ID AAB33424 standard; Protein; 328 AA.

XX AAB33424;
XX 29-JAN-2001 (first entry)
XX Human PRO272 protein UNQ239 SEQ ID NO:51.

DR WPI; 2001-408281/43.
 DR N-PSDB; AAS21425.
 XX
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
 PT lung, breast, prostate, cervical
 XX
 PS Claim 12; Fig 364; 813pp; English.
 XX
 CC AAU12172-AAU12446 represent novel human secretory and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful to detect other
 CC PRO polypeptides, to link bioactive molecules to cells expressing
 CC PRO polypeptides, to modulate biological activities of cells expressing
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample.
 CC Some of the 275 sequences are also useful to stimulate the release of
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
 CC proliferation or differentiation of chondrocytes, the proliferation or
 CC gene expression in pericyte cells, the release of proteoglycans from
 CC cartilage, the proliferation of inner ear utricular supporting cells or
 CC of T-lymphocytes, the release of a cytokine from peripheral blood
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
 CC to factor VIIa. The PRO polypeptides can be used in assays to identify
 CC molecules involved in binding interactions. The polynucleotides encoding
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy.
 XX
 SQ Sequence 328 AA;

Query Match 100.0%; Score 1772; DB 22; Length 328;
 Best Local Similarity 100.0%; Pred. No. 1.7e-155;
 Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMWRPSVLLLLLRHGAQGKPSDAGPHGQGRVHQAPLSDAPHDHAGNFQYDHEAFL 60
 DB 1 MMWRPSVLLLLLRHGAQGKPSDAGPHGQGRVHQAPLSDAPHDHAGNFQYDHEAFL 60
 QY 61 GREVAKEFDQLTPEESQARLGRIVDMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSA 120
 DB 61 GREVAKEFDQLTPEESQARLGRIVDMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSA 120
 QY 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEADAETTKMLARDERRFRVADQGD 180
 DB 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEADAETTKMLARDERRFRVADQGD 180
 QY 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
 DB 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
 QY 241 WYQTERQOQFRDLNKGDLGSEVGHVWLPAPQDQPLVEANHLHESDTDKDGRLSKA 300
 DB 241 WYQTERQOQFRDLNKGDLGSEVGHVWLPAPQDQPLVEANHLHESDTDKDGRLSKA 300
 QY 301 EILGNWNNFVGSQATNYGEDLTRHDEL 328
 DB 301 EILGNWNNFVGSQATNYGEDLTRHDEL 328

RESULT 7
 AAG64865
 ID AAG64865 standard; protein; 328 AA.
 XX
 AC AAG64865;
 XX
 DT 21-SEP-2001 (first entry)
 XX Human calcium binding protein.
 DE Human;
 XX Human;
 KW Human; calcium binding protein; HCBP; cell proliferation disorder;

KW cancer.
 XX Homo sapiens.
 OS
 PN US2001012831-A1.
 XX
 PD 09-AUG-2001.
 XX
 PF 23-JAN-2001; 2001US-0768840.
 XX
 PR 21-MAR-1997; 97US-0828212.
 PR 07-DEC-1998; 98US-0206499.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Hillman JL, Goli SK;
 XX WPI; 2001-464391/50.
 DR N-PSDB; AAH48279.
 XX
 PT Human calcium-binding protein, useful in the diagnosis, prevention, and
 PT treatment of disorders associated with cell proliferation, e.g.
 PT adenocarcinoma, leukemia, lymphoma, melanoma, sarcoma, or
 PT teratocarcinoma
 XX
 PS Claim 1; Fig 1; 30pp; English.
 XX
 CC The present invention provides the protein and coding sequences of human
 CC calcium binding protein (HCBP). The sequences can be used in the
 CC diagnosis, prevention and treatment of cell proliferation disorders, such
 CC as cancer. The present sequence is the protein of the invention.
 XX
 SQ Sequence 328 AA;

Query Match 100.0%; Score 1772; DB 22; Length 328;
 Best Local Similarity 100.0%; Pred. No. 1.7e-155;
 Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 MMWRPSVLLLLLRHGAQGKPSDAGPHGQGRVHQAPLSDAPHDHAGNFQYDHEAFL 60
 QY 61 GREVAKEFDQLTPEESQARLGRIVDMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSA 120
 DB 61 GREVAKEFDQLTPEESQARLGRIVDMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSA 120
 QY 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEADAETTKMLARDERRFRVADQGD 180
 DB 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEADAETTKMLARDERRFRVADQGD 180
 QY 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
 DB 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
 QY 241 WYQTERQOQFRDLNKGDLGSEVGHVWLPAPQDQPLVEANHLHESDTDKDGRLSKA 300
 DB 241 WYQTERQOQFRDLNKGDLGSEVGHVWLPAPQDQPLVEANHLHESDTDKDGRLSKA 300
 QY 301 EILGNWNNFVGSQATNYGEDLTRHDEL 328
 DB 301 EILGNWNNFVGSQATNYGEDLTRHDEL 328

RESULT 8
 AAB80250
 ID AAB80250 standard; protein; 328 AA.
 XX
 AC AAB80250;
 XX
 DT 24-APR-2001 (first entry)
 XX Human
 DE Human
 XX Human PRO272 protein.

KW Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
 KW antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant;
 KW antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
 KW antiarthritic; antinfertility; antidiabetic; antiviral; diabetes;
 KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
 KW ischemia; inflammation.
 XX
 OS Homo sapiens.
 XX WO200104311-A1.
 PN 18-JAN-2001.
 PD 22-FEB-2000; 2000WO-US04414.
 XX 07-JUL-1999; 99US-0143048.
 PR 26-JUL-1999; 99US-0145698.
 PR 28-JUL-1999; 99US-0146222.
 PR 08-SEP-1999; 99WO-US20594.
 PR 13-SEP-1999; 99WO-US20944.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 29-NOV-1999; 99WO-US28214.
 PR 30-NOV-1999; 99WO-US28313.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 05-JAN-2000; 99WO-US00219.
 XX (GETH) GENENTECH INC.
 PA Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
 XX Flivaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kijavini LJ;
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
 PI Williams PM, Wood WI;
 XX WPI: 2001-081051/09.
 DR N-PSDB; AAF72411.
 XX
 PT Sixty one nucleic acids encoding PRO polypeptides which are useful in
 PT the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung
 PT squamous cell carcinoma) and neurodegenerative diseases (e.g.
 PT Alzheimer's disease).
 XX
 PS Claim 1: Fig 80; 393pp; English.
 XX
 CC The present sequence is one of sixty one novel secreted and
 CC transmembrane PRO polypeptides. The PRO polypeptides are
 CC useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung
 CC squamous cell carcinoma), gastrointestinal disorders (e.g.
 CC enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,
 CC Parkinson's disease), wound repair, cardiovascular disorders (e.g.
 CC endometrial bleeding angiogenesis), ischaemias such as coronary
 CC ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma,
 CC rheumatoid arthritis, multiple sclerosis), infertility, AIDS and
 CC diabetes and retinal disorders such as retinitis pigmentosum.
 CC The PRO nucleic acids have applications in molecular biology, including
 CC use as hybridization probes, and in chromosome and gene mapping.
 XX
 SQ Sequence 328 AA;
 Query Match
 Best Local Similarity 100.0%; Score 1772; DB 22; Length 328;
 Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMWRPVLVLLLLRHGAGKPSDPAGPHGGRVHQAPLSDAPHDHAGNFQYDHEAFL 60
 DB 1 MMWRPVLVLLLLRHGAGKPSDPAGPHGGRVHQAPLSDAPHDHAGNFQYDHEAFL 60
 QY 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGGVSLAEALRAWIAHTOORHSDVSA 120
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Db 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGGVSLAEALRAWIAHTOORHSDVSA 120
 QY 121 AWDTYDTRDRGRVGEELRNATYGHVAPGEEFHVDVEDAETTKMLARDERRFRVADQGD 180
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 Db 121 AWDTYDTRDRGRVGEELRNATYGHVAPGEEFHVDVEDAETTKMLARDERRFRVADQGD 180
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 QY 181 SMATREELTAFLHPEEFPHMRDIIAETLEDLDRNKDGVQVVEYIADLYSAEPGEEPA 240
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 Db 181 SMATREELTAFLHPEEFPHMRDIIAETLEDLDRNKDGVQVVEYIADLYSAEPGEEPA 240
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 QY 241 WYOTERQOQFRDLNKNKDLGSEVGHVWLPAPQOPLVEANHLHESDTRDKDGRLSKA 300
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 Db 241 WYOTERQOQFRDLNKNKDLGSEVGHVWLPAPQOPLVEANHLHESDTRDKDGRLSKA 300
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 301 EILGNMNFVGSQATNYGEDLTRHDEL 328
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 EILGNMNFVGSQATNYGEDLTRHDEL 328
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 RESULT 9
 AAB53085
 ID AAB53085 standard; Protein; 328 AA.
 XX
 AC AAB53085;
 XX
 DT 28-FEB-2001 (first entry)
 XX
 DE Human angiogenesis-associated protein PRO272, SEQ ID NO:113.
 XX
 KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;
 KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
 KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
 KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
 KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;
 KW Alzheimer's disease; Huntington's disease; stroke; drug screening;
 KW gene therapy; transgenic animal.
 XX
 OS Homo sapiens.
 XX
 PN WO2000053753-A2.
 XX
 PD 14-SEP-2000.
 PF
 XX 05-JAN-2000; 2000WO-US00219.
 PR 08-MAR-1999; 99WO-US05028.
 PR 12-MAR-1999; 99US-0123957.
 PR 14-MAY-1999; 99US-0134287.
 PR 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 30-NOV-1999; 99WO-US28313.
 PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 XX
 XX (GETH) GENENTECH INC.
 PA Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;
 XX Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;
 PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;
 XX WPI: 2001-090793/10.
 DR N-PSDB; AAC97455.
 XX
 PT New isolated nucleic acid for producing a PRO polypeptide, analyzing
 PT genetic disorders and treating cardiovascular, endothelial or

RESULT 10
AAU87402
ID AAU87402 standard; Protein; 343 AA
XX
XX
AC
XX

Db	256	WVQTERQQFWDFRDLNKGDLGSEVGHVWLP	PAQDQPLVEANHLLHESDTDKDGLSKA	315
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Db	316	EILGNWNNFVGSQATNYGEDLTRHDEL	343	
RESULT 11				
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ID	AA443584 standard; Protein; 343 AA.			
XX	AA443584;			
DT	22-OCT-2001 (first entry)			
XX	Human polypeptide SEQ ID NO 262.			
DE	Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;			
KW	cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;			
KW	fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;			
KW	neuroprotective; antiallergic; hepatotropic; antidiabetic;			
KW	antiinflammatory; antitumor; antileukemic; anticonvulsant; antibacterial;			
KW	antiparasitic; cardiac; gene therapy; cancer; immune disorder;			
KW	cardiovascular disorder; neurological disease; infection; human.			
OS	Homo sapiens.			
XX	WO200155308-A2.			
PN	02-AUG-2001.			
XX	17-JAN-2001; 2001WO-US01309.			
XX	31-JAN-2000; 2000US-0179065.			
PR	04-FEB-2000; 2000US-0180628.			
PR	24-FEB-2000; 2000US-0184664.			
PR	02-MAR-2000; 2000US-0186350.			
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PR	17-MAR-2000; 2000US-0190076.			
PR	18-MAR-2000; 2000US-0198123.			
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PR	17-NOV-2000; 2000US-0249207.			
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PR	17-NOV-2000; 2000US-0249215.			


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PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
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PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
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PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
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PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(PA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
WPI; 2001-465568/50.
N-PSDB; AAS31631.
Isolated nucleic acid molecule encoding a calcium-binding protein is
used in preventing, treating or ameliorating a medical condition -
Claim 11; SEQ ID NO 143; 542pp; English.
The present invention relates to the isolation of novel human
calcium-binding proteins, and cDNA (AAS31577-AAS31634) and genomic
sequences encoding for these proteins. The sequences of the invention
are useful in the diagnosis, prevention and/or prognosis of diseases
associated with aberrant calcium flux. Such disorders include
neurological diseases (e.g. amyotrophic lateral sclerosis, ALS),
immune dysfunction (e.g. severe combined immunodeficiency, SCID),
digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic
disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or
infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The
novel calcium-binding proteins are also useful as screening tools to
identify antagonists and/or agonists that may enhance or inhibit
activities mediated by calcium-binding proteins. The polynucleotides of
the invention are also useful in gene therapy. AAU19892-AAU19969
represent the novel human calcium-binding proteins.
Note: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.
Sequence 343 AA;
Query Match 99.5%; Score 1764; DB 22; Length 343;
Best Local Similarity 99.7%; Pred. NO. 9.9e-155;
Matches 327; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MMWRPSVLLLLLLRHGAQKPSDPAGHGQGRVHQAAAPLSDAPHDDAHGNGFYDHEAFL 60
Db 16 MMWRPSVLLLLLLRHGAQKPSDPAGHGQGRVHQAAAPLSDAPHDDAHGNGFYDHEAFL 75
QY 61 GREVAKFQDLTPESQARLGRIVDRMDRAGDGDGWVSLAEURLAWIAHTQQRHIRDVSVA 120
Db 76 GREVAKFQDLTPESQARLGRIVDRMDRAGDGDGWVSLAEURLAWIAHTQQRHIRDVSVA 135
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OY 121 AWDYTDTRDGRVGEELRNATYGHVAPGEEFHDVEDAETKKMLARDERRFRVADODGD 180
Db 136 AWDYTDTRDGRVGEELRNATYGHVAPGEEFHDVEDAETKKMLARDERRFRVADODGD 195
OY 181 SMATRELTAFHPPEFPHMRDIVIAETLEDLRNKGQVQVEEYIADLYSAEPGEPEPA 240
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OY 241 WYQTERQOFRDRLNKGDLGSEVGHVLPAPQDQPLVEANHLHESDTDKDGRLSKA 300
Db 256 WYQTERQOFRDRLNKGDLGSEVGHVLPAPQDQPLVEANHLHESDTDKDGRLSKA 315
OY 301 EILGNWNVFVGSQATNYGEDLTRHDEL 328
Db 316 EILGNWNVFVGSQATNYGEDLTRHDEL 343

RESULT 13
AAW67852
ID AAW67852 standard; Protein; 328 AA.
XX
AC AAW67852;
XX
DT 25-MAR-1999 (first entry)
XX
DE Human secreted protein encoded by gene 46 clone H5JBQ79.
XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
OS Homo sapiens.

Key Location/Qualifiers
FT Misc-difference 300
FT /label= unknown
FT Misc-difference 328
FT /label= unknown
XX
XX WO9842738-A1.
XX
XX PD 01-OCT-1998.
XX
XX PF 19-MAR-1998; 98WO-US05311.
XX
XX PR 30-MAY-1997; 97US-0050937.
XX PR 21-MAR-1997; 97US-0041276.
XX PR 21-MAR-1997; 97US-0041277.
XX PR 21-MAR-1997; 97US-0041281.
XX PR 21-MAR-1997; 97US-0042344.
XX PR 30-MAY-1997; 97US-0048069.
XX PR 30-MAY-1997; 97US-0048094.
XX PR 30-MAY-1997; 97US-0048095.
XX PR 30-MAY-1997; 97US-0048096.
XX PR 30-MAY-1997; 97US-0048099.
XX PR 30-MAY-1997; 97US-0048131.
XX PR 30-MAY-1997; 97US-0048135.
XX PR 30-MAY-1997; 97US-0048154.
XX PR 30-MAY-1997; 97US-0048160.
XX PR 30-MAY-1997; 97US-0048186.
XX PR 30-MAY-1997; 97US-0048187.
XX PR 30-MAY-1997; 97US-0048188.
XX PR 30-MAY-1997; 97US-0048350.
XX PR 30-MAY-1997; 97US-0048351.
XX PR 30-MAY-1997; 97US-0048352.
XX PR 30-MAY-1997; 97US-0048355.
XX PR 05-AUG-1997; 97US-0054804.

(HUMA-) HUMAN GENOME SCI INC.
Brewer LA, Duan R, Ebner R, Ferrie AM, Florence KA,
Greene JM, Hu JS, Lafleur DW, Moore PA, Ni J, Olsen HS;
Rosen CA, Ruben SM, Shi Y, Young P;
XX WPI; 1999-070065/06.
DR N-PSDB; AAX00656.
XX
XX New isolated human genes and the secreted polypeptides they encode -
XX useful for diagnosis and treatment of e.g. cancers, neurological
XX disorders, immune diseases, inflammation or blood disorders
XX
XX Claim 11: Page 297-298; 385pp; English.
XX
XX This sequence represents a secreted human protein encoded by the gene
XX clone detailed in the descriptor line. The gene can be used to generate
XX fusion proteins by linking to the gene to a human immunoglobulin FC
XX portion (e.g. AAX00602) for increasing the stability of the fused
XX protein as compared to the human protein only.
XX The invention relates to 87 novel genes and their fragments (nucleic
XX acid sequences: AAX00611-X00724; amino acid sequences AAW67807-W68004)
XX which are useful for preventing, treating or ameliorating medical
XX conditions e.g. by protein or gene therapy. Also, pathological
XX polypeptides can be diagnosed by determining the amount of the new
XX polypeptides in a sample or by determining the presence of mutations in
XX the new polynucleotides. Specific uses are described for each of the 87
XX polynucleotides, based on which tissues they are most highly expressed in
XX (see AAX00611 for described uses).

Sequence 328 AA;
OY 2 MWPSVILLLLLRHGAQKPSDAGPHGGRVHQAPLSDAPHDHAGNFQYDHEAF 61
Db 1 MWPSVILLLLLRHGAQKPSDAGPHGGRVHQAPLSDAPHDHAGNFQYDHEAF 60
OY 62 REVAKFEDQLTPEESQARIGRIVDRMDRAGDGDGWSVLAELRAWTQORHRSVSA 121
Db 61 REVAKFEDQLTPEESQARIGRIVDRMDRAGDGDGWSVLAELRAWTQORHRSVSA 120
OY 122 WDTYTDTRDGRVGEELRNATYGHVAPGEEFHDVEDAETKKMLARDERRFRVADODGD 181
Db 121 WDTYTDTRDGRVGEELRNATYGHVAPGEEFHDVEDAETKKMLARDERRFRVADODGD 180
OY 182 MATRELTAFHPPEFPHMRDIVIAETLEDLRNKGQVQVEEYIADLYSAEPGEPEPA 241
Db 181 MATRELTAFHPPEFPHMRDIVIAETLEDLRNKGQVQVEEYIADLYSAEPGEPEPA 240
OY 242 VQTERQOFRDRLNKGDLGSEVGHVLPAPQDQPLVEANHLHESDTDKDGRLSKA 301
Db 241 VQTERQOFRDRLNKGDLGSEVGHVLPAPQDQPLVEANHLHESDTDKDGRLSKA 300
OY 302 ILGNWNVFVGSQATNYGEDLTRHDEL 328
Db 301 ILGNWNVFVGSQATNYGEDLTRHDEL 327

Query Match 99.4%; Score 1761; DB 20; Length 328;
Best Local Similarity 99.4%; Pred. No. 1.8e-154;
Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 14
AAG75587
ID AAG75587 standard; Protein; 240 AA.
XX
AC AAG75587;
XX
XX 03-SEP-2001 (first entry)
XX
XX Human colon cancer antigen protein SEQ ID NO:6351.
XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
XX colorectal carcinoma.
KW

XX	Homo sapiens.
OS	WO20012929-A2.
PX	
PP	05-APR-2001.
PD	
PF	28-SEP-2000; 2000WO-US26524.
PR	29-SEP-1999; 99US-0157137.
PT	03-NOV-1999; 99US-0163280.
PS	(HUMA-) HUMAN GENOME SCI INC.
RUBEN SM,	Barash SC, Birse CE, Rosen CA;
WPI:	2001-235357/24.
N-PSDB:	AHH34992.
Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -	
Claim 11; Page 7803-7804; 9803pp; English.	
AHH32943 to AAH37195 and AAG773514 to AG777788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate p expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of p by expressing inactive proteins or to supplement the patients own production of p. Additionally, N may be used to produce the colon cancer-associated ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and p can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the present invention.	
N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.	
Sequence 240 AA;	
Query Match 55.2%; Score 978; DB 22; Length 240; Best Local Similarity 92.9%; Pred. No. 3.3e-82; Matches 184; Conservative 2; Mismatches 12; Indels 0; Gaps	
QY 131 GRVGWEELRNATYGHYAPGEFFHDVEDAEYYKKMLARDERRFRVADODGDSMATREelta 190 : : Db 43 GRASVDRAHAATAHTGLGEFHDVEDAEYYKKMLARDERRFRVADODGDSMATREelta 102	
QY 191 FLHPPEFPHMrdIVTAETLEDLDRNKDGYGVVEEYIADLYSAEPGEEPAWVTROOFR 250 Db 103 FLHPPEFPHMrdIVTAETLEDLDRNKDGYGVVEEYIADLYSAEPGEEPAWVTROOFR 162	
QY 251 DFRDLKNDCHLDGSEVGHWWLPPAQDQLPVANHLHESDTDKGRLSKAELLGNWNMFV 310 Db 163 DFRDLKNDCHLDGSEVGHWWLPPAQDQLPVANHLHESDTDKGRLSKAELLGNWNMFV 222	
QY 311 GSQATNYGEDLTRHDEL 328 Db 223 GSQATNYGEDLTRHDEL 240	
RESULT 15 AAW67906 ID AAW67906 standard; Protein; 184 AA. XX AAW67906.	

CC fusion proteins by linking to the gene to a human immunoglobulin Fc
CC portion (e.g. AAX00602) for increasing the stability of the fused
CC protein as compared to the human protein only.
CC The invention relates to 87 novel genes and their fragments (nucleic
CC acid sequences: AAX00611-X00724; amino acid sequences AAW67807-W68004)
CC which are useful for preventing, treating or ameliorating medical
CC conditions e.g. by protein or gene therapy. Also, pathological
CC conditions can be diagnosed by determining the amount of the new
CC polypeptides in a sample or by determining the presence of mutations in
CC the new polynucleotides. Specific uses are described for each of the 87
CC polynucleotides, based on which tissues they are most highly expressed in
CC (see AAX00611 for described uses).

XX SQ Sequence 184 AA;

Query Match 54.68; Score 967; DB 20; Length 184;
Best Local Similarity 97.3%; Pred. No. 2.3e-81;
Matches 179; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2 MWRPSVLLLLLLLRHGAQKPSDPAGPHGQGRVHQAAPLSDAPHDHAGNFQYDHEAFLG 61
Db 1 MWRPSVLLLLLLLRHGAQKPSDPAGPHGQGRVHQAAPLSDAPHDHAGNFQYDHEAFLG 60
Qy 62 REVAKFEDLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWIAHTQQRHIRDSVSA 121
Db 61 REVAKFEDLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWIAHTQQRHIRDSVSA 120
Qy 122 WDTYDTRDGRGVGWEELRNATYGHYAPGEEFHDEDAETTKMLARDERRFRVADODGDS 181
Db 121 WDTYDTRDGRGVGWEELRNATYGHYAPGEEFHDEDAETTKMLARDERRFRVADODGDS 180
Qy 182 MATR 185
Db 181 MATR 184

Search completed: May 14, 2003, 10:42:56
Job time : 105.883 secs

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OM protein - protein search, using sw model

Run on: May 14, 2003, 10:41:13 ; Search time 37,5132 Seconds
(without alignments)
257.262 Million cell updates/sec

Title: US-09-768-840-1

Perfect score: 1772

Sequence: 1 MMWRPSVLLLLLRHGAQG.....FVGSQATNYGDLTRHDEL 328

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1772	100.0	328	2	US-08-828-242-1
2	1772	100.0	328	2	US-08-910-927B-1
3	1772	100.0	328	4	US-09-206-499-1
4	1772	100.0	328	4	US-09-270-270-1
5	944	53.3	331	2	US-08-828-242-3
6	944	53.3	331	2	US-08-910-927B-5
7	944	53.3	331	4	US-09-206-499-3
8	944	53.3	331	4	US-09-270-270-5
9	938	52.9	325	2	US-08-828-242-4
10	938	52.9	325	4	US-09-206-499-4
11	842.5	47.5	315	2	US-08-910-927B-3
12	842.5	47.5	315	4	US-09-270-270-3
13	481	27.1	98	2	US-08-910-927B-6
14	481	27.1	98	4	US-09-270-270-6
15	456.5	25.8	317	2	US-08-555-722-8
16	456.5	25.8	317	4	US-09-384-301-8
17	362.5	20.5	220	2	US-08-840-683-8
18	134.5	7.6	276	3	US-09-048-889-4
19	128	7.2	456	1	US-08-464-164-2
20	128	7.2	456	1	US-08-338-057-2
21	128	7.2	456	2	US-08-668-416-2
22	124	7.0	146	3	US-08-963-409-1
23	122.5	6.9	619	3	US-08-813-150-6
24	118.5	6.7	145	4	US-08-720-625-5
25	117.5	6.6	642	2	US-08-818-253-2
26	117.5	6.6	642	4	US-08-818-252-2
27	117.5	6.6	652	2	US-08-818-253-4

28	117.5	6.6	652	4	US-08-818-252-4	Sequence 4, Appl1
29	114.5	6.5	642	2	US-08-818-253-6	Sequence 6, Appl1
30	114.5	6.5	642	4	US-08-818-252-6	Sequence 6, Appl1
31	114.5	6.5	656	2	US-08-818-253-8	Sequence 8, Appl1
32	114.5	6.5	656	4	US-08-818-252-8	Sequence 8, Appl1
33	112.5	6.3	179	3	US-08-764-563-4	Sequence 4, Appl1
34	111	6.3	257	4	US-09-399-913-16	Sequence 16, Appl1
35	111	6.3	257	4	US-09-399-913-16	Sequence 16, Appl1
36	108	6.1	270	4	US-09-399-913-18	Sequence 18, Appl1
37	108	6.1	270	4	US-09-399-913-18	Sequence 18, Appl1
38	107.5	6.1	150	4	US-09-329-909-2	Sequence 2, Appl1
39	107.5	6.1	160	2	US-08-602-941-1	Sequence 1, Appl1
40	107.5	6.1	160	3	US-08-961-264-1	Sequence 1, Appl1
41	107.5	6.1	160	4	US-09-442-099A-1	Sequence 1, Appl1
42	107.5	6.1	169	4	US-08-720-625-4	Sequence 4, Appl1
43	107.5	6.1	170	3	US-08-764-563-5	Sequence 5, Appl1
44	107	6.0	270	4	US-09-399-913-14	Sequence 14, Appl1
45	107	6.0	270	4	US-09-398-731-14	Sequence 14, Appl1

ALIGNMENTS

RESULT 1
US-08-828-242-1
; Sequence 1, Application US/08828242
; Patent No. 5871970 ✓
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L. **SAFE**
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,242
; FILING DATE: Filed Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0261 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: CONUTUR01
; CLONE: 2509570
US-08-828-242-1

Query Match 100.0%; Score 1772; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.1e-168;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CLONE: 922578
US-08-910-927B-1
Query Match 100.0%; Score 1772; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.1e-168; Indels 0; Gaps 0;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLLLRRHGAQKSPDAGPHGQGRVHQAAPLSDAPHDHDAHGNFYDHEAFL 60
DB 1 MMWRPSVLLLLLLLRRHGAQKSPDAGPHGQGRVHQAAPLSDAPHDHDAHGNFYDHEAFL 60
QY 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSA 120
DB 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSA 120
QY 121 ANDTYDTRDGRGVGWEELRNATYGHVAPGEEFHDVEDAETTKKMLARDERRFRVADQDGD 180
DB 121 ANDTYDTRDGRGVGWEELRNATYGHVAPGEEFHDVEDAETTKKMLARDERRFRVADQDGD 180
QY 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
DB 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
QY 241 WVQTERQQFRDRLNKGHLGDSVGHVLPAPQDQPLVEANHLHESDTRDKDGRLSKA 300
DB 241 WVQTERQQFRDRLNKGHLGDSVGHVLPAPQDQPLVEANHLHESDTRDKDGRLSKA 300
QY 301 EILGNMFMVGSQATNYGEDLTRHDEL 328
DB 301 EILGNMFMVGSQATNYGEDLTRHDEL 328

RESULT 3
US-09-206-499-1
Sequence 1, Application US/09206499
Patent No. 6194385
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L. — SAME
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL CALCIUM-BINDING
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/206,499
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,242
FILING DATE: 03/31/1997
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0261 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 328 amino acids
TYPE: amino acid
STRANDEDNESS: single
LIBRARY: RATRNOT02

QY 1 MMWRPSVLLLLLLLRRHGAQKSPDAGPHGQGRVHQAAPLSDAPHDHDAHGNFYDHEAFL 60
DB 1 MMWRPSVLLLLLLLRRHGAQKSPDAGPHGQGRVHQAAPLSDAPHDHDAHGNFYDHEAFL 60
QY 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSA 120
DB 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSA 120
QY 121 ANDTYDTRDGRGVGWEELRNATYGHVAPGEEFHDVEDAETTKKMLARDERRFRVADQDGD 180
DB 121 ANDTYDTRDGRGVGWEELRNATYGHVAPGEEFHDVEDAETTKKMLARDERRFRVADQDGD 180
QY 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
DB 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
QY 241 WVQTERQQFRDRLNKGHLGDSVGHVLPAPQDQPLVEANHLHESDTRDKDGRLSKA 300
DB 241 WVQTERQQFRDRLNKGHLGDSVGHVLPAPQDQPLVEANHLHESDTRDKDGRLSKA 300
QY 301 EILGNMFMVGSQATNYGEDLTRHDEL 328
DB 301 EILGNMFMVGSQATNYGEDLTRHDEL 328

RESULT 2
US-08-910-927B-1
Sequence 1, Application US/08910927B
Patent No. 5976801
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,927B
FILING DATE: Hereewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0358 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 328 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: RATRNOT02

11/2/99 } Different

3/16/99 8/8/97

TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: CONUTUT01
CLONE: 2509570
US-09-206-499-1

Query Match 100.0%; Score 1772; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.1e-168;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLRHGAQKSPDAGPHGQGRVHQAPLSDAPHDDAHGNFQYDHEAFL 60
DB 1 MMWRPSVLLLLLRHGAQKSPDAGPHGQGRVHQAPLSDAPHDDAHGNFQYDHEAFL 60
QY 61 GREVAKEDQLTPEESQARLGRIVDRMDRAGDGGVSLAEALRAWIAHTQORHIRDSVSA 120
DB 61 GREVAKEDQLTPEESQARLGRIVDRMDRAGDGGVSLAEALRAWIAHTQORHIRDSVSA 120
QY 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETYYKMLARDERRFRVADODGD 180
DB 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETYYKMLARDERRFRVADODGD 180
QY 181 SMATREELTAPLHPEEPHMRDIVIAETLEDLRNKDGYVQVEEYIADLYSAEPGEEPA 240
DB 181 SMATREELTAPLHPEEPHMRDIVIAETLEDLRNKDGYVQVEEYIADLYSAEPGEEPA 240
QY 241 WVOTERQQRFRDLNKGHLGDSGVGHVWLPAPADQPLVEANHLHESDTDKDGRLSKA 300
DB 241 WVOTERQQRFRDLNKGHLGDSGVGHVWLPAPADQPLVEANHLHESDTDKDGRLSKA 300
QY 301 EILGNWNVGSOATNYGDELTRHHDEL 328
DB 301 EILGNWNVGSOATNYGDELTRHHDEL 328

RESULT 4

US-09-270-270-1
; Sequence 1, Application US/09270270
; Patent No. 6235477 5/22/01
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/270,270
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/910,927
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0358 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166

TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: RATRNOT02
; CLONE: 922578
; US-09-270-270-1

Query Match 100.0%; Score 1772; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.1e-168;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLRHGAQKSPDAGPHGQGRVHQAPLSDAPHDDAHGNFQYDHEAFL 60
DB 1 MMWRPSVLLLLLRHGAQKSPDAGPHGQGRVHQAPLSDAPHDDAHGNFQYDHEAFL 60
QY 61 GREVAKEDQLTPEESQARLGRIVDRMDRAGDGGVSLAEALRAWIAHTQORHIRDSVSA 120
DB 61 GREVAKEDQLTPEESQARLGRIVDRMDRAGDGGVSLAEALRAWIAHTQORHIRDSVSA 120
QY 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETYYKMLARDERRFRVADODGD 180
DB 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETYYKMLARDERRFRVADODGD 180
QY 181 SMATREELTAPLHPEEPHMRDIVIAETLEDLRNKDGYVQVEEYIADLYSAEPGEEPA 240
DB 181 SMATREELTAPLHPEEPHMRDIVIAETLEDLRNKDGYVQVEEYIADLYSAEPGEEPA 240
QY 241 WVOTERQQRFRDLNKGHLGDSGVGHVWLPAPADQPLVEANHLHESDTDKDGRLSKA 300
DB 241 WVOTERQQRFRDLNKGHLGDSGVGHVWLPAPADQPLVEANHLHESDTDKDGRLSKA 300
QY 301 EILGNWNVGSOATNYGDELTRHHDEL 328
DB 301 EILGNWNVGSOATNYGDELTRHHDEL 328

RESULT 5

US-08-828-242-3
; Sequence 3, Application US/08828242
; Patent No. 5871970
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,242
; FILING DATE: Filed Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0261 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 331 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1262329
US-08-910-927B-5

Query Match 53.3%; Score 944; DB 2; Length 331;
Best Local Similarity 54.7%; Pred. No. 4.5e-86;
Matches 181; Conservative 51; Mismatches 75; Indels 24; Gaps 5;

Qy 7 VLLLLLLRHGAQKPS-----PDAGPHGQGRVHQAAPLSDAPHDHAGNFQYDHEA 58
Db 16 LLLALVLAAPVLRKPTVRKERVVRPD-----SELGERPPED-NQSFQYDHEA 62
Qy 59 FLGREVAKFDPQLTPESQARLGRIVDRMDRAGDGGWVSLAELRAWIAHTQQRHIRDSV 118
Db 63 FLGKEDSKTFQQLPDKESKELGKIVDRID--NDGDFVTTTELKTKWIKRVQRYIFDNV 120
Qy 119 SAAMDVTYDTRDGRVGEELRNATYGHYAPG-EEFHDEVEDAETYYKKMLARDERRFRVADQ 177
Db 121 AKWKYDVRDOKDKISWEEKYQATYGYLGNPAEFHDSHHTFKMLPRDERFKAADL 180
Qy 178 DGSMTAREELTAFLHPEEPHMRDVIATLELDLDRNKDGYQVVEEYIADLYSAEPGEE 237
Db 181 NGDLTATREETAFLHPEEFHMRDVIATLELDLDRNKDGYQVVEEYIADLYSAEPGEE 240
Qy 238 EPWVQTEROQFRDLNKGDLGSEVGHVWLPAPQDQPLVEANHLHSDTDKGRDL 297
Db 241 EPDWVLSEREQNEFRDLNKGDLKDKDEIRHWILPQDYDHAQAARHLVYESDKNDEKL 300
Qy 298 SKAEILGNWNNFVGSQATNYGDLTRHDEL 328
Db 301 TKEILENNWNNFVGSQATNYGDLTKNHDEL 331

RESULT 7
US-09-206-499-3
Sequence 3, Application US/09206499
Patent No. 6194385
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL CALCIUM-BINDING
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: Hereewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

REFERENCE/DOCKET NUMBER: PF-0261 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 331 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1262329
US-08-910-927B-5

Query Match 53.3%; Score 944; DB 2; Length 331;
Best Local Similarity 54.7%; Pred. No. 4.5e-86;
Matches 181; Conservative 51; Mismatches 75; Indels 24; Gaps 5;

Qy 7 VLLLLLLRHGAQKPS-----PDAGPHGQGRVHQAAPLSDAPHDHAGNFQYDHEA 58
Db 16 LLLALVLAAPVLRKPTVRKERVVRPD-----SELGERPPED-NQSFQYDHEA 62
Qy 59 FLGREVAKFDPQLTPESQARLGRIVDRMDRAGDGGWVSLAELRAWIAHTQQRHIRDSV 118
Db 63 FLGKEDSKTFQQLPDKESKELGKIVDRID--NDGDFVTTTELKTKWIKRVQRYIFDNV 120
Qy 119 SAAMDVTYDTRDGRVGEELRNATYGHYAPG-EEFHDEVEDAETYYKKMLARDERRFRVADQ 177
Db 121 AKWKYDVRDOKDKISWEEKYQATYGYLGNPAEFHDSHHTFKMLPRDERFKAADL 180
Qy 178 DGSMTAREELTAFLHPEEPHMRDVIATLELDLDRNKDGYQVVEEYIADLYSAEPGEE 237
Db 181 NGDLTATREETAFLHPEEFHMRDVIATLELDLDRNKDGYQVVEEYIADLYSAEPGEE 240
Qy 238 EPWVQTEROQFRDLNKGDLGSEVGHVWLPAPQDQPLVEANHLHSDTDKGRDL 297
Db 241 EPDWVLSEREQNEFRDLNKGDLKDKDEIRHWILPQDYDHAQAARHLVYESDKNDEKL 300
Qy 298 SKAEILGNWNNFVGSQATNYGDLTRHDEL 328
Db 301 TKEILENNWNNFVGSQATNYGDLTKNHDEL 331

RESULT 6
US-08-910-927B-5
Sequence 5, Application US/08910927B
Patent No. 5976801
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: Hereewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US/09/206,499
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: 08/828,242
; APPLICATION NUMBER: 08/828,242
; FILING DATE: 03/31/1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0261 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 331 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1262329
; US-09-206-499-3

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Query Match          53.3%; Score 944; DB 4; Length 331;
Best Local Similarity 54.7%; Pred. No. 4.5e-86;
Matches 181; Conservative 51; Mismatches 75; Indels 24; Gaps 5;

QY 7 VLLLLLLRHGAQGRPS-----PDAGPHGGRVHQAAPLSDAPHDHAGNFQYDHEA 58
Db 16 LLLALLVAPRLVRAKPTVKERVVRPD-----SELGERPPED-NQSFQYDHEA 62
QY 59 FLGREVAKEFQQLTPESQARLGRIVDRMDRAGDGGVSLAEURLAWIAHTQQRHIRDSV 118
Db 63 FLGKEDSKTFQQLTPDESKERLGIIVRID--NDGCGFVTEELKTWIKRVQRYIFDNV 120
QY 119 SAANDTDTDRGVRGVEELRNATYGHYAPG-EFFHDEVEDAEYKMKLARDERRFRVADQ 177
Db 121 AKVWKDYDRDKDDKISWEYKQATYGYLGNPAEFHDSDDHHTFKKMLPRDRERRFKAADL 180
QY 178 DGSNATREELTAFLHPPEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAPFGEE 237
Db 181 NGDLTATREETAFLHPPEEFHMKIIVLETLEDIDKNGDGFVDQDEYIADMFSEHNGP 240
QY 238 EPAWVQTERQOFRDLNKGDLGSEVGHVWLPAPQOQPLVEANHLHESDTDKGRL 297
Db 241 EPDWLSEREQFNEFRDLNKGDLKDKDEIRHILWPIDYDHAQAEARHLVYESDKNKDEKL 300
QY 298 SKAEILGNMNMFGSOATNYGDLTRHDEL 328
Db 301 TKEEILNMMNMFVGSQATNYGDLTKNHDEL 331

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RESULT 8
US-09-270-270-5
; Sequence 5, Application US/09270270
; Patent No. 6235477
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/270,270
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/910,927
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0358 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 331 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1262329
; US-09-270-270-5

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Query Match          53.3%; Score 944; DB 4; Length 331;
Best Local Similarity 54.7%; Pred. No. 4.5e-86;
Matches 181; Conservative 51; Mismatches 75; Indels 24; Gaps 5;

QY 7 VLLLLLLRHGAQGRPS-----PDAGPHGGRVHQAAPLSDAPHDHAGNFQYDHEA 58
Db 16 LLLALLVAPRLVRAKPTVKERVVRPD-----SELGERPPED-NQSFQYDHEA 62
QY 59 FLGREVAKEFQQLTPESQARLGRIVDRMDRAGDGGVSLAEURLAWIAHTQQRHIRDSV 118
Db 63 FLGKEDSKTFQQLTPDESKERLGIIVRID--NDGCGFVTEELKTWIKRVQRYIFDNV 120
QY 119 SAANDTDTDRGVRGVEELRNATYGHYAPG-EFFHDEVEDAEYKMKLARDERRFRVADQ 177
Db 121 AKVWKDYDRDKDDKISWEYKQATYGYLGNPAEFHDSDDHHTFKKMLPRDRERRFKAADL 180
QY 178 DGSNATREELTAFLHPPEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAPFGEE 237
Db 181 NGDLTATREETAFLHPPEEFHMKIIVLETLEDIDKNGDGFVDQDEYIADMFSEHNGP 240
QY 238 EPAWVQTERQOFRDLNKGDLGSEVGHVWLPAPQOQPLVEANHLHESDTDKGRL 297
Db 241 EPDWLSEREQFNEFRDLNKGDLKDKDEIRHILWPIDYDHAQAEARHLVYESDKNKDEKL 300
QY 298 SKAEILGNMNMFGSOATNYGDLTRHDEL 328
Db 301 TKEEILNMMNMFVGSQATNYGDLTKNHDEL 331

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```

RESULT 9
US-08-828-242-4
; Sequence 4, Application US/08828242
; Patent No. 5871970
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto

```

us-09-768-840-1-rai

Tue May 20 14:43:27 2003

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/206,499

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA: 08/828,242

APPLICATION NUMBER: 03/31/1997

FILING DATE: 03/31/1997

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0261 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 325 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GenBank

CLONE: 220582

US-09-206-499-4

Query Match 52.9%; Score 938; DB 2; Length 325;

Best Local Similarity 55.2%; Pred. No. 1.7e-85;

Matches 181; Conservative 47; Mismatches 76; Indels 24; Gaps 5;

QY 10 LLLLRHGAQKPS-----PDAGPHGQGRVHQAPLSDAPHDHAGNFQYDHEAFLG 61

DB 13 LLLALVALRAKPTVRKRVVRPD-----SELGERPPED-NQSFQYDHEAFLG 59

QY 62 REVAKFDPOLTPESQARLGRIVDRMDRAGDGGWVSLAELRAWIAHTQOHRIRDSVSA 121

DB 60 KEDSKTFDQSPDSKSKRLGKIVDRID--SDGSLVTTELKWKIKRVQKRYIYDNVAKV 117

QY 122 WDTYDTRDGRVGVWEELRNATYGHYAPG-EFHDVEDAEIYKKMLARDERRFVADQGD 180

DB 118 WKDYDRDKDEKISWEYKQATYGYLGNPAEFHDSDDHHTFKMLPRDERFRKASDLGD 177

QY 181 SMATREELTAFHPPEEPHMRDIVIAETLEDLRNKDGYVQVEEYIADLYSAEPGEEPA 240

DB 178 LTATREETAFHPPEEFHMKIEIVVLETDIDKNGDGFVDQDEYIADMFSHEDNGPEPD 237

QY 241 WYOTERQOQFRDLNKGDLGDSGVGHVLPAPQOQPLVEANHLHESDTDKGRLSKA 300

DB 238 WLSEREQNFDFRLNKGDLGDKLDEIRHWILPDQYDHAQAARHLVYESDKNKDEMLTKE 297

QY 301 EILGNMNFVGSQATNYGDLTRHDEL 328

DB 298 EILDNNMNFVGSQATNYGDLTKNHDEL 325

RESULT 10

US-09-206-499-4

; Sequence 4, Application US/09206499

; Patent No. 6194385

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: NOVEL CALCIUM-BINDING

; TITLE OF INVENTION: NOVEL CALCIUM-BINDING

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

RESULT 11

US-08-910-927B-3

; Sequence 3, Application US/08910927B

; Patent No. 5976801

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Lal, Preeti


```

; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,927B
; FILING DATE: Hereewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0358 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BLADNOT03
; CLONE: 1601793
; US-08-910-927B-3

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Query Match 47.5% Score 842.5; DB 2; Length 315;
Best Local Similarity 50.5%; Pred. No. 5.6e-76;
Matches 161; Conservative 60; Mismatches 87; Indels 11; Gaps 4;

QY 8 LLLLLLHGAQGKPSDPAGPHGQGRVHQAPLSDAPHDDAHGNFYDHEAFLGREVAKE 67
Db 7 LMCLSLCTAFALSAPT-----EKKDRVHHEPQLSDKVHNDQAQ-SFDYDHDALGAEAKT 60
QY 68 FDLTPESQARLGRIVDRMDRAGDGGWVSLAELRAWIAHTQORHIRDSVSAANDTYDT 127
Db 61 FDLTPESKERLGVKISKID--GDKDGFVTVDELKDWIFAKRWIYEDVERQWKGHDL 118
QY 128 DRGRVGEELRNATYGHVAPGEEFHDVEDAETKKMLARDERRFRVADQDGSMTREE 187
Db 119 NEDGLVSWEEYKNATYGYVL---DDPPDDGFNYKQMVYDERFRKMDKGDGLIATKEE 175
QY 188 LTAFLPEEPHMRDVIATLLEDLRNKGQYVQVEEYIADLYSAEPGEEPAWQTERQ 247
Db 176 FTAFLPEEYDMKDIVVQETMEDIDKNADGFDLLEEYIGDMYSHDGNTPDEPWKTERE 235
QY 248 QFRDRLNKGDLGSEYGHVLPAPQDQPLVEANHLHESDTDKDGLSKAEILGNWN 307
Db 236 QFVEFRDKNRDGMKEETKDWILPSDYDHAEAEARHLVYESDQNKDGKLTKEEIVDKYD 295
QY 308 MFVGSQATNYGEDLTRHHD 326
Db 296 LFVGSQATDFGEALVRHDE 314

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RESULT 12
US-09-270-270-3

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; Sequence 3, Application US/09270270
; Patent No. 6235477
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/270,270
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/910,927
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0358 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BLADNOT03
; CLONE: 1601793
; US-09-270-270-3

```

```

Query Match 47.5% Score 842.5; DB 4; Length 315;
Best Local Similarity 50.5%; Pred. No. 5.6e-76;
Matches 161; Conservative 60; Mismatches 87; Indels 11; Gaps 4;

QY 8 LLLLLLHGAQGKPSDPAGPHGQGRVHQAPLSDAPHDDAHGNFYDHEAFLGREVAKE 67
Db 7 LMCLSLCTAFALSAPT-----EKKDRVHHEPQLSDKVHNDQAQ-SFDYDHDALGAEAKT 60
QY 68 FDLTPESQARLGRIVDRMDRAGDGGWVSLAELRAWIAHTQORHIRDSVSAANDTYDT 127
Db 61 FDLTPESKERLGVKISKID--GDKDGFVTVDELKDWIFAKRWIYEDVERQWKGHDL 118
QY 128 DRGRVGEELRNATYGHVAPGEEFHDVEDAETKKMLARDERRFRVADQDGSMTREE 187
Db 119 NEDGLVSWEEYKNATYGYVL---DDPPDDGFNYKQMVYDERFRKMDKGDGLIATKEE 175
QY 188 LTAFLPEEPHMRDVIATLLEDLRNKGQYVQVEEYIADLYSAEPGEEPAWQTERQ 247
Db 176 FTAFLPEEYDMKDIVVQETMEDIDKNADGFDLLEEYIGDMYSHDGNTPDEPWKTERE 235
QY 248 QFRDRLNKGDLGSEYGHVLPAPQDQPLVEANHLHESDTDKDGLSKAEILGNWN 307
Db 236 QFVEFRDKNRDGMKEETKDWILPSDYDHAEAEARHLVYESDQNKDGKLTKEEIVDKYD 295
QY 308 MFVGSQATNYGEDLTRHHD 326

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[illegible]

Search completed: May 14, 2003, 10:47:14
Job time : 39.5132 secs

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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 14, 2003, 10:43:07 ; Search time 31.7419 Seconds
(without alignments)
950.932 Million cell updates/sec

Title: US-09-768-840-1
Perfect score: 1772
Sequence: 1 MMWRPSVLLLLLRHGAQG.....FVGSQATNYCEDTRRHDEL 328

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 349150 seqs, 92025710 residues

Total number of hits satisfying chosen parameters: 349150

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA.*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/PCQUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1772	100.0	328	9	US-09-905-291A-221
2	1772	100.0	328	9	US-09-902-853-221
3	1772	100.0	328	9	US-09-907-824-221
4	1772	100.0	328	9	US-09-907-841-221
5	1772	100.0	328	9	US-09-904-011-221
6	1772	100.0	328	9	US-10-028-072-364
7	1772	100.0	328	9	US-09-906-742-221
8	1772	100.0	328	9	US-10-121-049-364
9	1772	100.0	328	9	US-10-123-904-364
10	1772	100.0	328	9	US-10-140-470-364
11	1772	100.0	328	9	US-09-906-838-221
12	1772	100.0	328	9	US-09-907-813-221
13	1772	100.0	328	9	US-10-175-746-364
14	1772	100.0	328	9	US-10-176-918-364
15	1772	100.0	328	9	US-10-176-921-364
16	1772	100.0	328	9	US-10-137-865-364
17	1772	100.0	328	9	US-10-140-474-364
18	1772	100.0	328	9	US-09-904-820-221
19	1772	100.0	328	9	US-09-904-820-221

20	1772	100.0	328	9	US-09-904-859-221	Sequence 221, App
21	1772	100.0	328	9	US-09-909-204-221	Sequence 221, App
22	1772	100.0	328	9	US-10-142-431-364	Sequence 364, App
23	1772	100.0	328	9	US-10-143-114-364	Sequence 364, App
24	1772	100.0	328	9	US-09-904-786-221	Sequence 221, App
25	1772	100.0	328	9	US-09-906-646-221	Sequence 221, App
26	1772	100.0	328	9	US-09-906-700-221	Sequence 221, App
27	1772	100.0	328	9	US-10-140-002-364	Sequence 364, App
28	1772	100.0	328	9	US-09-902-903-221	Sequence 221, App
29	1772	100.0	328	9	US-09-903-749A-221	Sequence 221, App
30	1772	100.0	328	9	US-09-903-786-221	Sequence 221, App
31	1772	100.0	328	9	US-10-142-419-364	Sequence 364, App
32	1772	100.0	328	9	US-09-902-736-221	Sequence 221, App
33	1772	100.0	328	9	US-09-904-119-221	Sequence 221, App
34	1772	100.0	328	9	US-09-904-956-221	Sequence 221, App
35	1772	100.0	328	9	US-09-907-794-221	Sequence 364, App
36	1772	100.0	328	9	US-10-123-262-364	Sequence 364, App
37	1772	100.0	328	9	US-09-902-692-221	Sequence 221, App
38	1772	100.0	328	9	US-09-903-520-221	Sequence 221, App
39	1772	100.0	328	9	US-09-903-943-221	Sequence 221, App
40	1772	100.0	328	9	US-09-904-462-221	Sequence 221, App
41	1772	100.0	328	9	US-09-905-056-221	Sequence 221, App
42	1772	100.0	328	9	US-09-907-925-221	Sequence 364, App
43	1772	100.0	328	9	US-10-121-050-364	Sequence 364, App
44	1772	100.0	328	9	US-10-141-755-364	Sequence 364, App
45	1772	100.0	328	9	US-10-141-755-364	Sequence 364, App

ALIGNMENTS

RESULT 1

US-09-905-291A-221
; Sequence 221, Application US/09050291A
; Patent No. US20020160374A1

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumes, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,291A
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222

APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Guiney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,853
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US/09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 221
LENGTH: 328
TYPE: PRT
ORGANISM: Homo Sapien
US-09-902-853-221

Query Match 100.0%; Score 1772; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 2.1e-143;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 241 WQOTERQOQFRDLNKGDLGSEVGHVLPQAQDQPLVEANHLHSDTDKDGRLSKA 300
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US-09-902-853-221
; Sequence 221, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.

QY 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWYSLAELRAWIAHTQQRHIRDSVSA 120
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Db 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWYSLAELRAWIAHTQQRHIRDSVSA 120
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Db 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEFHDVEADATYKKMLARDERRFRVADODGD 180
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RESULT 3

US-09-907-824-221
; Sequence 221, Application US/09907824
; Publication No. US20020197671A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Grittsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Macher, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,824
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 221
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-824-221

Query Match

Best Local Similarity 100.0%; Score 1772; DB 9; Length 328;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEFHDVEADATYKKMLARDERRFRVADODGD 180
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|||||
Db 181 SMATREELTAPLHPPEEPHMRDVIATLLEDLRNKDGYVQVEEYIADLYSAPGEEPA 240
QY 241 WVOTEROQFRDLNKGDLGSEVGHVWVLPQAQDQPLVEANHLHESDTDKDGRLSKA 300
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Db 241 WVOTEROQFRDLNKGDLGSEVGHVWVLPQAQDQPLVEANHLHESDTDKDGRLSKA 300
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RESULT 4

US-09-907-841-221
; Sequence 221, Application US/09907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Grittsen, Mary E.
; APPLICANT: Goddard, A.


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; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 221
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-011-221

Query Match      100.0%   Score 1772; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 2.1e-143;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MMRRPSVLLLLLLLRRGAGKSPDAGPHGQGRVHQAAPLSDAPHDHAGNFQYDHEAFL 60
   |||||
QY 61 GREVAKFQDLTPESQARLGRVDRMDRAGDGDGWSLAELRAWIAHTQQRHIRDSVSA 120
   |||||
Db 61 GREVAKFQDLTPESQARLGRVDRMDRAGDGDGWSLAELRAWIAHTQQRHIRDSVSA 120
   |||||
QY 121 AWDYTDTRDGRVGVHEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQGD 180
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Db 121 AWDYTDTRDGRVGVHEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQGD 180
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QY 181 SMATREELTAFLHPPEEFHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEPEPA 240
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Db 181 SMATREELTAFLHPPEEFHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEPEPA 240
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QY 241 WYQTERQQRFRDLNKGCHLDGSEVGHVWLPAPQDQPLVEANHLHESDTDKDGRLSKA 300
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Db 241 WYQTERQQRFRDLNKGCHLDGSEVGHVWLPAPQDQPLVEANHLHESDTDKDGRLSKA 300
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QY 301 ETLGNMNFVGSQATNYGDELTRHDEL 328
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RESULT 6
US-10-028-072-364
; Sequence 364, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/028,072
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
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; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1998-02-04
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
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; PRIOR FILING DATE: 1997-09-19
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; PRIOR FILING DATE: 1997-09-24
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/063082
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; PRIOR APPLICATION NUMBER: 60/074086
; PRIOR FILING DATE: 1998-02-09
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; PRIOR FILING DATE: 1998-02-09
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; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081818
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082999
; PRIOR FILING DATE: 1998-04-24
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085149
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086414
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/086430
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088730
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088741
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089907

Query Match          100.0%; Score 1772; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 2.1e-143;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLRRHGAQKPSPDAGPHCGQGRVHQAAPLSDAPHDDAHGNFOYDHEAFL 60
Db 1 MMWRPSVLLLLLRRHGAQKPSPDAGPHCGQGRVHQAAPLSDAPHDDAHGNFOYDHEAFL 60
QY 61 GREVAKFEDQLTPESQARLGRIVDRMDRAGDGDGVWSLAELRAWTIAHTQQRHIRDSVSA 120
Db 61 GREVAKFEDQLTPESQARLGRIVDRMDRAGDGDGVWSLAELRAWTIAHTQQRHIRDSVSA 120
QY 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEADTYKKMLARDERRFRVADQGD 180
Db 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEADTYKKMLARDERRFRVADQGD 180
QY 181 SMATREELTAPLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
Db 181 SMATREELTAPLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
QY 241 WVQTERQQFRDLINKDGLDSEGVGHVWLPAAQDQPLVEANHLHSHESDTDKDGRLSKA 300
Db 241 WVQTERQQFRDLINKDGLDSEGVGHVWLPAAQDQPLVEANHLHSHESDTDKDGRLSKA 300
QY 301 EILGNMNMVGSQATNYGEDLTRHDEL 328
Db 301 EILGNMNMVGSQATNYGEDLTRHDEL 328

RESULT 7
US-09-906-742-221
; Sequence 221, Application US/09906742
; Publication No. US20030023054A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavina, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
```

APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,742
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 221
LENGTH: 328
TYPE: PRT
ORGANISM: Homo Sapien
US-09-906-742-221

Query Match 100.0%; Score 1772; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 2,1e-143;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLLLRHGAQKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60
DB 1 MMWRPSVLLLLLLLRHGAQKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60

QY 61 GREVAKFEDLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWIAHTQORHIRDSVSA 120
DB 61 GREVAKFEDLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWIAHTQORHIRDSVSA 120

QY 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQGD 180
DB 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQGD 180

QY 181 SMATREELTAFLLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAPGEEPEA 240
DB 181 SMATREELTAFLLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAPGEEPEA 240

QY 241 WYQTERQQFRDRLDNKKGHLDSGSEVGHVWLPAPQDQPLVEANHLHESDTDKDGRLSKA 300
DB 241 WYQTERQQFRDRLDNKKGHLDSGSEVGHVWLPAPQDQPLVEANHLHESDTDKDGRLSKA 300

QY 301 EILGNMNFVGSQATNYGEDLTRHHDEL 328
DB 301 EILGNMNFVGSQATNYGEDLTRHHDEL 328

RESULT 8

US-10-121-049-364
Sequence 364, Application US/10121049
Publication No. US2003002239A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C17
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 364
LENGTH: 328
TYPE: PRT
ORGANISM: Homo Sapien
US-10-121-049-364

Query Match 100.0%; Score 1772; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 2,1e-143;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLLLRHGAQKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60
DB 1 MMWRPSVLLLLLLLRHGAQKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60

QY 61 GREVAKFEDLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWIAHTQORHIRDSVSA 120
DB 61 GREVAKFEDLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWIAHTQORHIRDSVSA 120

QY 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQGD 180
DB 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQGD 180

QY 181 SMATREELTAFLLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAPGEEPEA 240
DB 181 SMATREELTAFLLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAPGEEPEA 240

QY 241 WYQTERQQFRDRLDNKKGHLDSGSEVGHVWLPAPQDQPLVEANHLHESDTDKDGRLSKA 300
DB 241 WYQTERQQFRDRLDNKKGHLDSGSEVGHVWLPAPQDQPLVEANHLHESDTDKDGRLSKA 300

QY 301 EILGNMNFVGSQATNYGEDLTRHHDEL 328
DB 301 EILGNMNFVGSQATNYGEDLTRHHDEL 328

RESULT 9

US-10-123-904-364

; Sequence 364, Application US/10123904

; Publication No. US20030022328A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3330R1C54

; CURRENT APPLICATION NUMBER: US/10/123,904

; CURRENT FILING DATE: 2002-04-16

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 364

; LENGTH: 328

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-123-904-364

Query Match 100.0%; Score 1772; DB 9; Length 328;

Best Local Similarity 100.0%; Pred. No. 2.1e-143;

Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLLRHGAQKSPDAGHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFL 60

Db 1 MMWRPSVLLLLLLRHGAQKSPDAGHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFL 60

QY 61 GREVAKEFDLTPESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSA 120

Db 61 GREVAKEFDLTPESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSA 120

QY 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETTKKMLARDERRFRVADQGD 180

Db 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETTKKMLARDERRFRVADQGD 180

QY 181 SMATRELTAFLEPPEPHEPMDIVIAETLEDLRNKGDDGYVQVEEYIADLYSAEPGEEPA 240

Db 181 SMATRELTAFLEPPEPHEPMDIVIAETLEDLRNKGDDGYVQVEEYIADLYSAEPGEEPA 240

QY 241 WVQTERQOQFRDLNKGDLGSEVGHVWLPVPAQDQPLVEANHLHESDTDKDGRLSKA 300

Db 241 WVQTERQOQFRDLNKGDLGSEVGHVWLPVPAQDQPLVEANHLHESDTDKDGRLSKA 300

QY 301 EILGNWNNFVGSQATNYGEDLTRHDEL 328

Db 301 EILGNWNNFVGSQATNYGEDLTRHDEL 328

RESULT 10

US-10-140-470-364

; Sequence 364, Application US/10140470

; Publication No. US20030022331A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

RESULT 11

US-09-906-838-221

; Sequence 221, Application US/09906838

; Publication No. US20030027143A1

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3330R1C160

; CURRENT APPLICATION NUMBER: US/10/140,470

; CURRENT FILING DATE: 2002-05-06

; Prior Application removed - See Palm or File Wrapper

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 364

; LENGTH: 328

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-140-470-364

Query Match 100.0%; Score 1772; DB 9; Length 328;

Best Local Similarity 100.0%; Pred. No. 2.1e-143;

Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLLRHGAQKSPDAGHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFL 60

Db 1 MMWRPSVLLLLLLRHGAQKSPDAGHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFL 60

QY 61 GREVAKEFDLTPESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSA 120

Db 61 GREVAKEFDLTPESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSA 120

QY 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETTKKMLARDERRFRVADQGD 180

Db 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETTKKMLARDERRFRVADQGD 180

QY 181 SMATRELTAFLEPPEPHEPMDIVIAETLEDLRNKGDDGYVQVEEYIADLYSAEPGEEPA 240

Db 181 SMATRELTAFLEPPEPHEPMDIVIAETLEDLRNKGDDGYVQVEEYIADLYSAEPGEEPA 240

QY 241 WVQTERQOQFRDLNKGDLGSEVGHVWLPVPAQDQPLVEANHLHESDTDKDGRLSKA 300

Db 241 WVQTERQOQFRDLNKGDLGSEVGHVWLPVPAQDQPLVEANHLHESDTDKDGRLSKA 300

QY 301 EILGNWNNFVGSQATNYGEDLTRHDEL 328

Db 301 EILGNWNNFVGSQATNYGEDLTRHDEL 328

```

; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,838
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 221
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-838-221

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Query Match 100.0%; Score 1772; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 2.1e-143;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLRHGAQKSPDAGPHGGRVHQAPLSDAPHDHAGNFQYDHEAFL 60
DB 1 MMWRPSVLLLLLRHGAQKSPDAGPHGGRVHQAPLSDAPHDHAGNFQYDHEAFL 60
QY 61 GREVAKETDQTPESQARLGRIVDMDRAGDGDGWYSLAELRAWIAHTQORHROSVA 120
DB 61 GREVAKETDQTPESQARLGRIVDMDRAGDGDGWYSLAELRAWIAHTQORHROSVA 120

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QY 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETYYKKMLARDERRFRVADQGD 180
DB 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETYYKKMLARDERRFRVADQGD 180
QY 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKGQYVQVEEYIADLYSAEPGEEPA 240
DB 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKGQYVQVEEYIADLYSAEPGEEPA 240
QY 241 WVQTERQQFRDRLNKGDLGSEYGHVWLPVPAQDQPLVEANHLHESDTRKDGRLSKA 300
DB 241 WVQTERQQFRDRLNKGDLGSEYGHVWLPVPAQDQPLVEANHLHESDTRKDGRLSKA 300
QY 301 EILGNMFMVGSQATNYGEDLRRHDEL 328
DB 301 EILGNMFMVGSQATNYGEDLRRHDEL 328

RESULT 12
US-09-907-613-221
; Sequence 221, Application US/09907613
; Publication No. US20030027145A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,613
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313

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Tue May 20 14:43:28 2003

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; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 221
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-613-221

Query Match      100.0%; Score 1772; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 2.1e-143;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLHGAQGPSDPAGPHGQGRVHQAPLSDAPHDHDAHGNFYDHEAFL 60
DB 1 MMWRPSVLLLLLHGAQGPSDPAGPHGQGRVHQAPLSDAPHDHDAHGNFYDHEAFL 60
QY 61 GREVAKEFDQLTPEESQARLGRIVDMDRAGDGDGWSLAELRAWIAHTQQRHTRDSVSA 120
DB 61 GREVAKEFDQLTPEESQARLGRIVDMDRAGDGDGWSLAELRAWIAHTQQRHTRDSVSA 120
QY 121 AMDTYDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERFRVADQGD 180
DB 121 AMDTYDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERFRVADQGD 180
QY 181 SMATREELTAFLLHPEEFPHMRDIVIAETLEDLDRNKDGYGVQVEEYIADLYSAEPGEEPPA 240
DB 181 SMATREELTAFLLHPEEFPHMRDIVIAETLEDLDRNKDGYGVQVEEYIADLYSAEPGEEPPA 240
QY 241 WVOTERQQRDFRDLNKGDLGSEVGHVWLPADQDPLVEANHLHESDITDKDGRLSKA 300
DB 241 WVOTERQQRDFRDLNKGDLGSEVGHVWLPADQDPLVEANHLHESDITDKDGRLSKA 300
QY 301 EILGNMFMVGSQATNYGDLTRHDEL 328
DB 301 EILGNMFMVGSQATNYGDLTRHDEL 328

RESULT 13
US-09-907-942-221
; Sequence 221, Application US/09907942
; Publication No. US20030027146A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
```

```

; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,942
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 221
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-942-221

Query Match      100.0%; Score 1772; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 2.1e-143;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 MMWRPSVLLLLLHGAQGPSDPAGPHGQGRVHQAPLSDAPHDHDAHGNFYDHEAFL 60
DB 1 MMWRPSVLLLLLHGAQGPSDPAGPHGQGRVHQAPLSDAPHDHDAHGNFYDHEAFL 60
QY 61 GREVAKEFDQLTPEESQARLGRIVDMDRAGDGDGWSLAELRAWIAHTQQRHTRDSVSA 120
DB 61 GREVAKEFDQLTPEESQARLGRIVDMDRAGDGDGWSLAELRAWIAHTQQRHTRDSVSA 120
QY 121 AMDTYDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERFRVADQGD 180
DB 121 AMDTYDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERFRVADQGD 180
QY 181 SMATREELTAFLLHPEEFPHMRDIVIAETLEDLDRNKDGYGVQVEEYIADLYSAEPGEEPPA 240
DB 181 SMATREELTAFLLHPEEFPHMRDIVIAETLEDLDRNKDGYGVQVEEYIADLYSAEPGEEPPA 240
QY 241 WVOTERQQRDFRDLNKGDLGSEVGHVWLPADQDPLVEANHLHESDITDKDGRLSKA 300
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Db 241 WYOTERQQRFRDLNKGDLGSEVGHVLPAPQDQPLVEANHLHESDTRHDELSKA 300
QY 301 EILGNMNFVGSQATNYGDLTRHDEL 328
Db 301 EILGNMNFVGSQATNYGDLTRHDEL 328

RESULT 14

US-10-175-746-364
; Sequence 364, Application US/10175746
; Publication No. US20030027270A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3330R1C353

; CURRENT APPLICATION NUMBER: US/10/175,746

; CURRENT FILING DATE: 2002-06-19

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 364

; LENGTH: 328

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-175-746-364

Query Match 100.0%; Score 1772; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 2,1e-143;

Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MMWRPSVLLLLLLLRHGAQKSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60

QY 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWTIAHTQQRHIRDSVSA 120
Db 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWTIAHTQQRHIRDSVSA 120

QY 121 AWDTYDTRDGRVGEELRNATYGHYAPGEEFHDVEDAETYYKKMLARDERRFRVADQGD 180
Db 121 AWDTYDTRDGRVGEELRNATYGHYAPGEEFHDVEDAETYYKKMLARDERRFRVADQGD 180

QY 181 SMATREELTAFLEHPEEFPHMRDIVIAETLEDLDRNKGQYVQVEEYIADLYSAEPGEEPA 240
Db 181 SMATREELTAFLEHPEEFPHMRDIVIAETLEDLDRNKGQYVQVEEYIADLYSAEPGEEPA 240

QY 241 WYOTERQQRFRDLNKGDLGSEVGHVLPAPQDQPLVEANHLHESDTRHDELSKA 300
Db 241 WYOTERQQRFRDLNKGDLGSEVGHVLPAPQDQPLVEANHLHESDTRHDELSKA 300

QY 301 EILGNMNFVGSQATNYGDLTRHDEL 328
Db 301 EILGNMNFVGSQATNYGDLTRHDEL 328

RESULT 15

US-10-176-918-364
; Sequence 364, Application US/10176918
; Publication No. US20030027275A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3330R1C382

; CURRENT APPLICATION NUMBER: US/10/176,918

; CURRENT FILING DATE: 2002-06-20

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 364

; LENGTH: 328

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-176-918-364

Query Match 100.0%; Score 1772; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 2,1e-143;

Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MMWRPSVLLLLLLLRHGAQKSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60

QY 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWTIAHTQQRHIRDSVSA 120
Db 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWTIAHTQQRHIRDSVSA 120

QY 121 AWDTYDTRDGRVGEELRNATYGHYAPGEEFHDVEDAETYYKKMLARDERRFRVADQGD 180
Db 121 AWDTYDTRDGRVGEELRNATYGHYAPGEEFHDVEDAETYYKKMLARDERRFRVADQGD 180

QY 181 SMATREELTAFLEHPEEFPHMRDIVIAETLEDLDRNKGQYVQVEEYIADLYSAEPGEEPA 240
Db 181 SMATREELTAFLEHPEEFPHMRDIVIAETLEDLDRNKGQYVQVEEYIADLYSAEPGEEPA 240

QY 241 WYOTERQQRFRDLNKGDLGSEVGHVLPAPQDQPLVEANHLHESDTRHDELSKA 300
Db 241 WYOTERQQRFRDLNKGDLGSEVGHVLPAPQDQPLVEANHLHESDTRHDELSKA 300

QY 301 EILGNMNFVGSQATNYGDLTRHDEL 328
Db 301 EILGNMNFVGSQATNYGDLTRHDEL 328

Search completed: May 14, 2003, 10:47:54
Job time : 34.7419 secs

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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 14, 2003, 10:43:43 ; Search time 38 Seconds
(without alignments)
1150.163 Million cell updates/sec

Title: US-09-768-840-1

Perfect score: 328

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Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_101002.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	328	100.0	328	19	AAW80746
2	328	100.0	328	20	AA13382
3	328	100.0	328	20	AA100916
4	328	100.0	328	21	AA133424
5	328	100.0	328	21	AA153640
6	328	100.0	328	22	AAU12353
7	328	100.0	328	22	AAG64865
8	328	100.0	328	22	AAB80250
9	328	100.0	328	22	AAB53085
10	299	91.2	328	20	AAW67852

11	249	75.9	343	22	AAU87402
12	249	75.9	343	22	AAW43584
13	249	75.9	343	22	AAU19946
14	180	54.9	240	22	AAW67587
15	139	42.4	184	20	AAW67906
16	89	27.1	96	20	AAV11333
17	26	7.9	26	20	AAU01002
18	18	5.5	311	23	ABP41959
19	18	5.5	325	22	AAG64867
20	18	5.5	331	22	AAG64866
21	18	5.5	331	23	AAO17363
22	10	3.0	100	22	ABG20510
23	10	3.0	146	22	AAB88445
24	10	3.0	217	19	AAW37863
25	10	3.0	217	19	AAW37863
26	9	2.7	94	20	AAW48334
27	9	2.7	94	20	AAW12347
28	9	2.7	315	19	AAW37865
29	9	2.7	315	20	AAW00917
30	9	2.7	315	20	AAW67886
31	9	2.7	315	22	AAW93808
32	9	2.7	315	22	AAW94090
33	8	2.4	14	22	AAU84387
34	8	2.4	19	22	AAW98435
35	8	2.4	20	21	AAW53453
36	8	2.4	20	21	AAW30673
37	8	2.4	21	14	AAW28679
38	8	2.4	21	14	AAW30656
39	8	2.4	21	14	AAW30657
40	8	2.4	21	20	AAW88193
41	8	2.4	21	20	AAW88194
42	8	2.4	21	22	AAW49688
43	8	2.4	21	22	AAW49689
44	8	2.4	21	22	AAW46105
45	8	2.4	21	22	AAW46106
			23	14	AAW31606

ALIGNMENTS

RESULT 1

AAW80746

ID AAW80746 standard; Protein; 328 AA.

AC AAW80746;

DT 15-DEC-1998 (first entry)

DE Human calcium-binding protein.

DE Human; calcium-binding protein; reticulocalbin; sickle cell anaemia;

KW HCBP; beta thalassaemia; cell proliferation; cancer; adenocarcinoma;

KW leukemia; lymphoma; melanoma; sarcoma.

OS Homo sapiens.

PN WO9844114-A1.

PD 08-OCT-1998.

PF 30-MAR-1998; 98WO-US06233.

PR 31-MAR-1997; 97US-0828242.

PA (INCY-) INCYTE PHARM INC.

PI Goli SK, Hillman JL;

XX WPI; 1998-542704/46.

XX N-PSDB; AAV57600.

XX A new human calcium binding protein - useful for treating or

XX preventing disorders associated with the expression of HCBP

Novel central nerv
Human polypeptide
Novel human calciu
Human colon cancer
Human secreted pro
Human 5' EST seque
Human 5' EST seque
Human ovarian anti
Murine reticulocalb
Human reticulocalb
Human reticulocalb
Novel human diagno
Human membrane or
Amino acid sequenc
Human T1 receptor-
Human 5' EST seque
Human protein comp
Human reticulocalb
Human secreted pro
Human polypeptide,
Human protein sequ
Novel human secret
Human peptide #171
Peptide SEQ ID NO:
Amino acid sequenc
Synthetic chimeric
Peptide contg. alt
Peptide contg. alt
Surfactant peptide
Surfactant peptide
Modified surfactan
Modified surfactan
Human surfactant p
Human surfactant p
Protein XIX encode

XX PS Claim 1; Page 42-43; 60pp; English.

XX CC The present sequence is a new human calcium binding protein (HCBP).

CC A pharmaceutical composition which includes the HCBP protein is claimed

CC and can be added directly to cells in vivo to promote regeneration or

CC differentiation of cells. HCBP can also be added to cells, cell lines,

CC tissue or organ culture to stimulate cell proliferation for heterologous

CC and autologous transplantation. The cells can be selected for their

CC ability to inhibit development of an infection or to correct a genetic

CC HCBP can be administered to a subject to treat or prevent a disorder

CC associated with cell proliferation e.g. many cancers including

CC adenocarcinoma, leukemia, lymphoma, melanoma, sarcoma and particularly

CC cancers of bladder, bone, brain, heart, kidney, liver. Antibodies

CC specific for HCBP may be used directly as an antagonist or indirectly as

CC a targeting or delivery mechanism for delivering pharmaceutical agents

CC to cell or tissue which express protein HCBP. A method is claimed for

CC treating or preventing a disorder associated with cell proliferation

CC which involves adding pharmaceutical composition of antagonist of HCBP.

XX CC

XX SQ Sequence 328 AA;

Query Match 100.08; Score 328; DB 19; Length 328;

Best Local Similarity 100.08; Pred. No. 4.9e-295; Indels 0; Gaps 0;

Matches 328; Conservative 0; Mismatches 0;

QY 1 MMWRPSVLLLLLRHGAQKPSDPAGPHGQGRVHQAAPLSDAPHDHAGNFQYDHEAFL 60

Db 1 MMWRPSVLLLLLRHGAQKPSDPAGPHGQGRVHQAAPLSDAPHDHAGNFQYDHEAFL 60

QY 61 GREVAKFEDLTPEESQARLGRIIVDRMDRAGDGDGWSLAELRAWIAHTQQRHIDSVA 120

Db 61 GREVAKFEDLTPEESQARLGRIIVDRMDRAGDGDGWSLAELRAWIAHTQQRHIDSVA 120

QY 121 AWDYTDTRDGRVGYWEELRNATYGHVAPGEFHDVEDAETYYKKMLARDERRFRVADQGD 180

Db 121 AWDYTDTRDGRVGYWEELRNATYGHVAPGEFHDVEDAETYYKKMLARDERRFRVADQGD 180

QY 181 SMATRELTAFHPPEPHMRDIVIAETLEDLRNKGDVQVVEEYIADLYSAEPGEPEPA 240

Db 181 SMATRELTAFHPPEPHMRDIVIAETLEDLRNKGDVQVVEEYIADLYSAEPGEPEPA 240

QY 241 WQTERQOQFRDLNKGDLGSEVGHVWVLPQAQDQPLVEANHLHESDTDKDGLSKA 300

Db 241 WQTERQOQFRDLNKGDLGSEVGHVWVLPQAQDQPLVEANHLHESDTDKDGLSKA 300

QY 301 EILGNWNMFVGSQATNYGDELTRHDEL 328

Db 301 EILGNWNMFVGSQATNYGDELTRHDEL 328

RESULT 2

AAV13382

ID AAV13382 standard; Protein; 328 AA.

XX AC AAV13382;

XX DT 25-JUN-1999 (first entry)

XX DE Amino acid sequence of protein PRO272.

XX Secreted protein; transmembrane protein; human; enterocolitis;

KW Zollinger-Ellison syndrome; gastrointestinal ulceration;

KW congenital microvillus atrophy; skin disease; cell growth;

KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;

KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy;

KW fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;

XX anti-thrombotic; wound healing; tissue repair.

OS Homo sapiens.

XX WO914328-A2.

PN

XX PD 25-MAR-1999.

XX PF 16-SEP-1998; 98WO-US19330.

XX 25-NOV-1997; 97US-0066840.

PR 17-SEP-1997; 97US-0059113.

PR 17-SEP-1997; 97US-0059115.

PR 17-SEP-1997; 97US-0059117.

PR 17-SEP-1997; 97US-0059119.

PR 17-SEP-1997; 97US-0059121.

PR 17-SEP-1997; 97US-0059122.

PR 17-SEP-1997; 97US-0059184.

PR 18-SEP-1997; 97US-0059263.

PR 18-SEP-1997; 97US-0059266.

PR 15-OCT-1997; 97US-0062125.

PR 17-OCT-1997; 97US-0062285.

PR 17-OCT-1997; 97US-0062287.

PR 21-OCT-1997; 97US-0063486.

PR 24-OCT-1997; 97US-0062814.

PR 24-OCT-1997; 97US-0062816.

PR 24-OCT-1997; 97US-0063045.

PR 24-OCT-1997; 97US-0063120.

PR 24-OCT-1997; 97US-0063121.

PR 24-OCT-1997; 97US-0063127.

PR 27-OCT-1997; 97US-0063329.

PR 27-OCT-1997; 97US-0063327.

PR 28-OCT-1997; 97US-0063541.

PR 28-OCT-1997; 97US-0063542.

PR 28-OCT-1997; 97US-0063544.

PR 28-OCT-1997; 97US-0063549.

PR 28-OCT-1997; 97US-0063550.

PR 28-OCT-1997; 97US-0063564.

PR 29-OCT-1997; 97US-0063435.

PR 29-OCT-1997; 97US-0063704.

PR 29-OCT-1997; 97US-0063732.

PR 29-OCT-1997; 97US-0063738.

PR 29-OCT-1997; 97US-0063734.

PR 29-OCT-1997; 97US-0064215.

PR 29-OCT-1997; 97US-0063735.

PR 31-OCT-1997; 97US-0063870.

PR 31-OCT-1997; 97US-0064103.

PR 03-NOV-1997; 97US-0064248.

PR 07-NOV-1997; 97US-0064809.

PR 12-NOV-1997; 97US-0065186.

PR 17-NOV-1997; 97US-0065846.

PR 18-NOV-1997; 97US-0065693.

PR 21-NOV-1997; 97US-0066120.

PR 21-NOV-1997; 97US-0066364.

PR 24-NOV-1997; 97US-0066772.

PR 24-NOV-1997; 97US-0066466.

PR 24-NOV-1997; 97US-0066770.

PR 24-NOV-1997; 97US-0066511.

PR 24-NOV-1997; 97US-0066453.

XX PA (GETH) GENENTECH INC.

XX PI Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;

XX WPI; 1999-229533/19.

DR N-PSDB; AAX52253.

DR New isolated human genes and polypeptides used in, e.g. treatment of

XX gastrointestinal ulceration

XX Claim 12; Fig 80; 320pp; English.

XX AAY13344-403 represent secreted and transmembrane human proteins.

CC The cDNA sequences are obtained from cDNA libraries, prepared from

CC fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.

CC The encoded polypeptides have specific uses based on their homology to

CC known polypeptides, e.g. PRO211 and PRO217 can be used for disorders

CC associated with the preservation and maintenance of gastrointestinal
 CC mucosa and the repair of acute and chronic mucosal lesions
 CC (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal
 CC ulceration and congenital microvillus atrophy), skin diseases associated
 CC with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial
 CC cancers such as lung squamous cell carcinoma of the vulva and gliomas),
 CC potent effects on cell growth and development, diseases related to
 CC growth or survival of nerve cells including Parkinson's disease,
 CC Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as
 CC as a target for anti-tumor drugs. PRO533 may be used in the treatment
 CC of Usher Syndrome or Atrophia areata; PRO269 can be used as an
 CC anti-thrombotic agent; PRO287 polypeptides and portions may have
 CC therapeutic applications in wound healing and tissue repair; PRO317 can
 CC be used for treating problems of the kidney, uterus, endometrium, blood
 CC vessels, or related tissue, e.g. in the heart of genital tract.

XX Sequence 328 AA;

Query Match 100.0%; Score 328; DB 20; Length 328;
 Best Local Similarity 100.0%; Pred. No. 4.9e-295;
 Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLRHGAQKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60
 DB 1 MMWRPSVLLLLLRHGAQKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60

QY 61 GREVAKEFDOLTPEESQARLGRIVDRMDRAGDGGWVSLAELRAWIHTQORHIRDSVSA 120
 DB 61 GREVAKEFDOLTPEESQARLGRIVDRMDRAGDGGWVSLAELRAWIHTQORHIRDSVSA 120

QY 121 AWDTYDTRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETTKKMLARDERRFRVADQGD 180
 DB 121 AWDTYDTRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETTKKMLARDERRFRVADQGD 180

QY 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKGQYVQVEEYIADLYSAEPGEEPA 240
 DB 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKGQYVQVEEYIADLYSAEPGEEPA 240

QY 241 WYQTERQQRFRDLNKGDLGSEVGHVWLPQAQDQPLVEANHLHESDTRDKGRLSKA 300
 DB 241 WYQTERQQRFRDLNKGDLGSEVGHVWLPQAQDQPLVEANHLHESDTRDKGRLSKA 300

QY 301 EILGNWNNFVGSQATNYGDELTRHDEL 328
 DB 301 EILGNWNNFVGSQATNYGDELTRHDEL 328

RESULT 3
 AAY00916

XX ID AAY00916 standard; Protein; 328 AA.

XX AC AAY00916;

XX XX 28-MAY-1999 (first entry)

XX DE Human reticulocalbin gamma protein sequence.

XX KW Human; reticulocalbin gamma; RCNgamma; reticulocalbin delta; RCNdelta;
 KW developmental disorder; neoplastic disorder; immunological disorder;
 KW infection.

XX OS Homo sapiens.

XX PN WO9907849-A2.

XX PD 18-FEB-1999.

XX XX 05-AUG-1998; 98WO-US16259.

XX PF 08-AUG-1997; 97US-0910927.

XX PR (INCY-) INCYTE PHARM INC.

XX PA

XX

PI Bandman O, Corley NC, Hillman JL, Lal P, Shah P;

XX WPI; 1999-180492/15.

DR N-PSDB; AAX27229.

XX New human reticulocalbin isoforms - useful to diagnose, prevent,
 PT and treat infectious, developmental, neoplastic, and immunological
 PT disorders

XX Claim 1; Fig 1; 82pp; English.

XX This sequence is the human reticulocalbin gamma (RCNgamma) of the
 CC invention. RCNgamma and RCNdelta are used to treat an infectious or
 CC developmental disorder, and antagonists of them are used to treat a
 CC neoplastic or immunological disorder. Infectious disorders include e.g.
 CC pneumonia, lymphocytic choriomeningitis, Hantavirus, chronic bronchitis,
 CC mumps, rhinovirus, poliovirus, coxsackie-virus, smallpox, Colorado tick
 CC fever, HIV, rabies, gastroenteritis, and rubella, encephalitis, and
 CC bacterial, fungal, parasitic, protozoal, or helminthic infections.
 CC Developmental disorders include e.g. renal tubular acidosis, anaemia,
 CC Cushing's syndrome, achondroplastic dwarfism, epilepsy, gonadal
 CC dysgenesis, hereditary neuropathies such as Charcot-Marie-Tooth disease,
 CC and neurofibromatosis, hypothyroidism, hydrocephalus, seizure disorders
 CC such as Sydenham's chorea and cerebral palsy, spinal bifida, and
 CC congenital glaucoma, cataract, or sensorineural hearing loss. Neoplastic
 CC disorders include e.g. adenocarcinoma, leukaemia, lymphoma, melanoma,
 CC myeloma, sarcoma and teratocarcinoma. Overexpression of reticulocalbin
 CC mRNA has been associated with increased metastatic properties of
 CC three human breast cancer lines.

XX Sequence 328 AA;

Query Match 100.0%; Score 328; DB 20; Length 328;
 Best Local Similarity 100.0%; Pred. No. 4.9e-295;
 Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLRHGAQKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60
 DB 1 MMWRPSVLLLLLRHGAQKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60

QY 61 GREVAKEFDOLTPEESQARLGRIVDRMDRAGDGGWVSLAELRAWIHTQORHIRDSVSA 120
 DB 61 GREVAKEFDOLTPEESQARLGRIVDRMDRAGDGGWVSLAELRAWIHTQORHIRDSVSA 120

QY 121 AWDTYDTRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETTKKMLARDERRFRVADQGD 180
 DB 121 AWDTYDTRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETTKKMLARDERRFRVADQGD 180

QY 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKGQYVQVEEYIADLYSAEPGEEPA 240
 DB 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKGQYVQVEEYIADLYSAEPGEEPA 240

QY 241 WYQTERQQRFRDLNKGDLGSEVGHVWLPQAQDQPLVEANHLHESDTRDKGRLSKA 300
 DB 241 WYQTERQQRFRDLNKGDLGSEVGHVWLPQAQDQPLVEANHLHESDTRDKGRLSKA 300

QY 301 EILGNWNNFVGSQATNYGDELTRHDEL 328
 DB 301 EILGNWNNFVGSQATNYGDELTRHDEL 328

RESULT 4
 AAB33424

XX ID AAB33424 standard; Protein; 328 AA.

XX AC AAB33424;

XX XX 29-JAN-2001 (first entry)

XX DT Human PRO272 protein UNQ239 SEQ ID NO:51.

XX DE

XX XX

Tue May 20 14:43:20 2003

Human; immune related disease; diagnosis; antiinflammatory; cardiant;
dermatologic; antiarthritic; antirheumatic; immunosuppressive;
haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
antianemic; hepatotropic; virucide; antipsoriatic; antiallergic;
osteoarthritic; spondyloarthropathy; systemic sclerosis; sarcoidosis;
idiopathic inflammatory myopathy; Sjogren's syndrome; rheumatoid arthritis;
systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
autoimmune thrombocytopenia; immune-mediated renal disease;
denervating disease; hepatobiliary disease; Whipple's disease;
inflammatory bowel disease; gluten-sensitive enteropathy;
autoimmune disease; immune-mediated skin disease; allergic disease;
immunological disease; transplantation associated disease;
graft rejection; graft-versus-host-disease.

Homo sapiens.

WO200053758-A2.

14-SEP-2000.

02-MAR-2000; 2000WO-US05841.

08-MAR-1999; 99WO-US05028.

10-MAR-1999; 99US-0123618.

12-MAR-1999; 99US-0123957.

23-MAR-1999; 99US-0125775.

12-APR-1999; 99US-0128849.

20-APR-1999; 99WO-US08615.

28-APR-1999; 99US-0131445.

04-MAY-1999; 99US-0132371.

14-MAY-1999; 99US-0134287.

02-JUN-1999; 99WO-US12252.

23-JUN-1999; 99US-0141037.

20-JUL-1999; 99US-0144758.

26-JUL-1999; 99US-0145698.

28-JUL-1999; 99US-0146222.

01-SEP-1999; 99WO-US20111.

08-SEP-1999; 99WO-US20594.

13-SEP-1999; 99WO-US20944.

15-SEP-1999; 99WO-US21090.

15-SEP-1999; 99WO-US21547.

05-OCT-1999; 99WO-US23089.

29-OCT-1999; 99US-0162506.

29-NOV-1999; 99WO-US28214.

30-NOV-1999; 99WO-US28313.

30-NOV-1999; 99WO-US28409.

01-DEC-1999; 99WO-US28301.

01-DEC-1999; 99WO-US28634.

02-DEC-1999; 99WO-US28551.

02-DEC-1999; 99WO-US28564.

02-DEC-1999; 99WO-US28565.

16-DEC-1999; 99WO-US30095.

20-DEC-1999; 99WO-US30999.

30-DEC-1999; 99WO-US31274.

05-JAN-2000; 2000WO-US00219.

06-JAN-2000; 2000WO-US00277.

06-JAN-2000; 2000WO-US00376.

11-FEB-2000; 2000WO-US03565.

18-FEB-2000; 2000WO-US04341.

18-FEB-2000; 2000WO-US04342.

22-FEB-2000; 2000WO-US04414.

(GETH) GENENTECH INC.

Ashtkenari AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;

Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;

Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;

WPI; 2000-572271/53.

N-PSDB; AAC58589.

Sixty four PRO polypeptides, useful in the diagnosis and treatment of

immune related disorders, e.g. systemic lupus erythematosus, rheumatoid

arthritis, osteoarthritis, thyroiditis and diabetes mellitus -

Claim 33; Fig 22; 309pp; English..

The present invention describes sixty four human PRO proteins which can
be used in the treatment of immune related diseases. The human PRO
proteins, anti-PRO antibodies, agonists and antagonists are useful for
treating and diagnosing immune related disorders. The disorders are
selected from systemic lupus erythematosus, rheumatoid arthritis,
osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
syndrome, systemic vasculitis, sarcoidosis, thyroiditis, diabetes mellitus,
anaemia, autoimmune thrombocytopenia, demyelinating diseases of the central
and peripheral nervous systems, hepatobiliary and Whipple's disease,
bowel disease, gluten-sensitive enteropathy and allergic diseases,
autoimmune or immune-mediated skin diseases, allergic diseases,
immunological diseases of the lung, and transplantation associated
diseases including graft rejection and graft-versus-host-disease.
RAC58397 to AAC58578 represent PCR primers and hybridisation probes used
in the isolation of human PRO sequences. AAC58579 to AAC58642 and
AAB33414 to AAB33477 represent human PRO polynucleotide and protein
sequences given in the exemplification of the present invention.

Sequence 328 AA;

Query Match 100.0%; Score 328; DB 21; Length 328;

Best Local Similarity 100.0%; Pred. No. 4.9e-295;

Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY ° 1 MMWRPSVILLLLLRHGAQKSPDAGPHGQGRVHQAAPLSDAPHDHAGNFQYDHEAFL 60

Db 1 MMWRPSVILLLLLRHGAQKSPDAGPHGQGRVHQAAPLSDAPHDHAGNFQYDHEAFL 60

QY 61 GREVAKFEDQLTPESQARLGRIVDRMDRAGDGGVSWLAELRAWTAAHTQORHRSVSA 120

Db 61 GREVAKFEDQLTPESQARLGRIVDRMDRAGDGGVSWLAELRAWTAAHTQORHRSVSA 120

QY 121 AWDTYDTRDGRVGEELRNATYGHYAPGEFHDVEAETTKMLARDERRFRVADODGD 180

Db 121 AWDTYDTRDGRVGEELRNATYGHYAPGEFHDVEAETTKMLARDERRFRVADODGD 180

QY 181 SMATREELTAFLEPPEFPHMRDIVIAETLEDLRNKGIVQVVEYIADLYSAEPEEPA 240

Db 181 SMATREELTAFLEPPEFPHMRDIVIAETLEDLRNKGIVQVVEYIADLYSAEPEEPA 240

QY 241 WYQTERQOFRDRLNKGHLGDSVGHVWLPAPQDQPLVEANHLHESDTPDKGRLSKA 300

Db 241 WYQTERQOFRDRLNKGHLGDSVGHVWLPAPQDQPLVEANHLHESDTPDKGRLSKA 300

QY 301 EILGNMNFVGSQATNYGDELTRHDEL 328

Db 301 EILGNMNFVGSQATNYGDELTRHDEL 328

RESULT 5

AAY53640

ID AAY53640 standard; Protein; 328 AA.

XX AAY53640;

AC AAY53640;

XX 22-FEB-2000 (first entry)

DT 22-FEB-2000 (first entry)

XX A bone marrow secreted protein designated BMS37.

XX Bone marrow secreted protein; bone marrow stromal cell; cytokine;
XX cell proliferation; cell differentiation; hematopoiesis; anaemia;
XX myeloid cell deficiency; lymphoid cell deficiency; myeloid cell;
XX erythroid progenitor cell; colony stimulating factor; granulocyte;
XX monocyte; macrophage; myelo-suppression; megakaryocyte; platelet;
XX platelet disorder; thrombocytopenia; hematopoietic stem cell;
XX stem cell disorder; aplastic anaemia; bone differentiation;

KW paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon;
 KW ligament; nerve; wound healing; tissue repair; burn; incision; ulcer;
 XX bone fracture; cartilage damage; artificial joint.
 OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT /note= "signal peptide"
 XX
 XX W09333979-A2.
 XX
 PD 08-JUL-1999.
 XX
 XX 18-DEC-1998; 98WO-US27008.
 XX
 XX 30-DEC-1997; 97US-0068958.
 PR 24-SEP-1998; 98US-0101603.
 PR 30-SEP-1998; 98US-0102540.
 XX
 XX (CHIR) CHIRON CORP.
 PA
 XX Lin H, Cao L;
 XX
 XX WPI; 2000-038344/03.
 DR N-PSDB: AAZ36246.
 XX
 XX New isolated human polynucleotide and secreted proteins can induce
 FT production of other cytokines in certain cell populations -
 XX
 XX Claim 2; Page 113; 120pp; English.
 XX
 CC AAV53622-43 represent bone marrow secreted proteins of human bone marrow
 CC stromal cells. The proteins can exhibit cytokine, cell proliferation, or
 CC cell differentiation activity (either inducing or inhibiting). They can
 CC be used to support colony forming cells or factor-dependent cell lines,
 CC to regulate hematopoiesis, and to treat myeloid or lymphoid cell
 CC deficiencies. In addition, they may be used to support the growth and
 CC proliferation of erythroid progenitor cells, and to treat various
 CC anemias. They can have colony stimulating factor (CSF) activity and can
 CC be used to support the growth and proliferation of myeloid cells such as
 CC granulocytes, monocytes or macrophages, to prevent or treat
 CC myelo-suppression, to support the growth and proliferation of
 CC megakaryocytes and platelets, thereby allowing prevention or treatment
 CC of platelet disorders such as thrombocytopenia, to support the growth
 CC such as aplastic anaemia and paroxysmal nocturnal hemoglobinuria, or to
 CC conjunction with platelet transfusions, to treat stem cell disorders,
 CC repopulate the stem cell compartment after irradiation or chemotherapy.
 CC They can be used for growth or differentiation of bone, cartilage,
 CC tendon, ligament, or nerve tissue, as well as for wound healing and
 CC tissue repair and replacement, and in the treatment of burns, incisions
 CC and ulcers, to induce cartilage and/or bone growth in circumstances
 CC where bone is not normally formed and thus have an application in healing
 CC bone fractures and cartilage damage or defects, prophylactic use in
 CC fracture reduction and also in the improved fixation of artificial
 CC joints.
 XX
 XX Sequence 328 AA;
 SQ
 Query Match 100.0%; Score 328; DB 21; Length 328;
 Best Local Similarity 100.0%; Pred. No. 4,9e-295;
 Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMWRPVSLLLLLLRGAGGKSPDAGPHGQGRVHOAQLSDAPHDHDAHNFQYDHEAFL 60
 DB 1 MMWRPVSLLLLLLRGAGGKSPDAGPHGQGRVHOAQLSDAPHDHDAHNFQYDHEAFL 60
 QY 61 GREVAKEFDQLTPESQARLGRIIVDRMDRAGDGGVHSLAELRAWTAHTQQRHSDVSA 120
 DB 61 GREVAKEFDQLTPESQARLGRIIVDRMDRAGDGGVHSLAELRAWTAHTQQRHSDVSA 120
 QY 121 AWDYTDTRDRGVRGVEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRRVADQGD 180

Db 121 AWDYTDTRDRGVRGVEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRRVADQGD 180
 QY 181 SMATREELTAFLHPPEEPHMRDIVIAETLDRNKDGYVQVEEYIADLYSAEPGEERPA 240
 Db 181 SMATREELTAFLHPPEEPHMRDIVIAETLDRNKDGYVQVEEYIADLYSAEPGEERPA 240
 QY 241 WVQTERQQFRDRLNKGDLGSEVGHVLPAPADQDPLVEANHLHESDTRDKGRLSKA 300
 Db 241 WVQTERQQFRDRLNKGDLGSEVGHVLPAPADQDPLVEANHLHESDTRDKGRLSKA 300
 QY 301 EILGNWNMFVGSQATNYGDELTRHDEL 328
 Db 301 EILGNWNMFVGSQATNYGDELTRHDEL 328
 RESULT 6
 AAU12353
 ID AAU12353 standard; Protein; 328 AA.
 XX AC AAU12353;
 XX XX
 DT 24-OCT-2001 (first entry)
 DE Human PRO272 polypeptide sequence.
 XX
 KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
 KW adipocyte; A-peptide; factor VIIA; gene therapy.
 XX
 OS Homo sapiens.
 XX
 XX WO200140466-A2.
 XX 07-JUN-2001.
 XX
 XX 01-DEC-2000; 2000WO-US32678.
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 PR 09-DEC-1999; 99US-0170262.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 30-DEC-1999; 99WO-US31243.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 11-FEB-2000; 2000WO-US00376.
 PR 18-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04342.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 10-NOV-2000; 2000WO-US30873.
 XX (GETH) GENENTECH INC.
 PA
 XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sharwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX

DR WPI; 2001-408281/43.
DR N-PSDB; AAS21425.
XX Isolated, secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing
PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
PT lung, breast, prostate, cervical
XX
XX Claim 12; Fig 364; 813pp; English.
XX
XX AAU12172-AAU12446 represent novel human secretory and transmembrane
CC PRO polypeptides. The PRO polypeptides are useful to detect other
CC PRO polypeptides, to link bioactive molecules to cells expressing
CC PRO polypeptides, to modulate biological activities of cells expressing
CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample.
CC Some of the 275 sequences are also useful to stimulate the release of
CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
CC proliferation or differentiation of chondrocytes, the proliferation or
CC gene expression in pericyte cells, the release of proteoglycans from
CC cartilage, the proliferation of inner ear utricular supporting cells or
CC of T-lymphocytes, the release of a cytokine from peripheral blood
CC monocytes (PMNCs), or the proliferation of endothelial cells. Some of
CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
CC to factor VIIa. The PRO polypeptides can be used in assays to identify
CC molecules involved in binding interactions. The polynucleotides encoding
CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy.
XX
XX Sequence 328 AA;

Query Match 100.0%; Score 328; DB 22; Length 328;
Best Local Similarity 100.0%; Pred. No. 4.9e-295;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MMWRPSVLLLLLLLRHGAQKPSDPAGPHGQGRVHQAAAPLSDAPHDDAHGNFYDHEAFL 60
Db 1 MMWRPSVLLLLLLLRHGAQKPSDPAGPHGQGRVHQAAAPLSDAPHDDAHGNFYDHEAFL 60
Qy 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGVWSLAELRAWIAHTQQRHIRDSVSA 120
Db 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGVWSLAELRAWIAHTQQRHIRDSVSA 120
Qy 121 AWDYTDTRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQDGD 180
Db 121 AWDYTDTRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQDGD 180
Qy 181 SMATREELTAFLHPEEFPHMRDIVIAETLEDLDRNKDGVVQVEEYIADLYSAEPGEEPPA 240
Db 181 SMATREELTAFLHPEEFPHMRDIVIAETLEDLDRNKDGVVQVEEYIADLYSAEPGEEPPA 240
Qy 241 WYQTERQQFRDRLNKDGLDGVSEVHWVLPAPQDQPLVEANHLHSHDSTDKDGRLSKA 300
Db 241 WYQTERQQFRDRLNKDGLDGVSEVHWVLPAPQDQPLVEANHLHSHDSTDKDGRLSKA 300
Qy 301 EILGNMNFVGSQATNYGDELTRHHDEL 328
Db 301 EILGNMNFVGSQATNYGDELTRHHDEL 328

RESULT 7
AAG64865
ID AAG64865 standard; protein; 328 AA.
XX AAG64865;
XX
XX 21-SEP-2001 (first entry)
XX Human calcium binding protein.
XX Human; calcium binding protein; HCBP; cell proliferation disorder;
XX

KW cancer.
XX Homo sapiens.
XX US2001012831-A1.
XX 09-AUG-2001.
XX 23-JAN-2001; 2001US-0768840.
XX 21-MAR-1997; -97US-0828212.
XX 07-DEC-1998; 98US-0206499.
XX (INCY-) INCYTE PHARM INC.
XX Hillman JL, Goli SK;
XX WPI; 2001-464391/50.
XX N-PSDB; AAH48279.
XX Human calcium-binding protein, useful in the diagnosis, prevention, and
XX treatment of disorders associated with cell proliferation, e.g.
XX adenocarcinoma, leukemia, lymphoma, melanoma, sarcoma, or
XX teratocarcinoma
XX
XX Claim 1; Fig 1; 30pp; English.
XX The present invention provides the protein and coding sequences of human
XX calcium binding protein (HCBP). The sequences can be used in the
XX diagnosis, prevention and treatment of cell proliferation disorders, such
XX as cancer. The present sequence is the protein of the invention.
XX
XX Sequence 328 AA;

Query Match 100.0%; Score 328; DB 22; Length 328;
Best Local Similarity 100.0%; Pred. No. 4.9e-295;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MMWRPSVLLLLLLLRHGAQKPSDPAGPHGQGRVHQAAAPLSDAPHDDAHGNFYDHEAFL 60
Db 1 MMWRPSVLLLLLLLRHGAQKPSDPAGPHGQGRVHQAAAPLSDAPHDDAHGNFYDHEAFL 60
Qy 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGVWSLAELRAWIAHTQQRHIRDSVSA 120
Db 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGVWSLAELRAWIAHTQQRHIRDSVSA 120
Qy 121 AWDYTDTRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQDGD 180
Db 121 AWDYTDTRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQDGD 180
Qy 181 SMATREELTAFLHPEEFPHMRDIVIAETLEDLDRNKDGVVQVEEYIADLYSAEPGEEPPA 240
Db 181 SMATREELTAFLHPEEFPHMRDIVIAETLEDLDRNKDGVVQVEEYIADLYSAEPGEEPPA 240
Qy 241 WYQTERQQFRDRLNKDGLDGVSEVHWVLPAPQDQPLVEANHLHSHDSTDKDGRLSKA 300
Db 241 WYQTERQQFRDRLNKDGLDGVSEVHWVLPAPQDQPLVEANHLHSHDSTDKDGRLSKA 300
Qy 301 EILGNMNFVGSQATNYGDELTRHHDEL 328
Db 301 EILGNMNFVGSQATNYGDELTRHHDEL 328

RESULT 8
AAB80250
ID AAB80250 standard; protein; 328 AA.
XX AAB80250;
XX
XX 24-APR-2001 (first entry)
XX Human PRO272 protein.
XX

KW Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
 KW antiparkinsonian neurotropic; neuroprotective; vulnerary; cardiant;
 KW antiangiogenic; vasotropic; antiaschmatic; antirheumatic; cancer;
 KW antiarthritic; antinfertility; antidiabetic; antiviral; diabetes;
 KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
 KW ischaemia; inflammation.

XX Homo sapiens.

XX WO200104311-A1.

XX 18-JAN-2001.

XX 22-FEB-2000; 2000WO-US04414.

XX 07-JUL-1999; 99US-0143048.

XX 26-JUL-1999; 99US-0145698.

XX 28-JUL-1999; 99US-0146222.

XX 08-SEP-1999; 99WO-US20594.

XX 13-SEP-1999; 99WO-US20944.

XX 15-SEP-1999; 99WO-US21090.

XX 15-SEP-1999; 99WO-US21547.

XX 05-OCT-1999; 99WO-US23089.

XX 29-NOV-1999; 99WO-US28214.

XX 30-NOV-1999; 99WO-US28313.

XX 16-DEC-1999; 99WO-US30095.

XX 20-DEC-1999; 99WO-US30911.

XX 20-DEC-1999; 99WO-US30999.

XX 05-JAN-2000; 99WO-US00219.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;

XX Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;

XX Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kijavini IU;

XX Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;

XX Williams PM, Wood WI;

XX WPI: 2001-081051/09.

XX N-PSDB; AAF72411.

XX Sixty one nucleic acids encoding PRO polypeptides which are useful in
 the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung
 squamous cell carcinoma) and neurodegenerative diseases (e.g.
 Alzheimer's disease) -

XX Claim 1; Fig 80; 393pp; English.

XX The present sequence is one of sixty one novel secreted and

XX transmembrane PRO polypeptides. The PRO polypeptides are

XX useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung

XX squamous cell carcinoma), gastrointestinal disorders (e.g.

XX enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,

XX Parkinson's disease), wound repair, cardiovascular disorders (e.g.

XX endometrial bleeding angiogenesis, ischaemias such as coronary

XX ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma,

XX rheumatoid arthritis, multiple sclerosis), infertility, AIDS and

XX diabetes and retinal disorders such as retinitis pigmentosa.
 XX The PRO nucleic acids have applications in molecular biology, including
 XX use as hybridization probes, and in chromosome and gene mapping.

XX Sequence 328 AA;

XX Query Match 100.0%; Score 328; DB 22; Length 328;

XX Best Local Similarity 100.0%; Pred. No. 4.9e-295;

XX Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 MMWRPVLVLLLRHGAQCKSPDAGPHGQGRVHOAAPLSDAPHDDAHNGFYDHEAFL 60

XX 1 MMWRPVLVLLLRHGAQCKSPDAGPHGQGRVHOAAPLSDAPHDDAHNGFYDHEAFL 60

XX 61 GREVAKEFDLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWIAHTQQRHIRDSVSA 120

XX 121 AWDYTDTRDGRGVGHEELRNATYGHYAPGEEFHDVEDAETKKMLANDERRFRVADQDGD 180

XX 121 AWDYTDTRDGRGVGHEELRNATYGHYAPGEEFHDVEDAETKKMLANDERRFRVADQDGD 180

XX 181 SMATREELTAFLEHPEEPFPHMRDIVIAETLEDLDRNKDGYVOVEEYIADLYSAEPGESEPA 240

XX 181 SMATREELTAFLEHPEEPFPHMRDIVIAETLEDLDRNKDGYVOVEEYIADLYSAEPGESEPA 240

XX 241 WVQTERQQFRDLNKGDLGSEVGHVWLPAPQDQPLVEANHLHSHESDTDKDGLSKA 300

XX 241 WVQTERQQFRDLNKGDLGSEVGHVWLPAPQDQPLVEANHLHSHESDTDKDGLSKA 300

XX 301 EILGNWNNFVGSQATNYGDELTRHDEL 328

XX 301 EILGNWNNFVGSQATNYGDELTRHDEL 328

XX RESULT 9

XX AAB53085

XX ID AAB53085 standard; Protein; 328 AA.

XX AC AAB53085;

XX DT 28-FEB-2001 (first entry)

XX DE Human angiogenesis-associated protein PRO272, SEQ ID NO:113.

XX KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;

XX KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;

XX KW myogenic disorder; atherosclerosis; osteoporosis; hypertension;

XX KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;

XX KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;

XX KW Alzheimer's disease; Huntington's disease; stroke; drug screening;

XX KW gene therapy; transgenic animal.

XX OS Homo sapiens.

XX XX WO200053753-A2.

XX PD 14-SEP-2000.

XX XX 05-JAN-2000; 2000WO-US00219.

XX PR 08-MAR-1999; 99WO-US05028.

XX PR 12-MAR-1999; 99US-0123957.

XX PR 14-MAY-1999; 99US-0134287.

XX PR 02-JUN-1999; 99WO-US12252.

XX PR 23-JUN-1999; 99US-0141037.

XX PR 20-JUL-1999; 99US-0144758.

XX PR 26-JUL-1999; 99US-0145698.

DB

QY

DB

QY

DB

QY

DB

QY

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QY

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QY

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QY

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QY

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QY

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QY

DB

QY

PT angiogenic disorders, such as atherosclerosis, wounds or cancer -

XX Claim 69; Fig 44; 293pp; English.

XX The invention relates to novel human angiogenesis-associated proteins

CC designated PRO proteins (AA053064-B53097), and to nucleic acids encoding

CC PRO proteins. The invention also relates to vectors and host cells

CC comprising a PRO nucleic acid, the recombinant production of a PRO

CC protein, PRO antibodies specific for a PRO protein, fusion proteins

CC comprising a PRO protein, agonists or antagonists of a PRO protein, and

CC compounds which inhibit the expression of a PRO gene. The invention

CC additionally encompasses methods of identifying modulators of PRO

CC expression or activity; diagnosing a cardiovascular, endothelial or

CC angiogenic disorder, or a susceptibility to such a disorder by detecting

CC mutations in a PRO gene, or the expression level of a PRO gene within a

CC particular tissue; treating a cardiovascular, endothelial or angiogenic

CC disorder via the administration of a PRO protein, PRO nucleic acid, or

CC PRO agonist or antagonist; and methods of inhibiting or stimulating endothelial

CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the

CC administration of a PRO protein, or an agonist or antagonist thereof.

CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO

CC agonists and PRO antagonists may be used as therapeutic agents to treat

CC cardiovascular, endothelial or angiogenic disorders, such as

CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,

CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,

CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's

CC disease, or stroke. PRO nucleic acids are additionally useful in the

CC recombinant production of PRO proteins, as hybridisation probes to

CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,

CC to map genes encoding PRO proteins, to analyse genetic disorders, and in

CC gene therapy. PRO nucleic acids can also be used to produce transgenic

CC animals useful for the development and screening of potential

CC therapeutic agents. The present sequence represents a PRO protein of the

XX invention.

XX Sequence 328 AA;

Query Match 100.0%; Score 328; DB 22; Length 328;

Best Local Similarity 100.0%; Pred. No. 4.9e-295; Indels 0; Gaps 0;

Matches 328; Conservative 0; Mismatches 0;

QY 1 MMKRPVLLLLLRGAGCKPSDAGPHGQGRVHQAPLSDAPHDHAGNFQYDHEAPL 60

Db 1 MMKRPVLLLLLRGAGCKPSDAGPHGQGRVHQAPLSDAPHDHAGNFQYDHEAPL 60

QY 61 GREVAKFEDLTPEESQARLGRIVDRMDRAGDGDGHWVSLAELRAWTAAHQRRHDSVA 120

Db 61 GREVAKFEDLTPEESQARLGRIVDRMDRAGDGDGHWVSLAELRAWTAAHQRRHDSVA 120

QY 121 AWDTYDTRDGRGVWEELRNATYGHVAPGEFFHVDVDAETYYKKMLARDERRFRVADQDGD 180

Db 121 AWDTYDTRDGRGVWEELRNATYGHVAPGEFFHVDVDAETYYKKMLARDERRFRVADQDGD 180

QY 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKGIVQVEEYADLYSAEPGEEPA 240

Db 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKGIVQVEEYADLYSAEPGEEPA 240

QY 241 WVQTERQOQFRDLNKGDLGSEGVHVVLPQAQDQPLVEANHLHESDTRDGRLSKA 300

Db 241 WVQTERQOQFRDLNKGDLGSEGVHVVLPQAQDQPLVEANHLHESDTRDGRLSKA 300

QY 301 EILGNWNMFVGSQATNYGEDLTRHDEL 328

Db 301 EILGNWNMFVGSQATNYGEDLTRHDEL 328

RESULT 10

AAW67852

ID AAW67852 standard; Protein; 328 AA.

XX

AC AAW67852;

XX

DT 25-MAR-1999 (first entry)

XX Human secreted protein encoded by gene 46 clone HSJB079.

DE

XX

XX Human; secreted protein; fusion protein; gene therapy; protein therapy;

KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;

KW developmental abnormality; foetal deficiency; blood; allergy; renal;

KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;

KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;

KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;

KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;

XX endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

XX Homo sapiens.

OS

XX

XX Key Location/Qualifiers

FH Misc-difference 300 /label= unknown

FT Misc-difference 328 /label= unknown

FT

XX W09842738-A1.

XX 01-OCT-1998.

XX 19-MAR-1998; 98WO-US05311.

XX 30-MAY-1997; 97US-0050937.

XX 21-MAR-1997; 97US-0041276.

XX 21-MAR-1997; 97US-0041277.

XX 21-MAR-1997; 97US-0041281.

XX 21-MAR-1997; 97US-0042344.

XX 30-MAY-1997; 97US-0048069.

XX 30-MAY-1997; 97US-0048094.

XX 30-MAY-1997; 97US-0048095.

XX 30-MAY-1997; 97US-0048096.

XX 30-MAY-1997; 97US-0048099.

XX 30-MAY-1997; 97US-0048131.

XX 30-MAY-1997; 97US-0048135.

XX 30-MAY-1997; 97US-0048134.

XX 30-MAY-1997; 97US-0048160.

XX 30-MAY-1997; 97US-0048186.

XX 30-MAY-1997; 97US-0048187.

XX 30-MAY-1997; 97US-0048188.

XX 30-MAY-1997; 97US-0048350.

XX 30-MAY-1997; 97US-0048351.

XX 30-MAY-1997; 97US-0048352.

XX 30-MAY-1997; 97US-0048355.

XX 05-AUG-1997; 97US-0054804.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Brewer LA, Duan R, Ebner R, Ferrie AM, Florence KA;

PI Greene JM, Hu JS, Lafleur DW, Moore PA, Ni J, Olsen HS;

PI Rosen CA, Ruben SM, Shi Y, Young P;

XX WPI: 1999-070066/06.

XX N-PSDB; AAX00656.

XX New isolated human genes and the secreted polypeptides they encode -

DR useful for diagnosis and treatment of e.g. cancers, neurological

XX disorders, immune diseases, inflammation or blood disorders

XX Claim 11; Page 297-298; 385pp; English.

XX This sequence represents a secreted human protein encoded by the gene

CC clone detailed in the descriptor line. The gene can be used to generate

CC fusion proteins by linking to the gene to a human immunoglobulin Fc

CC portion (e.g. AAX00602) for increasing the stability of the fused

CC protein as compared to the human protein only.

CC The invention relates to 87 novel genes and their fragments (nucleic

CC acid sequences: AAX00611-X00724; amino acid sequences AAW67807-68004)

CC which are useful for preventing, treating or ameliorating medical

Tue May 20 14:43:20 2003

20-OCT-2000; 2000US-02411787.
20-OCT-2000; 2000US-02411808.
20-OCT-2000; 2000US-02411809.
20-OCT-2000; 2000US-0241826.
01-NOV-2000; 2000US-0244617.
08-NOV-2000; 2000US-0246474.
08-NOV-2000; 2000US-0246475.
08-NOV-2000; 2000US-0246476.
08-NOV-2000; 2000US-0246477.
08-NOV-2000; 2000US-0246478.
08-NOV-2000; 2000US-0246523.
08-NOV-2000; 2000US-0246524.
08-NOV-2000; 2000US-0246525.
08-NOV-2000; 2000US-0246526.
08-NOV-2000; 2000US-0246527.
08-NOV-2000; 2000US-0246528.
08-NOV-2000; 2000US-0246532.
08-NOV-2000; 2000US-0246609.
08-NOV-2000; 2000US-0246610.
08-NOV-2000; 2000US-0246611.
08-NOV-2000; 2000US-0246613.
17-NOV-2000; 2000US-0249207.
17-NOV-2000; 2000US-0249208.
17-NOV-2000; 2000US-0249209.
17-NOV-2000; 2000US-0249210.
17-NOV-2000; 2000US-0249211.
17-NOV-2000; 2000US-0249212.
17-NOV-2000; 2000US-0249213.
17-NOV-2000; 2000US-0249214.
17-NOV-2000; 2000US-0249215.
17-NOV-2000; 2000US-0249216.
17-NOV-2000; 2000US-0249217.
17-NOV-2000; 2000US-0249218.
17-NOV-2000; 2000US-0249244.
17-NOV-2000; 2000US-0249245.
17-NOV-2000; 2000US-0249264.
17-NOV-2000; 2000US-0249265.
17-NOV-2000; 2000US-0249297.
17-NOV-2000; 2000US-0249299.
17-NOV-2000; 2000US-0249300.
01-DEC-2000; 2000US-0250160.
01-DEC-2000; 2000US-0250391.
05-DEC-2000; 2000US-0251030.
05-DEC-2000; 2000US-0256719.
06-DEC-2000; 2000US-0251479.
06-DEC-2000; 2000US-0251856.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251989.
08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0259678.
(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
WPI; 2001-581633/65.
N-PSDB; ABR43732.
New isolated nucleic acid encoding a protein for diagnosing,
preventing, treating or ameliorating medical conditions and used as
food additives or preservatives -
Claim 9; SEQ ID NO 920; 837pp; English.
The invention describes an isolated nucleic acid molecule (I) encoding a
novel central nervous system protein. (I) and polypeptides (III) encoded
by (I), are used to treat a medical conditions and in diagnosis of a
pathological condition. Disorders which are diagnosed or treated include
autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
disorders e.g. neoplasms of the breast or liver, cardiovascular disorders

CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and
CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses
CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,
CC adenocarcinomas and irritable bowel syndrome, reproductive system
CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes
CC leukaemia, disorders involving neovascularisation e.g. malignancies, e.g.
CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.
CC acute kidney failure and blood related disorders e.g. myocardial
CC infarction. The polypeptides can also be used to aid wound healing and
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
CC maintain organs before transplantation, for supporting cell culture of
CC primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content, lipid, protein,
Query Match 75.9%; Score 249; DB 22; Length 343;
Best Local Similarity 100.0%; Pred. No. 6.2e-222; Indels 0; Gaps 0;
Matches 249; Conservative 0; Mismatches 0;
QY 1 MMWRPSVILLILLRGAQGKPSDPAGPHGQGRVHQAAPLSDAPHDHAGNFQDHEAFL 60
Db 16 MMWRPSVILLILLRGAQGKPSDPAGPHGQGRVHQAAPLSDAPHDHAGNFQDHEAFL 75
QY 61 GREVAKREFDQLTPEESQARLGRIVDRMDRAGDGDGVSLAELRAWTATQOHRHDSVSA 120
Db 76 GREVAKREFDQLTPEESQARLGRIVDRMDRAGDGDGVSLAELRAWTATQOHRHDSVSA 135
QY 121 AWDTYDTRDGRVGEELRNATYGHVAPGEEFHDVEDAETFKKMLARDERRFRVADQGD 180
Db 136 AWDTYDTRDGRVGEELRNATYGHVAPGEEFHDVEDAETFKKMLARDERRFRVADQGD 195
QY 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKGVOVEEYADLYSAEPGEEPA 240
Db 196 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKGVOVEEYADLYSAEPGEEPA 255
QY 241 WQTERQOF 249
Db 256 WQTERQOF 264
RESULT 12
AAM43584
ID AAM43584 standard; Protein; 343 AA.
XX AAM43584;
XX AC AAM43584;
XX DT 22-OCT-2001 (first entry)
XX DE Human polypeptide SEQ ID NO 262.
XX KW Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;
KW cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;
KW fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
KW neuroprotective; antiallergic; hepatotropic; antidiabetic;
KW antiinflammatory; antitumor; vulnery; anticonvulsant; antibacterial;
KW antiparasitic; cardiant; gene therapy; cancer; immune disorder;
KW cardiovascular disorder; neurological disease; infection; human.
XX OS Homo sapiens.
XX PN WO200155308-A2.
XX XX 02-AUG-2001.
XX PD 17-JAN-2001; 2001WO-US01309.
XX PF 31-JAN-2000; 2000US-0179065.
XX PR 04-FEB-2000; 2000US-0180628.
XX PR 24-FEB-2000; 2000US-0184664.
XX PR 02-MAR-2000; 2000US-0186350.

the encoded proteins (AA0434497-AA043660) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes were isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune hemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemia; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Query Match 75.9%; Score 249; DB 22; Length 343;
Best Local Similarity 100.0%; Pred. No. 6.2e-222;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 343 AA;

QY	1	MMWRPSVLLILLRRHGAQKPSDPAGPHGGRVHQAAAPLSDAPHDDAHGNFQYDHEAFL 60	
Db	16	MMWRPSVLLILLRRHGAQKPSDPAGPHGGRVHQAAAPLSDAPHDDAHGNFQYDHEAFL 75	
QY	61	GREVAKEFDQLTPESQARLGRIVDRMDRAGDGVSLAEALRWIAHTQQRHIDSVSA 120	
Db	76	GREVAKEFDQLTPESQARLGRIVDRMDRAGDGVSLAEALRWIAHTQQRHIDSVSA 135	
QY	121	ANDTDTDRDGRVGEELRNATYHYAGEEPHVEDAETTKKMLARDERRFRVADQGD 180	
Db	136	ANDTDTDRDGRVGEELRNATYHYAGEEPHVEDAETTKKMLARDERRFRVADQGD 195	
QY	181	SNATRELTAFLEPFPFMRDIVIAETLEDLRNKGQVQVEEYIADLYSAEPGEEPPA 240	
Db	196	SNATRELTAFLEPFPFMRDIVIAETLEDLRNKGQVQVEEYIADLYSAEPGEEPPA 255	
QY	241	WVQTERQQF 249	
Db	256	WVQTERQQF 264	
RESULT 13			
AAU19946			
ID	AAU19946	standard; Protein; 343 AA.	
XX	AAU19946;		
XX	04-DEC-2001	(first entry)	
DT			
XX		Novel human calcium-binding protein #55.	
DE			
XX		Human; calcium-binding protein; calcium flux; neurological disease;	
KW		immune dysfunction; digestive disorder; neoplastic disease;	
KW		blood disorder; infectious disease; gene therapy; immunosuppressive;	
KW		antiarthritic; cytostatic; vasotropic; antibacterial; nootropic;	
KW		virucide.	
XX			
OS		Homo sapiens.	
XX			
PN		W0200155304-A2.	
XX			
PD		02-AUG-2001.	
XX			
XX		17-JAN-2001; 2001WO-US01302.	
XX			
XX		31-JAN-2000; 2000US-0179065.	
PR		04-FEB-2000; 2000US-0180628.	
PR		24-FEB-2000; 2000US-0184564.	
PR		02-MAR-2000; 2000US-0186350.	

PR	16-MAR-2000;	2000US-0189874.	
PR	17-MAR-2000;	2000US-0190076.	
PR	18-APR-2000;	2000US-0198123.	
PR	19-MAY-2000;	2000US-0205515.	
PR	07-JUN-2000;	2000US-0209467.	
PR	28-JUN-2000;	2000US-0214886.	
PR	30-JUN-2000;	2000US-0215135.	
PR	07-JUL-2000;	2000US-0216647.	
PR	07-JUL-2000;	2000US-0216880.	
PR	11-JUL-2000;	2000US-0217487.	
PR	11-JUL-2000;	2000US-0217496.	
PR	14-JUL-2000;	2000US-0218290.	
PR	26-JUL-2000;	2000US-0220963.	
PR	26-JUL-2000;	2000US-0220964.	
PR	14-AUG-2000;	2000US-0224518.	
PR	14-AUG-2000;	2000US-0224519.	
PR	14-AUG-2000;	2000US-0225213.	
PR	14-AUG-2000;	2000US-0225214.	
PR	14-AUG-2000;	2000US-0225266.	
PR	14-AUG-2000;	2000US-0225267.	
PR	14-AUG-2000;	2000US-0225268.	
PR	14-AUG-2000;	2000US-0225270.	
PR	14-AUG-2000;	2000US-0225447.	
PR	14-AUG-2000;	2000US-0225757.	
PR	14-AUG-2000;	2000US-0225758.	
PR	14-AUG-2000;	2000US-0225759.	
PR	18-AUG-2000;	2000US-0226279.	
PR	22-AUG-2000;	2000US-0226681.	
PR	22-AUG-2000;	2000US-0226868.	
PR	22-AUG-2000;	2000US-0227182.	
PR	23-AUG-2000;	2000US-0227009.	
PR	30-AUG-2000;	2000US-0228924.	
PR	01-SEP-2000;	2000US-0229287.	
PR	01-SEP-2000;	2000US-0229343.	
PR	01-SEP-2000;	2000US-0229344.	
PR	01-SEP-2000;	2000US-0229345.	
PR	05-SEP-2000;	2000US-0229509.	
PR	05-SEP-2000;	2000US-0229513.	
PR	06-SEP-2000;	2000US-0230437.	
PR	06-SEP-2000;	2000US-0230438.	
PR	08-SEP-2000;	2000US-0231242.	
PR	08-SEP-2000;	2000US-0231243.	
PR	08-SEP-2000;	2000US-0231244.	
PR	08-SEP-2000;	2000US-0231413.	
PR	08-SEP-2000;	2000US-0231414.	
PR	08-SEP-2000;	2000US-0232080.	
PR	12-SEP-2000;	2000US-0232081.	
PR	12-SEP-2000;	2000US-0231968.	
PR	14-SEP-2000;	2000US-0232397.	
PR	14-SEP-2000;	2000US-0232398.	
PR	14-SEP-2000;	2000US-0232399.	
PR	14-SEP-2000;	2000US-0232400.	
PR	14-SEP-2000;	2000US-0232401.	
PR	14-SEP-2000;	2000US-0233063.	
PR	14-SEP-2000;	2000US-0233064.	
PR	14-SEP-2000;	2000US-0233065.	
PR	21-SEP-2000;	2000US-0234223.	
PR	21-SEP-2000;	2000US-0234274.	
PR	25-SEP-2000;	2000US-0234997.	
PR	25-SEP-2000;	2000US-0234998.	
PR	26-SEP-2000;	2000US-0235484.	
PR	27-SEP-2000;	2000US-0235834.	
PR	27-SEP-2000;	2000US-0235836.	
PR	29-SEP-2000;	2000US-0236327.	
PR	29-SEP-2000;	2000US-0236367.	
PR	29-SEP-2000;	2000US-0236368.	
PR	29-SEP-2000;	2000US-0236369.	
PR	29-SEP-2000;	2000US-0236370.	
PR	02-OCT-2000;	2000US-0236802.	
PR	02-OCT-2000;	2000US-0237037.	
PR	02-OCT-2000;	2000US-0237038.	
PR	02-OCT-2000;	2000US-0237039.	
PR	02-OCT-2000;	2000US-0237040.	

PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 01-NOV-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 17-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 11-DEC-2000; 2000US-0251990.
 PR 05-JAN-2001; 2000US-0254097.
 PR 05-JAN-2001; 2000US-0259678.
 (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI: 2001-465568/50.
 XX N-PSDB; AAS31631.
 XX
 PT Isolated nucleic acid molecule encoding a calcium-binding protein is
 PT used in preventing, treating or ameliorating a medical condition
 XX
 PS Claim 11; SEQ ID No 143; 542pp; English.
 XX
 XX The present invention relates to the isolation of novel human

CC calcium-binding proteins, and cDNA (AAS31577-AAS31654) and genomic
 CC sequences encoding for these proteins. The sequences of the invention
 CC are useful in the diagnosis, prevention and/or prognosis of diseases
 CC associated with aberrant calcium flux. Such disorders include
 CC neurological diseases (e.g. amyotrophic lateral sclerosis, ALS),
 CC immune dysfunction (e.g. severe combined immunodeficiency, SCID),
 CC digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic
 CC disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or
 CC infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The
 CC novel calcium-binding proteins are also useful as screening tools to
 CC identify antagonists and/or agonists that may enhance or inhibit
 CC activities mediated by calcium-binding proteins. The polynucleotides of
 CC the invention are also useful in gene therapy. AAU19892-AAU19969
 CC represent the novel human calcium-binding proteins.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX
 SQ Sequence 343 AA;

Query Match 75.9%; Score 249; DB 22; Length 343;
 Best Local Similarity 100.0%; Pred. No. 6.2e-222;
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLLLHGAQKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNGFYDHEAFL 60
 DB 16 MMWRPSVLLLLLLLHGAQKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNGFYDHEAFL 75
 QY 61 GREVAKFQDLTPESQARLGRIVDRMDRAGDGDGCHVSLAEALRAWTAHTQQRHIRDSVSA 120
 DB 76 GREVAKFQDLTPESQARLGRIVDRMDRAGDGDGCHVSLAEALRAWTAHTQQRHIRDSVSA 135
 QY 121 AWDYTDTRDGRVGEELRNATYGHVAPGEFHDVEDAETTKKMLARDERRFRVADQDGD 180
 DB 136 AWDYTDTRDGRVGEELRNATYGHVAPGEFHDVEDAETTKKMLARDERRFRVADQDGD 195
 QY 181 SMATREELTAFLHPEFPHMRDIVIAETLEDLRNKGQVYVEEYIADLYSAEPGEERPA 240
 DB 196 SMATREELTAFLHPEFPHMRDIVIAETLEDLRNKGQVYVEEYIADLYSAEPGEERPA 255
 QY 241 WYQTERQQF 249
 DB 256 WYQTERQQF 264

RESULT 14
 AAG75587

ID AAG75587 standard; Protein; 240 AA.

XX AAG75587;

XX
 DT 03-SEP-2001 (first entry)

XX Human colon cancer antigen protein SEQ ID NO:6351.

DE Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW colorectal carcinoma.
 XX Homo sapiens.

XX WO200122920-A2.

XX 05-APR-2001.

XX 28-SEP-2000; 2000WO-US26524.

XX 29-SEP-1999; 99US-0157137.

PR 03-NOV-1999; 99US-0163280.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Barash SC, Birse CE, Rosen CA;

XX

Db 1 MWRPSVLLLLLLRHCAQCKSPDAGPRGQGRVHQAAFLSDAPHDDAHGNFOYDHEAFLG 60
QY 62 REVAKFDOLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSA 121
Db 61 REVAKFDOLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSA 121
QY 122 WDTYDTRDGRVGVWEELRN 140
Db 121 WDTYDTRDGRVGVWEELRN 139

Search completed: May 14, 2003, 10:48:38
Job time : 40 secs

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 14, 2003, 10:47:23 ; Search time 20 Seconds
(without alignments)
1576.605 Million cell updates/sec

Title: US-09-768-840-1

Perfect score: 328

Sequence: 1 MWRPSVLLLLLLLRHGAQG.....FVGSQATNYGDLTRHDEL 328

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

PIR_73:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	5.5	325	2 A45337	reticulocalbin pre
2	18	5.5	331	2 JC4173	reticulocalbin pre
3	9	2.7	402	1 BOHUS	sex steroid-bindin
4	8	2.4	90	1 BCHUY	calcyclin - human
5	8	2.4	133	2 S57038	probable membrane
6	8	2.4	147	2 A53180	ribonuclease PL3 (
7	8	2.4	171	2 S19502	hypothetical prote
8	8	2.4	185	2 A49957	CD45-associated 30
9	8	2.4	197	2 S51372	membrane protein L
10	8	2.4	205	2 T48294	pathogenesis relat
11	8	2.4	206	2 A55412	lymphocyte phospho
12	8	2.4	209	1 A26166	Ig lambda-5 chain
13	8	2.4	263	2 S57346	interleukin 15 rec
14	8	2.4	271	2 A48826	low choriolytic ha
15	8	2.4	351	2 S20078	NOV protein - chic
16	8	2.4	356	2 S39605	class I histocompa
17	8	2.4	365	2 S66466	cathepsin E (EC 3.
18	8	2.4	376	2 T03988	Myb-like transcrip
19	8	2.4	381	2 S48049	cholecystokinin B
20	8	2.4	398	2 S66465	cathepsin E (EC 3.
21	8	2.4	399	1 A39697	maize myb-related
22	8	2.4	420	2 I51667	thrombin receptor
23	8	2.4	441	2 F71425	hypothetical prote
24	8	2.4	447	2 A47430	gastrin/cholecysto
25	8	2.4	452	2 A46195	cholecystokinin B
26	8	2.4	452	2 JC2459	gastrin/cholecysto
27	8	2.4	453	2 S32817	hypothetical prote
28	8	2.4	481	2 T22406	gastrin receptor -
29	8	2.4	491	2 A82053	DamX-related prote

ALIGNMENTS

RESULT 1

A45337

reticulocalbin precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 02-Aug-2002

C:Accession: A45337; I55203

R:Ozawa, M.; Muramatsu, T.

J. Biol. Chem. 268, 699-705, 1993

A:Title: Reticulocalbin, a novel endoplasmic reticulum resident Ca(2+)-binding protein

A:Reference number: A45337; MUID:93107083; PMID:8416973

A:Contents: teratocarcinoma OTT6050

A:Accession: A45337

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-325 <OZA>

A:Cross-references: GB:D13003; NID:9220581; PIDN:BAA02366.1; PID:d1002865; PID:g22058

A:Note: sequence extracted from NCBI backbone (NCBIP:121512)

R:Ozawa, M.

J. Biochem. 118, 154-160, 1995

A:Title: Structure of the gene encoding mouse reticulocalbin, a novel endoplasmic ret

A:Reference number: I55203; MUID:96015163; PMID:8537305

A:Accession: I55203

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-325 <RES>

A:Cross-references: GB:D43956; NID:g2130295; PIDN:BAA07896.1; PID:g968894

C:Genetics:

A:Introns: 79/2; 144/1; 203/3; 224/1; 290/3

C:Superfamily: reticulocalbin; calmodulin repeat homology

C:Keywords: EF hand

F:1-23/Domain: signal sequence #status predicted <SIC>

F:322-325/Region: endoplasmic reticulum retention signal

Query Match

Best Local Similarity 5.5%; Score 18; DB 2; Length 325;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 305 NNNMFVGSQATNYGDLT 322

Db 302 NNNMFVGSQATNYGDLT 319

RESULT 2

JC4173

reticulocalbin precursor - human

C:Species: Homo sapiens (man)

C>Date: 27-Aug-1995 #sequence_revision 27-Oct-1995 #text_change 02-Aug-2002

C:Accession: JC4173

R:Ozawa, M.

J. Biochem. 117, 1113-1119, 1995

A:Title: Cloning of a human homologue of mouse reticulocalbin reveals conservation of

C:Accession: A28363; A25645; A30356; PC1222
J. Murphy, L.C.; Murphy, L.J.; Tsuyuki, D.; Duckworth, M.L.; Shiu, R.P.C.
A:Title: Cloning and characterization of a cDNA encoding a highly conserved, putative calmodulin-binding protein
A:Reference number: A28363
A:Accession: A28363
A:Molecule type: mRNA
A:Residues: 1-90 <MUR>
A:Cross-references: GB:M18981; NID:g179767; PIDN:AAA51906.1; PID:g179768
R:Calabretta, B.; Battini, R.; Kaczmarek, L.; de Riel, J.K.; Baserga, R.
J. Biol. Chem. 261, 12628-12632, 1986
A:Title: Molecular cloning of the cDNA for a growth factor-inducible gene with strong homology to the protein tyrosine kinase substrate
A:Reference number: A25645; MUID:86304442; PMID:3755724
A:Accession: A25645
A:Molecule type: mRNA
A:Residues: 2-90 <CAL>
A:Cross-references: GB:M14300; NID:g183097; PIDN:AAA35886.1; PID:g183098
R:Gabius, H.J.; Bardos, A.; Gabius, S.; Hellmann, K.P.; Karas, M.; Kratzin, H.
Biochem. Biophys. Res. Commun. 163, 506-512, 1989
A:Title: Identification of a cell cycle-dependent gene product as a sialic acid-binding protein
A:Reference number: A30356; MUID:89374276; PMID:2775283
A:Accession: A30356
A:Molecule type: protein
A:Residues: 57-63, 'X', 65, 'X', 67-70, 'X', 72-74 <GAB>
A:Note: the amino end of the intact protein is blocked
R:Tomida, Y.; Terasawa, M.; Kobayashi, R.; Hidaka, H.
Biochem. Biophys. Res. Commun. 189, 1310-1316, 1992
A:Title: Calcyclin and calvasculin exist in human platelets.
A:Reference number: PC1222; MUID:93129189; PMID:1482346
A:Accession: PC1222
A:Molecule type: protein
A:Residues: 27-31; 48-87, 'XX' <TOM>
A:Experimental source: platelets
C:Comment: This protein is expressed in a cell cycle-specific manner. Not found in the high in cycling cells. It is overproduced in certain acute myeloid leukemias.
C:Comment: Homology of this protein to the S-100 proteins is of interest given the role of S-100 proteins in cell cycle regulation.
C:Comment: This protein binds sialic acid in the presence of calcium.
C:Genetics:
A:Gene: GDB:S100A6; CACV
A:Cross-references: GDB:I19048; OMIM:114110
A:Map position: 1q21-1q21
C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: calcium binding; EF hand; growth regulation; mitogen
F:7-41/Domain: calmodulin repeat homology <EF1>
F:48-80/Domain: calmodulin repeat homology <EF2>

Query Match 2.4%; Score 8; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 210 EDDLNRKD 217
|||||||
Db 58 EDDLNRKD 65

RESULT 5
S57038
N:Alternate names: hypothetical protein J1470; hypothetical protein YJR83.19
C:Species: Saccharomyces cerevisiae
C:Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 19-Apr-2002
C:Accession: S57038; S57041; S55212
R:de Haan, M.; Grivell, L.A.; Smits, P.H.M.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S56771
A:Accession: S57038
A:Molecule type: DNA
A:Residues: 1-133 <ZAG>
A:Cross-references: EMBL:249522; NID:g1015659; PID:g1015661
R:Zagulska, M.; Babinska, B.; Gronadka, R.; Migdalski, A.; Rytka, J.; Sulicka, J.; Herberich, J.
submitted to the Protein Sequence Database, September 1995

Query Match 2.4%; Score 8; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 210 EDDLNRKD 217
|||||||
Db 58 EDDLNRKD 65

RESULT 5
S57038
N:Alternate names: hypothetical protein J1470; hypothetical protein YJR83.19
C:Species: Saccharomyces cerevisiae
C:Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 19-Apr-2002
C:Accession: S57038; S57041; S55212
R:de Haan, M.; Grivell, L.A.; Smits, P.H.M.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S56771
A:Accession: S57038
A:Molecule type: DNA
A:Residues: 1-133 <ZAG>
A:Cross-references: EMBL:249522; NID:g1015659; PID:g1015661
R:Zagulska, M.; Babinska, B.; Gronadka, R.; Migdalski, A.; Rytka, J.; Sulicka, J.; Herberich, J.
submitted to the Protein Sequence Database, September 1995

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A:Accession: S19502
A:Molecule type: DNA
A:Residues: 1-171 <DUS>
A:Cross-references: EMBL:X59720; NID:g1907116; PID:g1907224; GSPDB:GN00003; MIPS:YCR087w
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: T48294
A:Gene: MIPS:YCR087w
A:Cross-references: SGD:S0000683
A:Map position: 3R
A:Superfamily: Saccharomyces hypothetical protein YCR087w

Query Match      2.4%; Score 8; DB 2; Length 171;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VLLLLLLL 14
   |||||
Db 83 VLLLLLLL 90

RESULT 8
A49957
CD45-associated 30k phosphoprotein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 11-Jan-2000
R:Okada, A.; Maizel, A.L.; Kitamura, K.; Ohta, T.; Kimura, S.
J. Biol. Chem. 269, 2357-2360, 1994
A:Title: Molecular cloning of the CD45-associated 30-kDa protein.
A:Reference number: A49957; MUID:94131987; PMID:8300558
A:Accession: A49957
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-185 <YAK>
A:Cross-references: NID:g454750; PIDN:AA67166.1; PID:g454751
C:Superfamily: human lymphocyte phosphatase-associated phosphoprotein
C:Keywords: phosphoprotein
F:2-185/Product: CD45-associated 30k phosphoprotein #status experimental <YAK>

Query Match      2.4%; Score 8; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VLLLLLLL 14
   |||||
Db 25 VLLLLLLL 32

RESULT 9
S51372
membrane protein LSM - mouse
C:Species: Mus musculus (house mouse)
C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 20-Jun-2000
C:Accession: S51372
R:Shimizu, Y.; Ogawa, H.; Oka, Y.; Mizuno, R.; Sakoda, S.; Kishimoto, T.; Sugiyama, H.
FEBS Lett. 355, 30-34, 1994
A:Title: Isolation of a cDNA clone encoding a novel membrane protein expressed in lymph
A:Reference number: S51372; MUID:95046370; PMID:7957956
A:Accession: S51372
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-197 <SHI>
A:Cross-references: EMBL:D10105; NID:g602769; PIDN:BAA00986.1; PID:g602770
C:Superfamily: human lymphocyte phosphatase-associated phosphoprotein

Query Match      2.4%; Score 8; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VLLLLLLL 14
   |||||
Db 37 VLLLLLLL 44

RESULT 10
T48294
pathogenesis related protein-like - Arabidopsis thaliana
N:Alternate names: protein F9G14.40
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: T48294
R:Bevan, M.; Terry, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.;
ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24491
A:Accession: T48294
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-205 <BEV>
A:Cross-references: EMBL:AL162973
A:Experimental source: cultivar Columbia; BAC clone F9G14
C:Genetics:
A:Map position: 5
A:Note: F9G14.40

Query Match      2.4%; Score 8; DB 2; Length 205;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SVLLLLLL 13
   |||||
Db 16 SVLLLLLL 23

RESULT 11
A55412
lymphocyte phosphatase-associated phosphoprotein - human
C:Species: Homo sapiens (man)
C:Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 10-Dec-1999
C:Accession: A55412
R:Schraven, B.; Schoenhaut, D.; Bruyns, E.; Koretzky, G.; Eckerskorn, C.; Wallich, R.
J. Biol. Chem. 269, 29102-29111, 1994
A:Title: LPPAP, a novel 32-kDa phosphoprotein that interacts with CD45 in human lympho
A:Reference number: A55412; MUID:95050730; PMID:7961877
A:Accession: A55412
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-206 <SCH>
A:Cross-references: GB:X81422; NID:g577060; PIDN:CAA57182.1; PID:g577061
C:Genetics:
A:Gene: GDB:LPPAP
A:Cross-references: GDB:439030
A:Superfamily: human lymphocyte phosphatase-associated phosphoprotein
C:Keywords: phosphoprotein

Query Match      2.4%; Score 8; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VLLLLLLL 14
   |||||
Db 37 VLLLLLLL 44

RESULT 12
A26166
Ig lambda-5 chain J region precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A26166; J10030; A26434
R:Kudo, A.; Sakauchi, N.; Melchers, F.
EMBO J. 6, 103-107, 1987
A:Title: Organization of the murine Ig-related lambda-5 gene transcribed selectively
A:Reference number: A26166; MUID:87218453; PMID:3107979
A:Accession: A26166
A:Molecule type: DNA
A:Residues: 1-209 <KUD>

```

R;Jongstra, J.; Jongstra-Bilen, J.; Tidmarsh, G.F.; Davis, M.M.
 Mol. Immunol. 25, 687-693, 1988
 A:Title: The in vitro translation product of the murine lambda 5 gene contains a functional protein
 A:Reference number: JLO030; MUID:89039915; PMID:2460755
 A:Accession: JLO030
 A:Molecule type: mRNA
 A:Residues: 1-123, 'ANKATL', 130-209 <JON>
 A:Experimental source: pre-B cell, cell lines A2-A15
 R;Sakaguchi, N.; Melchers, F.
 Nature 324, 579-582, 1986
 A:Title: Lambda-5, a new light-chain-related locus selectively expressed in pre-B lymphocytes
 A:Reference number: A26434; MUID:87065143; PMID:3024017
 A:Accession: A26434
 A:Molecule type: mRNA
 A:Residues: 92-104 <SAK>
 A:Cross-references: GB:M30387
 C:Comment: See also PIR:B26434.
 C:Comment: This protein is the transcript of immunoglobulin lambda light chain-related gene

C:Genetics:
 A:Gene: lambda-5
 A:Introns: 65/2, 104/1
 C:Superfamily: pre-B cell omega light chain; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-30/Domain: signal sequence #status predicted <SIG>
 F:31-209/Product: lambda-5 protein #status predicted <MLS>

Query Match 2.4%; Score 8; DB 1; Length 209;
 Best Local Similarity 100.0%; Pred. No. 8.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VLLLLLLL 14
 |||||
 DB 18 VLLLLLLL 25

RESULT 13
 S57346
 Interleukin 15 receptor precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 05-Nov-1999
 C:Accession: S57346
 R;Giri, J.G.; Kumaki, S.; Ahldeh, M.; Friend, D.J.; Loomis, A.; Shanebeck, K.; DuBose, R.
 EMBO J. 14, 3654-3663, 1995
 A:Title: Identification and cloning of a novel IL-15 binding protein that is structurally related to the IL-2 receptor
 A:Reference number: S57346; MUID:95369237; PMID:7641685
 A:Accession: S57346
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-263 <GIR>
 A:Cross-references: EMBL:U22339; NID:g951105; PIDN:AAC52240.1; PID:g951106
 C:Superfamily: complement factor H repeat homology
 C:Keywords: cytokine receptor
 F:36-96/Domain: complement factor H repeat homology <FH2>

Query Match 2.4%; Score 8; DB 2; Length 263;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VLLLLLLL 14
 |||||
 DB 16 VLLLLLLL 23

RESULT 14
 A48826
 low choriolytic hatching proteinase (EC 3.4.24.-) precursor - Japanese medaka
 C:Species: Oryzias latipes (Japanese medaka)
 C:Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
 C:Accession: A48826
 R;Yasumasa, S.; Yamada, K.; Akasaka, K.; Mitsunaga, K.; Iuchi, I.; Shimada, H.; Yamagami, Dev. Biol. 153, 250-258, 1992
 A:Title: Isolation of cDNAs for LCE and HCE, two constituent proteases of the hatching

A:Reference number: A48826; MUID:93012471; PMID:1397682
 A:Accession: A48826
 A:Molecule type: mRNA; protein
 A:Residues: 1-271 <YAS>
 A:Cross-references: GB:M96169; NID:g213505; PIDN:AAA49440.1; PID:g213506
 A:Experimental source: orange red variety, embryo
 A:Note: sequence extracted from NCBI backbone (NCBIN:114767, NCBIP:114768)
 C:Note: part of this sequence, including the amino end of the mature protein, was determined
 C:Superfamily: astacin; astacin homology
 C:Keywords: glycoprotein; hydrolase; metalloproteinase; zinc
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-71/Domain: propeptide #status predicted <PRO>
 F:72-271/Product: low choriolytic hatching proteinase #status predicted <MAT>
 F:91-271/Domain: astacin homology <AST>
 F:30, 54, 211/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:172, 176, 182, 228/Binding site: zinc (His, His, Tyr) #status predicted
 F:173/Active site: Glu #status predicted

Query Match 2.4%; Score 8; DB 2; Length 271;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SVLLLLLL 13
 |||||
 DB 8 SVLLLLLL 15

RESULT 15
 S20078
 NOV protein - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
 C:Accession: S20078
 R;Joliot, V.; Martinier, C.; Dambrine, G.; Plassiat, G.; Brisac, M.; Crochet, J.; P.
 Mol. Cell. Biol. 12, 10-21, 1992
 A:Title: Proviral rearrangements and overexpression of a new cellular gene (nov) in m
 A:Reference number: S20078; MUID:92107157; PMID:1309586
 A:Accession: S20078
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-351 <JOL>
 A:Cross-references: EMBL:X59284; NID:g63702; PIDN:CAA41975.1; PID:g63703
 C:Genetics:
 A:Gene: NOV

Query Match 2.4%; Score 8; DB 2; Length 351;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VLLLLLLL 14
 |||||
 DB 11 VLLLLLLL 18

Search completed: May 14, 2003, 10:50:07
 Job time : 22 secs

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GenCore version 5.1.4_p5-4578
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OM protein - protein search, using sw model

Run on: May 14, 2003, 10:45:38 ; Search time 14 Seconds
(without alignments)
971.731 Million cell updates/sec

Title: US-09-768-840-1
Perfect score: 328
Sequence: 1 MMWRPSVLLLLLRHGAQG.....FVGSQATNYGDLTRHDEL 328

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	5.5	325	1 RCNL_MOUSE	Q05186 mus musculus
2	18	5.5	331	1 RCNL_HUMAN	Q15293 homo sapien
3	10	3.0	215	1 YA09_HUMAN	Q9y3b3 homo sapien
4	9	2.7	114	1 NPFF_RAT	Q9wva9 rattus norv
5	9	2.7	315	1 CALU_HUMAN	O43852 homo sapien
6	9	2.7	315	1 CALU_MOUSE	O35887 mus musculus
7	9	2.7	402	1 SHBG_HUMAN	P04278 homo sapien
8	8	2.4	90	1 S106_HUMAN	P06703 homo sapien
9	8	2.4	92	1 S106_CHICK	Q98953 gallus.gall
10	8	2.4	110	1 GON2_SUNMU	O97686 suncus muri
11	8	2.4	133	1 YJ23_YEAST	P47094 saccharomyc
12	8	2.4	141	1 LSHB_TRIVU	O46482 trichosurus
13	8	2.4	147	1 RNL4_PIG	P15468 sus scrofa
14	8	2.4	171	1 YCX7_YEAST	P25652 saccharomyc
15	8	2.4	197	1 PTCA_MOUSE	Q64597 mus musculus
16	8	2.4	206	1 PTCA_HUMAN	Q14761 homo sapien
17	8	2.4	271	1 LCE_ORYLA	P31579 oryzias lat
18	8	2.4	273	1 SZ16_HUMAN	Q9h2a7 homo sapien
19	8	2.4	346	1 LICH_ACILW	Q9x2s4 acinetobact
20	8	2.4	351	1 NOV_CHICK	P28686 gallus gall
21	8	2.4	353	1 NOV_COTJA	P42642 coturnix co
22	8	2.4	377	1 MLC1_HUMAN	Q15049 homo sapien
23	8	2.4	397	1 CATE_MOUSE	P70269 mus musculus
24	8	2.4	398	1 CATE_RAT	P16228 rattus norv
25	8	2.4	399	1 MYBP_MAIZE	P27898 zea mays (m
26	8	2.4	420	1 PAR1_XENLA	P47749 xenopus lae
27	8	2.4	447	1 GASR_HUMAN	P32239 homo sapien
28	8	2.4	452	1 GASR_RABIT	P46627 oryctolagus
29	8	2.4	452	1 GASR_RAT	P30553 rattus norv
30	8	2.4	453	1 GASR_CANFA	P30552 canis fami
31	8	2.4	454	1 GASR_BOVIN	P79266 bos taurus
32	8	2.4	461	1 NCBI_HUMAN	Q02818 homo sapien
33	8	2.4	464	1 SRPX_HUMAN	P78539 homo sapien

34	8	2.4	501	1 PTGI_MOUSE	O35074 mus musculus
35	8	2.4	501	1 PTGI_RAT	Q62969 rattus norv
36	8	2.4	519	1 PPBT_CHICK	Q32058 gallus gall
37	8	2.4	633	1 HS7B_DROME	P11146 drosophila
38	8	2.4	732	1 CADL_CHICK	P33145 gallus gall
39	8	2.4	754	1 PURL_MYCTU	P54876 mycobacteri
40	8	2.4	975	1 KIT_CANFA	O97799 canis fami
41	8	2.4	977	1 KFMS_MOUSE	P09581 mus musculus
42	8	2.4	978	1 KFMS_RAT	Q00495 rattus norv
43	8	2.4	1310	1 ACE_RABIT	P12822 oryctolagus
44	7	2.1	31	1 LPL_BUCRP	Q53017 buchmera ap
45	7	2.1	61	1 DNBI_BFDV	P13893 budgerigar

ALIGNMENTS

RESULT 1

RCNL_MOUSE	ID	RCNL_MOUSE	STANDARD	PRT	325 AA.
AC	Q05186;				
DT	01-JUN-1994 (Rel. 29, Created)				
DT	01-JUN-1994 (Rel. 29, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Reticulocalbin 1 precursor.				
GN	RCN1 OR RCN OR RCAL				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=93107083; PubMed=8416973;				
RA	Ozawa M., Muramatsu T.;				
RT	"Reticulocalbin, a novel endoplasmic reticulum resident				
RT	Ca(2+)-binding protein with multiple EF-hand motifs and a				
RT	carboxyl-terminal HDEL sequence.";				
RL	J. Biol. Chem. 268:699-705(1993).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=129/SV; TISSUE=Liver;				
RX	MEDLINE=96015163; PubMed=8537305;				
RA	Ozawa M.;				
RT	"Structure of the gene encoding mouse reticulocalbin, a novel				
RT	endoplasmic reticulum-resident Ca(2+)-binding protein with multiple				
RT	EF-hand motifs.";				
RL	J. Biochem. 118:154-160(1995).				
RN	[3]				
RP	SEQUENCE OF 24-39.				
RC	TISSUE=Fibroblast;				
RX	MEDLINE=95009907; PubMed=7523108;				
RA	Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;				
RT	"Separation and sequencing of familial and novel murine proteins				
RT	using preparative two-dimensional gel electrophoresis.";				
RL	Electrophoresis 15:735-745(1994).				
CC	-1- FUNCTION: MAY REGULATE CALCIUM-DEPENDENT ACTIVITIES IN THE				
CC	ENDOPLASMIC RETICULUM LUMEN OR POST-ER COMPARTMENT.				
CC	-1- SURCELLULAR LOCATION: Endoplasmic reticulum lumen.				
CC	-1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING				
CC	SITES; POTENTIAL SITES II AND VI HAVE LOST AFFINITY FOR CALCIUM.				
CC	-1- SIMILARITY: BELONGS TO THE CREC FAMILY.				
CC	-1- SIMILARITY: CONTAINS 6 EF-HAND CALCIUM-BINDING DOMAINS.				
CC	-----				
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CC	use by non-profit institutions as long as its content is in no way				
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CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; D13003; BAA02366.1; -.				
DR	EMBL; D43956; BAA07896.1; -.				

DR EMBL; D43952; BAA07896.1; JOINED.
 DR EMBL; D43954; BAA07896.1; JOINED.
 DR EMBL; D43955; BAA07896.1; JOINED.
 DR PIR; A45337; A45337.
 DR MGD; MGI:104559; RGN.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR000886; EF-hand.
 DR Pfam; PF00036; ehand; 6.
 DR SMART; SM00054; EFh; 3.
 DR PROSITE; PS00014; EF_TARGET; 1.
 DR PROSITE; PS00018; EF_HAND; 3.
 KW Calcium-binding; Endoplasmic reticulum; Signal; Glycoprotein; Repeat;
 KW Repeat.
 FT SIGNAL 1 23 RETICULOCALBIN 1.
 FT CHAIN 24 325 EF-HAND 1.
 FT CA_BIND 86 97 EF-HAND 2 (POSSIBLY ANCESTRAL).
 FT CA_BIND 122 133 EF-HAND 3.
 FT CA_BIND 173 184 EF-HAND 4.
 FT CA_BIND 210 221 EF-HAND 5.
 FT CA_BIND 251 262 EF-HAND 6 (POSSIBLY ANCESTRAL).
 FT CA_BIND 287 298 PREVENT SECRETION FROM ER.
 FT SITE 322 325 K -> G (IN REF. 3).
 FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (PARTIAL).
 FT CONFLICT 24 24 K -> I (IN REF. 3).
 FT CONFLICT 34 34 R -> I (IN REF. 3).
 FT CONFLICT 37 39 SEL -> DEE (IN REF. 3).
 SQ SEQUENCE 325 AA; 38113 MW; 0470B10B5A8BC76D CRC64;

 Query Match 5.5%; Score 18; DB 1; Length 325;
 Best Local Similarity 100.0%; Pred. No. 2.2e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 305 NNNMFVGSQATNYGDELDT 322
 DB 302 NNNMFVGSQATNYGDELDT 319

 RESULT 2
 RCN1_HUMAN
 ID RCN1_HUMAN STANDARD; PRT; 331 AA.
 AC Q15293;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Reticulocalbin 1 precursor.
 GN RCN1 OR RCN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96172582; PubMed=8586628;
 RA Ozawa M.;
 RT "Cloning of a human homologue of mouse reticulocalbin reveals
 RT conservation of structural domains in the novel endoplasmic reticulum
 RT resident Ca(2+)-binding protein with multiple EF-hand motifs.";
 RL J. Biochem. 117:1113-1119(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Coville G.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: MAY REGULATE CALCIUM-DEPENDENT ACTIVITIES IN THE
 CC ENDOPLASMIC RETICULUM LUMEN OR POST-ER COMPARTMENT.
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -!- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
 CC SITES; POTENTIAL SITES II AND VI HAVE LOST AFFINITY FOR CALCIUM
 CC (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE CREC FAMILY.
 CC -!- SIMILARITY: CONTAINS 6 EF-HAND CALCIUM-BINDING DOMAINS.
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 or send an email to license@isb-sib.ch.

 DR EMBL; D42073; BAA07670.1; -.
 DR EMBL; AL078612; CAB53067.1; -.
 DR Genew; HGNC:9934; RCN1.
 DR MIM; 602735; -.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR000886; EF-hand.
 DR Pfam; PF00036; ehand; 6.
 DR SMART; SM00054; EFh; 3.
 DR PROSITE; PS00014; EF_TARGET; 1.
 DR PROSITE; PS00018; EF_HAND; 4.
 KW Calcium-binding; Endoplasmic reticulum; Signal; Glycoprotein; Repeat;
 KW Polymorphism.
 FT SIGNAL 1 29 RETICULOCALBIN 1.
 FT CHAIN 30 331 EF-HAND 1 (POTENTIAL).
 FT CA_BIND 92 103 EF-HAND 2 (POSSIBLY ANCESTRAL).
 FT CA_BIND 128 139 EF-HAND 3 (POTENTIAL).
 FT CA_BIND 179 190 EF-HAND 4 (POTENTIAL).
 FT CA_BIND 216 227 EF-HAND 5 (POTENTIAL).
 FT CA_BIND 257 268 EF-HAND 6 (POSSIBLY ANCESTRAL).
 FT CA_BIND 293 304 PREVENT SECRETION FROM ER.
 FT SITE 328 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 53 53 T -> N (IN DBSNP:1061145).
 FT VARIANT 71 71 /FTID-VAR_011964.
 FT VARIANT 73 73 D -> Y (IN DBSNP:1804281).
 FT VARIANT 74 74 Q -> E (IN DBSNP:1061143).
 FT VARIANT 188 188 /FTID-VAR_011966.
 FT SEQUENCE 331 AA; 38890 MW; 608AAD536963F789 CRC64;

 Query Match 5.5%; Score 18; DB 1; Length 331;
 Best Local Similarity 100.0%; Pred. No. 2.2e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 305 NNNMFVGSQATNYGDELDT 322
 DB 308 NNNMFVGSQATNYGDELDT 325

 RESULT 3
 YA09_HUMAN
 ID YA09_HUMAN STANDARD; PRT; 215 AA.
 AC Q9Y3B3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein CGI-109 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20272150; PubMed=10810093;
 RA Lai C.-H., Chou C.-Y., Ch'ang L.-Y., Liu C.-S., Lin W.-C.;
 RT "Identification of novel human genes evolutionarily conserved in
 RT Caenorhabditis elegans by comparative proteomics.";
 RL Genome Res. 10:703-713(2000).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Endoplasmic
 CC reticulum (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE EMP24/GP25L FAMILY.
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DR EMBL: AFI51867; AAD34104.1;
 DR InterPro: IPR000348; Emp24_gp25L_p24.
 DR Pfam: PF01105; EMP24_GP25L; 1.
 KW Hypothetical protein; Transmembrane; Signal;
 KW Endoplasmic reticulum.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 215 HYPOTHETICAL PROTEIN CGI-109.
 FT DOMAIN 24 176 LUMENAL (POTENTIAL).
 FT TRANSMEM 177 199 POTENTIAL.
 FT DOMAIN 200 215 CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 215 AA; 24354 MW; 5CAD5BBE8054857B CRC64;

Query Match 3.0%; Score 10; DB 1; Length 215;
 Best Local Similarity 100.0%; Pred. No. 0.054;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 SVLLLLLLL 15
 Db 10 SVLLLLLLL 19

RESULT 4 NPFF_RAT

ID NPFF_RAT STANDARD; PRT; 114 AA.
 AC Q9WV9;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE FMRamide-related peptides precursor [Contains: Neuropeptide SF
 DE (NPFF); Neuropeptide FF (NPFF); Neuropeptide AF-like (NPFF)].
 GN NPFF.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]

SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=99238783; PubMed=10220558;
 RA Vilim F.S., Aarnisalo A.A., Nieminen M.L., Lintunen M., Karlstedt K.,
 RA Kontinen V.K., Kalso E., States B., Panula P., Ziff E.;
 RT "Gene for pain modulatory neuropeptide NPFF: induction in spinal cord
 RT by noxious stimuli.";
 RL Mol. Pharmacol. 55:804-811(1999).

CC -1- FUNCTION: MORPHINE MODULATING PEPTIDES. HAVE WIDE-RANGING
 CC PHYSIOLOGIC EFFECTS, INCLUDING THE MODULATION OF MORPHINE-INDUCED
 CC ANALGESIA, ELEVATION OF ARTERIAL BLOOD PRESSURE, AND INCREASED
 CC SOMATOSTATIN SECRETION FROM THE PANCREAS.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.

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DR EMBL: AFI48700; AAD39828.1;
 KW Neuropeptide; Amidation; Cleavage on pair of basic residues; Signal.
 FT SIGNAL 1 21 POTENTIAL.
 FT PROPEP 22 69
 FT PEPTIDE 72 82 NEUROPEPTIDE SF.
 FT PEPTIDE 75 82 NEUROPEPTIDE FF.
 FT PROPEP 85 100
 FT PEPTIDE 101 111 NEUROPEPTIDE AF-LIKE.
 FT MOD_RES 82
 FT AMIDATION (G-83 PROVIDE AMIDE GROUP) (BY

FT MOD_RES 111 111 SIMILARITY).
 FT AMIDATION (G-112 PROVIDE AMIDE GROUP) (BY
 FT SIMILARITY).
 SO SEQUENCE 114 AA; 13152 MW; 482ABAB7BA28F9E4 CRC64;

Query Match 2.7%; Score 9; DB 1; Length 114;
 Best Local Similarity 100.0%; Pred. No. 0.27;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 VLLLLLLL 15
 Db 8 VLLLLLLL 16

RESULT 5 CALU_HUMAN

ID CALU_HUMAN STANDARD; PRT; 315 AA.
 AC Q43852; Q60456;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calumenin precursor (IEF SSP 9302).
 GN CALU
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CALCIUM-BINDING DATA.
 RC TISSUE=Keratinocytes;
 RX PubMed=9675259;
 RA Vorum H., Liu X., Madsen P., Rasmussen H.H., Honore B.;
 RT "Molecular cloning of a cDNA encoding human calumenin, expression in
 RT Escherichia coli and analysis of its Ca2+-binding activity.";
 RL Biochim. Biophys. Acta 1386:121-131(1998).
 RN [2]

SEQUENCE FROM N.A.
 RX MEDLINE=98260687; PubMed=9598325;
 RA Yabe D., Taniwaki M., Nakamura T., Kanazawa N., Tashiro K., Honjo T.;
 RT "Human calumenin gene (CALU): cDNA isolation and chromosomal mapping
 RT to 7q32.";
 RL Genomics 49:331-333(1998).
 RN [3]

RP SUBCELLULAR LOCATION.
 RX PubMed=10222138;
 RA Vorum H., Hager H., Christensen B.M., Nielsen S., Honore B.;
 RT "Human calumenin localizes to the secretory pathway and is secreted to
 RT the medium.";
 RL Exp. Cell Res. 248:473-481(1999).

CC -1- FUNCTION: NOT KNOWN. BINDS 7 CALCIUM IONS WITH A LOW AFFINITY.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen and secreted.
 CC -1- TISSUE SPECIFICITY: Ubiquitously expressed. Expressed at high
 CC levels in heart, placenta and skeletal muscle, at lower levels in
 CC lung, kidney and pancreas and at very low levels in brain and
 CC liver.

CC -1- SIMILARITY: BELONGS TO THE CREC FAMILY.
 CC -1- SIMILARITY: CONTAINS 7 EF-HAND CALCIUM-BINDING DOMAINS.
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DR EMBL: U67280; AAB97725.1;
 DR EMBL: AF013759; AAC17216.1;
 DR Genew; HGNC:1458; CALU.
 DR MIM; 603420;
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; efhand; 6.
 DR SMART; SM00054; Efh; 2.

Tue May 20 14:43:21 2003

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DR PROSITE; PS00018; EF_HAND; 4.
KW Calcium-binding; Endoplasmic reticulum; Signal; Repeat.
FT SIGNAL 1 19
FT CHAIN 20 315
FT CA_BIND 81 92
FT CA_BIND 117 128
FT CA_BIND 164 175
FT CA_BIND 201 212
FT CA_BIND 242 253
FT CA_BIND 278 289
FT CARBOHYD 131 131
FT SITE 312 315
FT CONFLICT 207 207
FT SEQUENCE 315 AA; 37107 MW; 25BAE5A9B527375 CRC64;

Query Match 2.7%; Score 9; DB 1; Length 315;
Best Local Similarity 100.0%; Pred.No. 0.68;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 FDQLTPES 76
DB 61 FDQLTPES 69

RESULT 6
CALU_MOUSE
ID CALU_MOUSE STANDARD; PRT; 315 AA.
AC 035887;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Calumenin precursor.
GN CALU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC MEDLINE=97364750; PubMed=9218460;
RA Yabe D., Nakamura T., Kanazawa N., Tashiro K., Honjo T.;
RT "Calumenin, a Ca2+-binding protein retained in the endoplasmic
RL reticulum with a novel carboxyl-terminal sequence, HDEF.";
RL J. Biol. Chem. 272:18232-18239(1997).
CC -!- FUNCTION: NOT KNOWN, BINDS 7 CALCIUM IONS WITH A LOW AFFINITY (BY
CC similarity).
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: BELONGS TO THE CREC FAMILY.
CC -!- SIMILARITY: CONTAINS 6 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U81829; AAC53316.1; -.
CC DR MGD; MGI:1097158; Calu.
CC DR InterPro; IPR002048; EF-hand.
CC DR Pfam; PF00036; efhand; 6.
CC DR SMART; SM00054; EFh; 2.
CC DR PROSITE; PS00018; EF_HAND; 4.
KW Calcium-binding; Endoplasmic reticulum; Signal; Repeat.
FT SIGNAL 1 19
FT CHAIN 20 315
FT CA_BIND 81 92
FT CA_BIND 117 128
FT CA_BIND 164 175
FT CA_BIND 201 212
FT CONFLICT 207 207
FT SEQUENCE 315 AA; 37107 MW; 25BAE5A9B527375 CRC64;

Query Match 2.7%; Score 9; DB 1; Length 315;
Best Local Similarity 100.0%; Pred.No. 0.68;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 FDQLTPES 76
DB 61 FDQLTPES 69

RESULT 7
SHBG_HUMAN
ID SHBG_HUMAN STANDARD; PRT; 402 AA.
AC P04278; Q16616; P14689;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sex hormone-binding globulin precursor (SHBG) (sex steroid-binding
DE protein) (SBP) (testis-specific androgen-binding protein) (ABP).
GN SHBG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Testis;
RC MEDLINE=90067924; PubMed=2587256;
RA Gershagen S., Lundwall A., Fernlund P.;
RT "Characterization of the human sex hormone binding globulin (SHBG)
RL gene and demonstration of two transcripts in both liver and testis.";
RL Nucleic Acids Res. 17:9245-9258(1989).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Testis;
RC MEDLINE=90114193; PubMed=2608061;
RA Hammond G.L., Underhill D.A., Rykse H.M., Smith C.L.;
RT "The human sex hormone-binding globulin gene contains exons for
RL androgen-binding protein and two other testicular messenger RNAs.";
RL Mol. Endocrinol. 3:1869-1876(1989).
RN [3]
RP SEQUENCE OF 22-402 FROM N.A. (ISOFORM 1).
RC TISSUE=Liver;
RC MEDLINE=87190990; PubMed=3569533;
RA Hammond G.L., Underhill D.A., Smith C.L., Goping I.S., Harley M.J.;
RT "The cDNA-deduced primary structure of human sex hormone-binding
RL globulin and location of its steroid-binding domain.";
RL FEBS Lett. 215:100-104(1987).
RN [4]
RP SEQUENCE OF 47-402 FROM N.A. (ISOFORM 1).
RC TISSUE=Liver;
RC MEDLINE=87276542; PubMed=2956126;
RA Gershagen S., Fernlund P., Lundwall A.;
RT "A cDNA coding for human sex hormone binding globulin. Homology to
RL vitamin K-dependent protein S.";
RL FEBS Lett. 220:129-135(1987).
RN [5]
RP SEQUENCE OF 121-402 FROM N.A. (ISOFORM 1).
RC TISSUE=Liver;
RC MEDLINE=87276521; PubMed=2956125;
RA Que B.G., Petra P.H.;
RT "Characterization of a cDNA coding for sex steroid-binding protein of
RL human plasma.";
RL FEBS Lett. 219:405-409(1987).
RN [6]
RP SEQUENCE OF 30-54.
RP MEDLINE=86201807; PubMed=3702459;

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Hammond G.L., Robinson P.A., Sugino H., Ward D.N., Finne J.;
 "Physicochemical characteristics of human sex hormone binding
 globulin: evidence for two identical subunits.",
 J. Steroid Biochem. 24:815-824(1986).
 [7]
 RP SEQUENCE OF 30-402.
 RX MEDLINE=87101042; PubMed=3542030;
 RA Walsh K.A., Titani K., Takio K., Kumar S., Hayes R., Petra P.H.;
 "Amino acid sequence of the sex steroid binding protein of human
 blood plasma.",
 Biochemistry 25:7584-7590(1986).
 RL [8]
 RP VARIANT ASN-356, AND CARBOHYDRATE-LINKAGE SITE ASN-356.
 RX MEDLINE=93016620; PubMed=1400872;
 RA Power S.G.A., Bocchinfuso W.P., Pallesen M., Wamels-Rodenhiiser S.,
 Van Baalen H., Hammond G.L.;
 "Molecular analyses of a human sex hormone-binding globulin variant:
 evidence for an additional carbohydrate chain.",
 J. Clin. Endocrinol. Metab. 75:1066-1070(1992).
 RL [9]
 RP VARIANT ASN-356.
 RX MEDLINE=95229819; PubMed=7714097;
 RA Hardy D.O., Carino C., Catterall J.F., Larrea F.;
 "Molecular characterization of a genetic variant of the steroid
 hormone-binding globulin gene in heterozygous subjects.",
 J. Clin. Endocrinol. Metab. 80:1253-1256(1995).
 RL [10]
 RP FUNCTION: Functions as an androgen transport protein, but may also
 be involved in receptor mediated processes. Each dimer binds one
 molecule of steroid. Specific for 5-alpha-dihydrotestosterone,
 testosterone, and 17-beta-estradiol. Regulates the plasma
 metabolic clearance rate of steroid hormones by controlling their
 plasma concentration.
 CC [11]
 RP SUBUNIT: Homodimer.
 CC [12]
 RP SUBCELLULAR LOCATION: Secreted. In testis, it is synthesized by
 the Sertoli cells, secreted into the lumen of the seminiferous
 tubule and transported to the epididymis (By similarity).
 CC [13]
 RP ALTERNATIVE PRODUCTS: At least 2 isoforms; 1/SHBG/SHBG-1 (shown
 here) and 2/sex hormone binding globulin-gene-related protein
 (SHBG-2); are produced by alternative splicing.
 CC [14]
 RP TISSUE SPECIFICITY: Isoforms 1 and 2 are present in liver and
 testis.
 CC [15]
 RP SIMILARITY: CONTAINS 2 LAMININ G-LIKE DOMAINS.
 CC
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 CC
 CC EMBL; X16349; CAA34398.1; -
 DR EMBL; X16350; CAA34399.1; -
 DR EMBL; X16351; CAA34400.1; -
 DR EMBL; X16352; AAC18778.1; -
 DR EMBL; X05403; CAA28987.1; -
 DR EMBL; X05885; CAA29309.1; -
 DR EMBL; X05792; CAA29234.1; -
 DR PIR; A03253; BOHUS
 DR PIR; A26339; A26339.
 DR PIR; A41402; A41402.
 DR PIR; S00077; S00077.
 DR PIR; S09606; S09606.
 DR GlycoSuiteDB; P04278; -
 DR Genew; HGNC:10839; SHBG.
 DR MIM; 182205; -
 DR InterPro; IPR001791; Laminin_G.
 DR Pfam; PF00054; Laminin_G.
 DR SMART; SM00282; Laminin_G.
 DR PROSITE; PS00025; LAM_G_DOMAIN; 1.
 KW Steroid-binding; Glycoprotein; Repeat; Signal; Alternative splicing;
 KW Polymorphism. 1 29
 FT SIGNAL

FT CHAIN 30 402
 FT DOMAIN 45 217
 FT DOMAIN 224 390
 FT DISULFID 193 217
 FT DISULFID 362 390
 FT CARBOHYD 36 36
 FT CARBOHYD 356 356
 FT CARBOHYD 380 380
 FT CARBOHYD 396 396
 FT VARSPLIC 1 37
 FT VARSPLIC 285 293
 FT VARSPLIC 294 402
 FT VARIANT 356 356
 FT CONFLICT 22 22
 FT CONFLICT 47 55
 FT CONFLICT 334 334
 FT CONFLICT 336 336
 SQ SEQUENCE 402 AA; 43779 MW; 5A3B1885E4E7A460 CRC64;
 Query Match 2.7%; Score 9; DB 1; Length 402;
 Best Local Similarity 100.0%; Pred. No. 0.85;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 8 LLLLLLLH 16
 Db 15 LLLLLLLH 23
 RESULT 8
 ID S106_HUMAN STANDARD; PRT; 90 AA.
 AC P06703;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JUN-1988 (Rel. 06, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calcyclin (Prolactin receptor associated protein) (PRA) (Growth
 factor-inducible protein 2A9) (S106 calcium-binding protein A6)
 DE (MLN 4).
 DE S100A6 OR CACY.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88115387; PubMed=2448309;
 RA Murphy L.C., Murphy L.J., Tsuyuki D., Duckworth M.L., Shiu R.P.C.;
 "Cloning and characterization of a cDNA encoding a highly conserved,
 putative calcium binding protein, identified by an anti-prolactin
 receptor antiserum.",
 RL J. Biol. Chem. 263:2397-2401(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Fibroblast;
 MEDLINE=86304442; PubMed=3755724;
 RA Calabretta B., Battini R., Kaczmarek L., de Riel J.K., Baserga R.;
 "Molecular cloning of the cDNA for a growth factor-inducible gene
 with strong homology to S-100, a calcium-binding protein.",
 RL J. Biol. Chem. 261:12628-12632(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87250432; PubMed=3036810;
 RA Ferrari S., Calabretta B., Deriel J.K., Battini R., Chezzo F.,
 Lauret E., Griffin C., Emanuel B.S., Gurrieri F., Baserga R.;
 "Structural and functional analysis of a growth-regulated gene, the
 human calcyclin.",
 RL J. Biol. Chem. 262:8325-8332(1987).
 RN [4]

SEX HORMONE-BINDING GLOBULIN.
 LAMININ G-LIKE 1.
 LAMININ G-LIKE 2.

O-LINKED.
 /FTID-CAR_000174.
 N-LINKED (GLCNAC. . .) (IN VARIANT ASN-
 356).
 N-LINKED (GLCNAC. . .).
 N-LINKED (GLCNAC. . .).
 MESRPLATSLRLLLLRHTRGHALRPVLPQTQ ->
 PRFGSPAVLEKLVAVITCSLRLTHPPRPW (IN
 ISOFORM 2).
 KVLSSSGS -> EKTLPPLPA (IN ISOFORM 2).
 MISSING (IN ISOFORM 2).
 D -> N.
 /FTID-VAR_013129.
 R -> Q (IN REF. 3).
 LNSGPGQEP -> VHSAAQTTL (IN REF. 4).
 A -> L (IN REF. 2).
 L -> S (IN REF. 2).

SEQUENCE FROM N.A.
 AC Q98953; STANDARD; PRT; 92 AA.
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Calyculin.
 DE S100A6.
 GN Gallus gallus (Chicken).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Glizzard
 RX MEDLINE=98262336; PubMed=9599662;
 RA Allen B.G., Andrea J.B., Sutherland C., Schonekess B.O., Walsh M.P.;
 RT "Molecular cloning of chicken calyculin (S100A6) and identification
 of putative isoforms";
 RL Biochem. Cell Biol. 75:733-738(1997).
 CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U76365; AAB18788.1; --
 DR HSSP; P30801; 1A03.
 DR InterPro; IPR001751; CaBP_S100.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; ehand; 1.
 DR Pfam; PF01023; S_100; 1.
 DR PRODOM; PD003407; CaBP_S100; 1.
 DR PROSITE; PS00018; EF-HAND; 1.
 DR PROSITE; PS00303; S100_CaBP; 1.
 DR Mitogen; Cell cycle; Calcium-binding.
 KW Mitogen; Cell cycle; Calcium-binding. (POTENTIAL).
 FT CA_BIND 20 33 EF-HAND 1 (LOW AFFINITY) (POTENTIAL).
 FT CA_BIND 61 72 EF-HAND 2 (HIGH AFFINITY) (POTENTIAL).
 FT SEQUENCE 92 AA; 10276 MW; 56B3D65BAA7BF7A4 CRC64;
 SQ
 Query Match 2.4%; Score 8; DB 1; Length 92;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 210 EDLDRNKD 217
 DB 58 EDLDRNKD 65
 RESULT 10
 GON2_SUNMU STANDARD; PRT; 110 AA.
 ID GON2_SUNMU
 AC Q97686;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Progonadoliberin II precursor [Contains: Gonadoliberin II (LHRH II)
 (Luteinizing hormone releasing hormone II) (Gonadotropin releasing
 hormone II) (GNRH II) (Luliberin II); GnRH-associated peptide II].
 DE GNRH2.
 GN Suncus murinus (House shrew) (Musk shrew).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Insectivora; Soricidae; Crocidurinae; Suncus.
 OX NCBI_TaxID=9378;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 White R.B., Kasten T.L., White S.A., Rissman E.F., Fernald R.D.;

SEQUENCE FROM N.A.
 RA Wu J., Liu W., Zhou Y., Zhao Z., Peng X., Yuan J., Qiang B.;
 RT "Cloning of human calyculin and calyculin binding protein (CacyBP).";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, and Placenta;
 RA Strausberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE OF 57-74.
 RX MEDLINE=89374276; PubMed=2775283;
 RA Galius H.J., Bardosi A., Galius S., Hellmann K.P., Karas M.,
 RA Kratzin H.;
 RT "Identification of a cell cycle-dependent gene product as a stalic
 acid-binding protein.";
 RL Biochem. Biophys. Res. Commun. 163:506-512(1989).
 CC -1- INDUCTION: THIS PROTEIN IS PREFERENTIALLY EXPRESSED WHEN QUIESCENT
 FIBROBLASTS ARE STIMULATED TO PROLIFERATE. IT IS INDUCIBLE BY
 GROWTH FACTORS AND OVEREXPRESSED IN ACUTE MYELOID LEUKEMIAS.
 CC -1- PTM: THE N-TERMINUS IS BLOCKED.
 CC -1- MISCELLANEOUS: THIS PROTEIN CO-PURIFIED WITH THE PROLACTIN
 RECEPTOR.
 CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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 CC -----
 CC EMBL; M18981; AAA51906.1; --
 DR EMBL; M14300; AAA35886.1; --
 DR EMBL; J02763; AAA51905.1; --
 DR EMBL; AY034480; AKK59702.1; --
 DR EMBL; BC001431; AAH01431.1; --
 DR EMBL; BC009017; AAH09017.1; --
 DR PIR; A28363; BCHUY.
 DR HSSP; P30801; 1A03.
 DR Genew; HGNC:10496; S100A6.
 DR MIM; 114110; --
 DR InterPro; IPR001751; CaBP_S100.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; ehand; 1.
 DR Pfam; PF01023; S_100; 1.
 DR PRODOM; PD003407; CaBP_S100; 1.
 DR PROSITE; PS00018; EF-HAND; 1.
 DR PROSITE; PS00303; S100_CaBP; 1.
 DR Mitogen; Cell cycle; Calcium-binding; Polymorphism.
 KW Mitogen; Cell cycle; Calcium-binding. (POTENTIAL).
 FT CA_BIND 20 33 EF-HAND 1 (LOW AFFINITY) (POTENTIAL).
 FT CA_BIND 61 72 EF-HAND 2 (HIGH AFFINITY) (POTENTIAL).
 FT VARIANT 27 27 H -> R (IN DBSNP:11974).
 FT VARIANT 69 69 N -> S (IN DBSNP:1802581).
 FT VARIANT 83 83 I -> T (IN DBSNP:1802582).
 FT /FTID=VAR_011984.
 FT /FTID=VAR_011984.
 FT /FTID=VAR_011984.
 FT SEQUENCE 90 AA; 10180 MW; 860CBBI416ACBACI CRC64;
 SQ
 Query Match 2.4%; Score 8; DB 1; Length 90;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 210 EDLDRNKD 217
 DB 58 EDLDRNKD 65
 RESULT 9
 S106_CHICK

RT "GnRH-II cDNA expression in the musk shrew.";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS; IT STIMULATES
 CC HORMONES (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: MIDBRAIN.
 CC -1- SIMILARITY: BELONGS TO THE GnRH FAMILY.
 CC
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 CC -----
 DR EMBL; AF107315; AAD09114.1;
 DR InterPro: IPR002012; GnRH.
 DR Pfam: PF00446; GnRH; 1.
 DR PROSITE: PS00473; GnRH; 1.
 KW Cleavage on pair of basic residues; Hormone; Amidation; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 110
 FT PEPTIDE 27 36
 FT PEPTIDE 40 110
 FT MOD_RES 27 27
 FT MOD_RES 36 36
 FT MOD_RES 110 AA; 12120 MW; A8986905FB83D9DB CRC64;
 SQ SEQUENCE 110 AA; 12120 MW; A8986905FB83D9DB CRC64;
 Query Match 2.4%; Score 8; DB 1; Length 110;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 VLLLLLLL 14
 Db 9 VLLLLLLL 16
 RESULT 11
 ID YJ23_YEAST STANDARD; PRT; 133 AA.
 AC P47094;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Hypothetical 15.3 kDa protein in MER2-BNA1 intergenic region.
 GN YJ023C OR J1470 OR YJR83.19.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288c / FY1679;
 RA de Haan M., Smits P.H.M., Grivell L.A.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 13-93 FROM N.A.
 RX MEDLINE=96109930; PubMed=8619316;
 RA Zagulski M., Babinska B., Gromadka R., Migdalski A., Rytka J.,
 RA Sulicka J., Herbert C.J.;
 RT "The sequence of 24.3 kb from chromosome X reveals five complete open
 RT reading frames, all of which correspond to new genes, and a tandem
 RT insertion of a Ty1 transposon.";
 RL Yeast 11:1179-1186(1995).
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 CC -----
 DR EMBL; X87611; CAA60946.1;
 DR EMBL; Z49522; CAA89548.1;
 DR SCD; S0003784; YJR023C.
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 8 28
 FT TRANSMEM 46 66
 FT DOMAIN 10 30
 FT POLY-LEU.
 FT CONFLICT 28 28
 FT MISSING (IN REF. 1).
 SQ SEQUENCE 133 AA; 15282 MW; 4303172FF2500008 CRC64;
 Query Match 2.4%; Score 8; DB 1; Length 133;
 Best Local Similarity 100.0%; Pred. No. 2.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 VLLLLLLL 14
 Db 9 VLLLLLLL 16
 RESULT 12
 LSHB_TRIVU STANDARD; PRT; 141 AA.
 ID LSHB_TRIVU
 AC O46482;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
 DE beta) (LSH-B) (LH-B).
 GN LHB.
 OS Trichosurus vulpecula (Brush-tailed possum).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
 OX NCBI_TaxID=9337;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pituitary;
 RX MEDLINE=98345424; PubMed=9680384;
 RA Harrison G.A., Deane E.M., Cooper D.W.;
 RT "cDNA cloning of luteinizing hormone subunits from brushtail possum
 RT and red kangaroo.";
 RL Mamm. Genome 9:638-642(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Lawrence S.B., McNatty K.P., Fidler A.E.;
 RA Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
 CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
 CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
 CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
 CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
 CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
 CC FAMILY.
 CC
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 CC -----
 DR EMBL; AF017448; AAC96019.1;
 DR EMBL; AF090388; AAC63526.1;
 DR HSSP; P01233; 1XUL.
 DR InterPro: IPR000359; Cys_knot.
 DR Pfam: PF00007; Cys_knot; 1.
 DR SMART: SM00068; GHB; 1.
 DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; 1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.

Hormone; Signal; Glycoprotein.

1 22 BY SIMILARITY.
CHAIN LUTROPIN BETA CHAIN.
23 141 BY SIMILARITY.
30 78 BY SIMILARITY.
44 93 BY SIMILARITY.
47 131 BY SIMILARITY.
55 109 BY SIMILARITY.
59 111 BY SIMILARITY.
114 121 BY SIMILARITY.
34 N-LINKED (GLCNAC...) (POTENTIAL).
SEQUENCE 141 AA; 15060 MW; C6CF98036B3C4EE0 CRC64;

2.4% Score 8; DB 1; Length 141;
Query Match Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VLLLLLLL 14
|||||||
DB 9 VLLLLLLL 16

RESULT 13
RNLA_PIG STANDARD; PRT; 147 AA.
ID RNLA_PIG
AC P15468;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Ribonuclease PL3 precursor (EC 3.1.27.-) (Ribonuclease 4) (RNase 4).
GN RNSE4 OR RNS4.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94290321; PubMed=8019417;
RA Vicentini A.M., Hemmings B.A., Hofsteenge J.;
RT Residues 36-42 of liver RNase PL3 contribute to its
RT uridine-prefering substrate specificity. Cloning of the cDNA and
RT site-directed mutagenesis studies.";
RL Protein Sci. 3:459-466(1994).
RN [2]
RP SEQUENCE OF 29-147.
RC TISSUE=Liver;
RX MEDLINE=90122868; PubMed=2611266;
RA Hofsteenge J., Matthies R., Stone S.R.;
RT Primary structure of a ribonuclease from porcine liver, a new member
RT of the ribonuclease superfamily.";
RL Biochemistry 28:9806-9813(1989).
CC -1- FUNCTION: THIS RNASE HAS MARKED SPECIFICITY TOWARDS THE 3' SIDE
CC OF URIDINE NUCLEOTIDES.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY. BL4
CC SUBFAMILY.
CC
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CC
CC EMBL; S73478; AAB31159.1; -
DR PIR; B33627; B33627.
DR KSSP; P34096; 1RNF.
DR GlycoSuiteDB; P15468; -
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR

```

DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein tyrosine phosphatase receptor type C-associated protein
DE (PTPRC-associated protein) (CD45-associated protein) (CD45-AP) (LSM-
DE 1).
GN PTPRCAP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Lymphoid;
RX MEDLINE=95046370; PubMed=7957956;
RA Shimizu Y., Ogawa H., Oka Y., Mizuno R., Sakoda S., Kishimoto T.,
RA Sugiyama H.;
RT "Isolation of a cDNA clone encoding a novel membrane protein expressed
RT in lymphocytes.";
RL FEBS Lett. 355:30-34(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Blood;
RX MEDLINE=94131987; PubMed=8300558;
RA Takeda A., Maizel A.L., Kitamura K., Ohta T., Kimura S.;
RT "Molecular cloning of the CD45-associated 30-kDa protein.";
RL J. Biol. Chem. 269:2357-2360(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
CC -|- SUBUNIT: Interacts with CD45/PTPRC.
CC -|- PTM: Phosphorylated on tyrosine residues.
CC -|- TISSUE SPECIFICITY: Leukocyte-specific. Expressed in B- and T-cell
CC lines, in spleen, thymus, and bone marrow of adult mice, and in
CC embryos.
CC -----
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CC -----
DR EMBL; D10105; BAA00986.1;
DR EMBL; U03856; AAA67166.1; ALT_INIT.
DR EMBL; BC013273; AAH13273.1;
DR MGD; MGI:97811; Ptpcap.
KW Transmembrane; Phosphorylation.
FT TRANSMEM 33 53
FT CONFLICT 55 55 POTENTIAL.
SQ SEQUENCE 197 AA; 20370 MW; B313F88693F084AA CRC64;
-----
Query Match
Best Local Similarity 2.4%; Score 8; DB 1; Length 197;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 7 VLLLLLLL 14
| | | | |
Db 37 VLLLLLLL 44

```

Search completed: May 14, 2003, 10:48:59
Job time : 16 secs

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GenCore version. 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 14, 2003, 10:46:38 ; Search time 34 Seconds
(without alignments)
1987.749 Million cell updates/sec

Title: US-09-768-840-1

Perfect score: 328

Sequence: 1 MMWRPSVLLLLLRHGAQG.....FVGSQATWNGDLTFHHDEL 328

Scoring table: OLIGO

Gapop 60.0 , Capext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	328	100.0	328	4	Q96D15	Q96d15 homo sapien
2	235	71.6	328	4	Q9HBZ8	Q9hbz8 homo sapien
3	57	17.4	259	11	Q9CTD4	Q9ctd4 mus musculus
4	57	17.4	315	11	Q9BK35	Q9bk35 mus musculus
5	57	17.4	328	11	Q9R137	Q9r137 mus musculus
6	25	7.6	98	11	Q93399	Q93399 rattus norv
7	19	5.8	322	13	Q93434	Q93434 fugu rubrip
8	10	3.0	217	4	Q9Y3Q3	Q9y3q3 homo sapien
9	9	2.7	269	12	Q9VAZ4	Q9vaz4 white spot
10	9	2.7	296	4	Q9NR43	Q9nr43 homo sapien
11	9	2.7	296	6	Q9WZ46	Q9wz46 sus scrofa
12	9	2.7	315	4	Q9RL3	Q9rl3 homo sapien
13	8	2.4	26	11	Q9ESQ6	Q9esq6 mus musculus
14	8	2.4	58	11	Q9JHQ7	Q9jhg7 mus musculus
15	8	2.4	62	5	Q9NLY0	Q9nly0 leishmania
16	8	2.4	70	5	Q9VUT7	Q9vut7 drosophila

17	8	2.4	100	5	Q9W4Q5	Q9w4q5 drosophila
18	8	2.4	100	10	Q9LDG6	Q9ldg6 oryza sativ
19	8	2.4	115	12	Q9L7I3	Q9l7i3 tupia herp
20	8	2.4	141	6	Q95J85	Q95j85 monodelphis
21	8	2.4	142	4	Q8W60	Q8w60 homo sapien
22	8	2.4	153	10	Q9XC81	Q9xc81 oryza sativ
23	8	2.4	179	2	Q93Q47	Q93q47 clostridium
24	8	2.4	190	4	Q8TBP5	Q8tbp5 homo sapien
25	8	2.4	197	11	Q64697	Q64697 mus musculus
26	8	2.4	200	11	Q9CRN2	Q9crn2 mus musculus
27	8	2.4	205	10	Q9LZ12	Q9lz12 arabidopsis
28	8	2.4	206	4	Q14761	Q14761 homo sapien
29	8	2.4	221	11	Q9D8Y6	Q9d8y6 mus musculus
30	8	2.4	230	13	Q9PU48	Q9pu48 gallus gall
31	8	2.4	254	4	Q9H2F6	Q9h2f6 homo sapien
32	8	2.4	254	4	Q9BXD6	Q9bx66 homo sapien
33	8	2.4	263	11	Q60819	Q60819 mus musculus
34	8	2.4	267	4	Q13261	Q13261 homo sapien
35	8	2.4	273	4	Q96K63	Q96k63 homo sapien
36	8	2.4	273	4	Q8TC80	Q8tc80 homo sapien
37	8	2.4	290	17	Q82X93	Q82x93 pyrobaculum
38	8	2.4	301	4	Q96K94	Q96k94 homo sapien
39	8	2.4	301	4	Q8TDQ0	Q8tdq0 homo sapien
40	8	2.4	307	11	Q922Q8	Q922q8 mus musculus
41	8	2.4	315	11	Q35783	Q35783 rattus norv
42	8	2.4	316	11	P89000	P89000 praonys nat
43	8	2.4	376	8	Q94Y43	Q94y43 tania stri
44	8	2.4	376	10	O24579	O24579 zea mays (m
45	8	2.4	377	4	Q8TAG4	Q8tag4 homo sapien

ALIGNMENTS

RESULT 1

Q96D15
ID Q96D15 PRELIMINARY; PRT; 328 AA.
AC Q96D15;
DC 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical 37.5 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013436; AAH13436.1; -
DR InterPro; IPR002048; EF-Hand.
DR InterPro; IPR000886; EF_target.
DR Pfam; PF00036; ehand; 5.
DR PROSITE; PS00018; EF_HAND; UNKNOWN 4.
DR PROSITE; PS00014; EF_TARGET; UNKNOWN 1.
KW Hypothetical protein.
SQ
SEQUENCE 328 AA; 37493 MW; B64EDB28B961088D CRC64;

Query Match 100.0%; Score 328; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MMWRPSVLLLLLRHGAQGKSPDAGPHQCGRVHQAPLSDAPHDDAHGNFYDHEAFL 60	
Db	1	MMWRPSVLLLLLRHGAQGKSPDAGPHQCGRVHQAPLSDAPHDDAHGNFYDHEAFL 60	
Qy	61	GREVAKEFDLTPEESQARLGRIVDRMDRAGDGGWVSLAELRAWTAHTQQRHRSVSA 120	
Db	61	GREVAKEFDLTPEESQARLGRIVDRMDRAGDGGWVSLAELRAWTAHTQQRHRSVSA 120	
Qy	121	AWDTYDTRDRGRVGEWELRNATYGHYAPGEEFHDVEDAETKKMLARDRRFRVADQDGD 180	

Tue May 20 14:43:22 2003

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DB 121 AWDYTDYDRGRVGEELRNATYGHYAPGEEHDEVEDAETKKMLARDERRFRVADQDGD 180
QY 181 SMATREELTAFLPPEEPHMRDIVIAETLEDLDRKNGYVQVEEYIADLYSAEPGEEPA 240
DB 181 SMATREELTAFLPPEEPHMRDIVIAETLEDLDRKNGYVQVEEYIADLYSAEPGEEPA 240
QY 241 WYQTERQFRDLNKGDLGSEVGHVLPAPQADQPLVEANHLHESDTDKDGRLSKA 300
DB 241 WYQTERQFRDLNKGDLGSEVGHVLPAPQADQPLVEANHLHESDTDKDGRLSKA 300
QY 301 ETLGNMNFVGSQATNYGDELTRHDEL 328
DB 301 ETLGNMNFVGSQATNYGDELTRHDEL 328

RESULT 2
Q9HBZ8 PRELIMINARY; PRT; 328 AA.
AC Q9HBZ8;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Reticulocabin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=HYPOTHALAMUS;
RA Feng Y., Gu Y., Huang C., Xu S., Han Z., Fu G., Chen Z.;
RT "A novel gene expressed in human hypothalamus.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF183423; AAG09692.1; -
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR000886; ER-target.
DR Pfam: PF00036; ehand; 4.
DR SMART: SM00054; EFH; 3.
DR PROSITE: PS00018; EF-HAND; UNKNOWN_4.
DR PROSITE: PS00014; ER-TARGET; UNKNOWN_1.
SQ SEQUENCE 328 AA; 37424 MW; 9D23648795D3C670 CRC64;

Query Match 71.6%; Score 235; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 2e-232;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 DGWVSLAEALRAWIAHTQOIRHSVSAANDTYDTRDGRVGEELRNATYGHYAPGEEPH 153
DB 94 DGWVSLAEALRAWIAHTQOIRHSVSAANDTYDTRDGRVGEELRNATYGHYAPGEEPH 153
QY 154 DVEAETKKMLARDERRFRVADQDGSMTARELTAFLEHPEEPHMRDIVIAETLEDLD 213
DB 154 DVEAETKKMLARDERRFRVADQDGSMTARELTAFLEHPEEPHMRDIVIAETLEDLD 213
QY 214 RNKDGIVQVEEYIADLYSAEPGEEPAWQTERQFRDLNKGDLGSEVGHVLP 273
DB 214 RNKDGIVQVEEYIADLYSAEPGEEPAWQTERQFRDLNKGDLGSEVGHVLP 273
QY 274 AQDQPLVEANHLHESDTDKDGRLSKAELLGNMNFVGSQATNYGDELTRHDEL 328
DB 274 AQDQPLVEANHLHESDTDKDGRLSKAELLGNMNFVGSQATNYGDELTRHDEL 328

RESULT 3
Q9CTD4 PRELIMINARY; PRT; 259 AA.
AC Q9CTD4;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE 6030455P07RIK protein (Fragment).
GN 6030455P07RIK.

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=EMBRYO;
RC MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Wagner L.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli J., Momberts P.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,
RA Lyons P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Nordone P., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Tovo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Suzuki H., Tovo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK003918; BAB23076.1; -
DR MGD: MGI:1915346; 6030455P07RIK.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR000886; ER-target.
DR Pfam: PF00036; ehand; 4.
DR SMART: SM00054; EFH; 3.
DR PROSITE: PS00018; EF-HAND; UNKNOWN_4.
DR PROSITE: PS00014; ER-TARGET; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 259 AA; 30163 MW; 7910A9F0476260A1 CRC64;

Query Match 17.4%; Score 57; DB 11; Length 259;
Best Local Similarity 100.0%; Pred. No. 6.9e-50;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 PGEEDHVEDAETKKMLARDERRFRVADQDGSMTARELTAFLEHPEEPHMRDIV 204
DB 79 PGEEDHVEDAETKKMLARDERRFRVADQDGSMTARELTAFLEHPEEPHMRDIV 135

RESULT 4
Q99K35 PRELIMINARY; PRT; 315 AA.
ID Q99K35;
AC Q99K35;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Similar to hypothetical protein LOC57333 (Fragment).
GN 6030455P07RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC005487; AA05487.1; -
DR MGD: MGI:1915346; 6030455P07RIK.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR000886; ER-target.
DR Pfam: PF00036; ehand; 4.
DR SMART: SM00054; EFH; 3.
DR PROSITE: PS00018; EF-HAND; UNKNOWN_4.
DR PROSITE: PS00014; ER-TARGET; UNKNOWN_1.

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KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 315 AA; 36269 MW; CECE4DAEES4D24E4 CRC64;
 Query Match 17.4%; Score 57; DB 11; Length 315;
 Best Local Similarity 100.0%; Pred. No. 8.2e-50;
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 PGEFHVDVDAETKKMLARDERRFRVADQDGDGSMATREELTAFLHPPEFPHMRDIV 204
 Db 135 PGEFHVDVDAETKKMLARDERRFRVADQDGDGSMATREELTAFLHPPEFPHMRDIV 191

RESULT 5
 Q8R137
 ID Q8R137 PRELIMINARY; PRT; 328 AA.
 AC Q8R137;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Similar to hypothetical protein LOC57333.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC025602; AAH25602.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 328 AA; 37973 MW; 913F5C6F0F8B8316 CRC64;

Query Match 17.4%; Score 57; DB 11; Length 328;
 Best Local Similarity 100.0%; Pred. No. 8.5e-50;
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 PGEFHVDVDAETKKMLARDERRFRVADQDGDGSMATREELTAFLHPPEFPHMRDIV 204
 Db 148 PGEFHVDVDAETKKMLARDERRFRVADQDGDGSMATREELTAFLHPPEFPHMRDIV 204

RESULT 6
 Q63399
 ID Q63399 PRELIMINARY; PRT; 98 AA.
 AC Q63399;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE (clone REM1) ORF (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-HOLZMAN; TISSUE=BRAIN;
 RC MEDLINE=96235155; PubMed=8642059;
 RA Asakura K., Pogulis R.J., Pease L.R., Rodriguez M.;
 RT "A monoclonal antibody which promotes central nervous system
 remyelination is highly polyreactive to multiple known and novel
 antigens.";
 RT J. Neuroimmunol. 65:11-19(1996).
 RL EMBL; L41683; AAB05841.1;
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00036; ehand; 1.
 DR PROSITE: PS00018; EF_HAND; UNKNOWN_1.
 FT NON_TER 1
 SQ SEQUENCE 98 AA; 11277 MW; FOA3D6D9EF624CE1 CRC64;

Query Match 7.6%; Score 25; DB 11; Length 98;
 Best Local Similarity 100.0%; Pred. No. 2e-17;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 VAKFEDQLTPESQARLGRIVDVDRMD 88
 Db 4 VAKFEDQLTPESQARLGRIVDVDRMD 28

RESULT 7
 Q93434
 ID Q93434 PRELIMINARY; PRT; 322 AA.
 AC Q93434;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Reticulocalbin.
 GN RCN1.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=99007268; PubMed=9789042;
 RA Miles C., Elgar G., Coles E., Kleinjan D.J., Van Heyningen V.,
 RA Hastie N.;
 RT "Complete sequencing of the Fugu WAGR region from WT1 to PAX6:
 RT Dramatic compaction and conservation of synteny with human chromosome
 RT 11p13.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:13068-13072(1998).
 DR EMBL; AL021531; CAA16492.1; -;
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00036; ehand; 5.
 DR SMART: SM00054; Efh; 2.
 DR PROSITE: PS00018; EF_HAND; UNKNOWN_4.
 DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
 SQ SEQUENCE 322 AA; 38207 MW; 85F99C053AC34C5C CRC64;

Query Match 5.8%; Score 19; DB 13; Length 322;
 Best Local Similarity 100.0%; Pred. No. 8.1e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 305 NWNMFVGSQATNYGEDLTLR 323
 Db 299 NWNMFVGSQATNYGEDLTLR 317

RESULT 8
 Q9Y303
 ID Q9Y303 PRELIMINARY; PRT; 217 AA.
 AC Q9Y303;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE P24B protein precursor (Integral type I protein).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE=PLACENTA;
 RC Blum R., Nastainczyk W., Kohler B., Schulz I.;
 RT "Cloning, localization and in vivo trafficking of p24B, a novel p24-
 RT member.";
 RT Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Carim L., Estivill X., Sumoy L., Escarceller M.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]

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SEQUENCE FROM N.A.
RA Auffray C., Ansong W., Ballabio A., Estivill X., Gibson K.,
RA Lehrach H., Poustka A., Lundeberg J.; Integrated Molecular analysis of
RT "The European IMAGE Consortium for integrated Molecular analysis of
RT human gene transcripts.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE-KIDNEY;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE-LUNG;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE-SKIN;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC TISSUE-LUNG;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ132270; CAB40416.1; -
DR EMBL; AL109672; CAB52017.1; -
DR EMBL; BC000027; AAH00027.1; -
DR EMBL; BC010853; AAH10853.1; -
DR EMBL; BC017495; AAH17495.1; -
DR EMBL; BC022232; AAH22232.1; -
DR InterPro; IPR000348; Emp24_gp25L_p24.
DR Pfam; PF01105; EMP24_GP25L; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
FT SEQUENCE 217 AA; 24777 MW; 515C3F0B6C17EBDD CRC64;
SQ SEQUENCE 217 AA; 24777 MW; 515C3F0B6C17EBDD CRC64;

Query Match 3.0%; Score 10; DB 4; Length 217;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SVLLLLLLL 15
DB 10 SVLLLLLLL 19

RESULT 9
Q8VAZ4 PRELIMINARY; PRT; 269 AA.
AC Q8VAZ4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE WSV221 (WSSV276).
OS White spot syndrome virus (WSSV).
OC Viruses; unclassified viruses.
OX NCBI_TaxID=92652;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21548311; PubMed=11689652;
RA Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
RT "Complete genome sequence of the shrimp white spot bacilliform
RT virus.";
RL J. Virol. 75:11811-11820(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-TAIWAN;

```

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RX MEDLINE=20517548; PubMed=11062040;
RA Tsai M.F., Yu H.T., Tzeng H.F., Leu J.H., Chou C.M., Huang C.J.,
RA Wang C.H., Lin J.Y., Kou G.H., Lo C.F.;
RT "Identification and characterization of a shrimp white spot syndrome
RT virus (WSSV) gene that encodes a novel chimeric polypeptide of
RT cellular-type thymidine kinase and thymidylate kinase.";
RL Virology 277:100-110(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-TAIWAN;
RX MEDLINE=21844071; PubMed=11853398;
RA Chen L.L., Leu J.H., Huang C.J., Chou C.M., Chen S.M., Wang C.H.,
RA Lo C.F., Kou G.H.;
RT "Identification of a nucleocapsid protein (VP35) gene of shrimp white
RT spot syndrome virus and characterization of the motif important for
RT targeting VP35 to the nuclei of transfected insect cells.";
RL Virology 293:44-53(2002).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN-TAIWAN;
RA Lo C.F., Kou G.H.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF332093; AAL33225.1; -
DR EMBL; AF440570; AAL89144.1; -
DR EMBL; AF440570; AAL89144.1; -
SQ SEQUENCE 269 AA; 29607 MW; D9A4112DED66E51D CRC64;

Query Match 2.7%; Score 9; DB 12; Length 269;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SVLLLLLLL 14
DB 185 SVLLLLLLL 193

RESULT 10
Q9NR43 PRELIMINARY; PRT; 296 AA.
AC Q9NR43;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Crocalbin-like protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE=99192326; PubMed=10094503;
RA Hsueh M.J., Yen C.H., Tzeng M.C.;
RT "Crocalbin: a new calcium-binding protein that is also a binding
RT protein for crotoxin, a neurotoxic phospholipase A2.";
RL FEBS Lett. 445:440-444(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Hsueh M.J., Tzeng M.C.;
RL Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF257659; AAF76141.1; -
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; efhand; 6.
DR SMART; SM00054; EFh; 3.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
FT NON_TER
SQ SEQUENCE 296 AA; 34990 MW; D011D029ADE2A02E CRC64;

Query Match 2.7%; Score 9; DB 4; Length 296;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 FQDLTPES 76

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Db 42 FDQLTPEES 50
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RESULT 11

Q9M246 PRELIMINARY: PRT; 296 AA.
ID Q9M246;
AC Q9M246;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Crocalbin-like protein (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=99192326; PubMed=10094503;
RA Hsue M.J., Yen C.H., Tzeng M.C.;
RT "Crocalbin: a new calcium-binding protein that is also a binding
RT protein for crotoxin, a neurotoxic phospholipase A2.";
RL FEBS Lett. 445:440-444(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Hsue M.J., Tzeng M.C.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF257660; AAF76142.1;
DR InterPro: IPR002048; EF-hand.
DR Pfam: PF00036; ehand; 6.
DR SMART: SM00054; EFh; 2.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_3.
FT NON_TER 1
FT NON_TER 296
SQ SEQUENCE 296 AA; 34896 MW; 7C01BB38C6275914 CRC64;

Query Match 2.7%; Score 9; DB 6; Length 296;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 FDQLTPEES 76
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RESULT 12

Q96RL3 PRELIMINARY: PRT; 315 AA.
ID Q96RL3;
AC Q96RL3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Calumenin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Peterson R.E. Jr., Watson D.K.;
RT "Novel splice variant of human calumenin.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF345637; AAK72908.1;
DR InterPro: IPR002048; EF-hand.
DR Pfam: PF00036; ehand; 6.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_4.
SQ SEQUENCE 315 AA; 37135 MW; E1BF415B25076676 CRC64;

Query Match 2.7%; Score 9; DB 4; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 FDQLTPEES 76
|||||

Db 61 FDQLTPEES 69

RESULT 13

Q9ESQ6 PRELIMINARY: PRT; 26 AA.
ID Q9ESQ6
AC Q9ESQ6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Prostacyclin synthase (Fragment).
GN PTGIS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129SVJ; TISSUE=SPLEEN;
RA Ohkawa S., Shimonishi M., Tanabe T., Yokoyama C.;
RT "Cloning and characterization of 5'-flanking region of mouse
RT prostacyclin synthase gene.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB040750; BAB12574.1;
DR MGD; MGI:1097156; Ptgis.
KW Cyclin
FT NON_TER 26
SQ SEQUENCE 26 AA; 2933 MW; 7C11084736AB9E0 CRC64;

Query Match 2.4%; Score 8; DB 11; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VLLLLLLL 14
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Db 12 VLLLLLLL 19

RESULT 14

Q9JHQ7 PRELIMINARY: PRT; 58 AA.
ID Q9JHQ7
AC Q9JHQ7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Laminin alpha 3B chain precursor (Fragment).
GN LAMA3B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21818471; PubMed=11829758;
RA Garbe J.H.O., Gohring W., Mann K., Timpl R., Sasaki T.;
RT "Complete sequence, recombinant analysis and binding to Laminins and
RT sulfated ligands of the N-terminal domains of Laminin alpha 3B and
RT alpha 5 chains.";
RL Biochem. J. 362:213-221(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Friedrich W.V.K.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ293592; CAB99254.2;
KW SIGNAL
FT SIGNAL 1 31
FT CHAIN 32 >58 LAMININ ALPHA 3B CHAIN.
FT NON_TER 58
SQ SEQUENCE 58 AA; 6464 MW; 96BB58C75E8C427F CRC64;

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Query Match 2.4%; Score 8; DB 11; Length 58;
 Best Local Similarity 100.0%; Pred. No. 3.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LLLLLLL 15
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 Db 18 LLLLLLL 25

RESULT 15

Q9NLYO PRELIMINARY; PRT; 62 AA.
 AC Q9NLYO;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE Hypothetical 6.7 kDa protein (Fragment).
 GN LM26.312.
 OS Leishmania major.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FRIEDLIN;
 RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL160493; CAB97930.1;
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 62 AA; 5695 MW; BBC186B54327F894 CRC64;

Query Match 2.4%; Score 8; DB 5; Length 62;
 Best Local Similarity 100.0%; Pred. No. 3.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VLLLLLL 14
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 Db 52 VLLLLLL 59

Search completed: May 14, 2003, 10:49:40
 Job time : 36 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: May 14, 2003, 10:47:58 ; Search time 14 Seconds
(without alignments)
689.337 Million cell updates/sec

Title: US-09-768-840-1
Perfect score: 328
Sequence: 1 MWPRPSVLLLLLLRHGAQG.....FVGSQATNYGDLFRHHDEL 328

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

- Database : Issued_Patents_AA.*
- 1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
 - 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
 - 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
 - 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
 - 5: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep.*
 - 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	328	100.0	328	2	US-08-828-242-1
2	328	100.0	328	2	US-08-910-927B-1
3	328	100.0	328	4	US-09-206-499-1
4	328	100.0	328	4	US-09-270-270-1
5	25	7.6	98	2	US-08-910-927B-6
6	25	7.6	98	4	US-09-270-270-6
7	18	5.5	325	2	US-08-828-242-4
8	18	5.5	325	4	US-09-206-499-4
9	18	5.5	331	2	US-08-828-242-3
10	18	5.5	331	2	US-08-910-927B-5
11	18	5.5	331	4	US-09-206-499-3
12	18	5.5	331	4	US-09-270-270-5
13	9	2.7	315	2	US-08-910-927B-3
14	9	2.7	315	4	US-09-270-270-3
15	8	2.4	21	3	US-08-848-580-6
16	8	2.4	21	3	US-08-848-580-7
17	8	2.4	21	5	PCT-US92-04537-2
18	8	2.4	21	5	PCT-US92-04537-3
19	8	2.4	45	1	US-08-056-200-107
20	8	2.4	45	2	US-08-800-644-107
21	8	2.4	54	1	US-08-464-339A-15
22	8	2.4	89	1	US-07-987-272A-10
23	8	2.4	90	4	US-09-370-838-200
24	8	2.4	206	1	US-08-197-793-2
25	8	2.4	206	2	US-08-636-176-2
26	8	2.4	206	5	PCT-US95-01618-2
27	8	2.4	234	1	US-08-300-903A-11

28	8	2.4	251	1	US-08-300-903A-7
29	8	2.4	254	4	US-09-449-437A-4
30	8	2.4	254	4	US-09-449-437A-6
31	8	2.4	254	4	US-09-195-106-2
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33	8	2.4	267	1	US-08-300-903A-15
34	8	2.4	279	1	US-08-300-903A-9
35	8	2.4	301	3	US-08-829-525-24
36	8	2.4	301	4	US-08-609-583A-24
37	8	2.4	301	4	US-08-937-399-24
38	8	2.4	301	4	US-09-310-367-24
39	8	2.4	301	4	US-09-032-337-24
40	8	2.4	351	1	US-08-468-847B-16
41	8	2.4	361	1	US-08-415-751-36
42	8	2.4	385	4	US-09-163-951-16
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44	8	2.4	447	1	US-07-978-892A-6
45	8	2.4	447	4	US-08-029-170-29

ALIGNMENTS

RESULT 1
US-08-828-242-1
; Sequence 1, Application US/08828242
; Patent No. 5871970
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,242
; FILING DATE: Filled Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0261 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: CONUTUT01
; CLONE: 2509570
US-08-828-242-1

Query Match 100.0%; Score 328; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 2.4e-299;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLLRHGAQKPSDAGPHGQGRVHQAAPLSDAPDDAHGNGFYDHEAFL 60
Db 1 MMWRPSVLLLLLLRHGAQKPSDAGPHGQGRVHQAAPLSDAPDDAHGNGFYDHEAFL 60
QY 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGGWVSLAELRAWIAHTQQRHIRDSVSA 120
Db 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGGWVSLAELRAWIAHTQQRHIRDSVSA 120
QY 121 AWDYTDTRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQGD 180
Db 121 AWDYTDTRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQGD 180
QY 181 SMATREELTAFHPPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPPA 240
Db 181 SMATREELTAFHPPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPPA 240
QY 241 WYQTERQQFRDRLNKDGLDGGSEVGHVLPAPQDQPLVEANHLHESDTRKGRLSKA 300
Db 241 WYQTERQQFRDRLNKDGLDGGSEVGHVLPAPQDQPLVEANHLHESDTRKGRLSKA 300
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Db 301 EILGNMNFVGSQATNYGEDLTRHDEL 328

RESULT 2

US-08-910-927B-1
; Sequence 1, Application US/08910927B
; Patent No. 5976801
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,927B
; FILING DATE: Hereewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0358 US
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: RATRNOT02

CLONE: 922578

US-08-910-927B-1

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Best Local Similarity 100.0%; Pred. No. 2.4e-299;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MMWRPSVLLLLLLRHGAQKPSDAGPHGQGRVHQAAPLSDAPDDAHGNGFYDHEAFL 60
QY 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGGWVSLAELRAWIAHTQQRHIRDSVSA 120
Db 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGGWVSLAELRAWIAHTQQRHIRDSVSA 120
QY 121 AWDYTDTRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQGD 180
Db 121 AWDYTDTRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQGD 180
QY 181 SMATREELTAFHPPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPPA 240
Db 181 SMATREELTAFHPPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPPA 240
QY 241 WYQTERQQFRDRLNKDGLDGGSEVGHVLPAPQDQPLVEANHLHESDTRKGRLSKA 300
Db 241 WYQTERQQFRDRLNKDGLDGGSEVGHVLPAPQDQPLVEANHLHESDTRKGRLSKA 300
QY 301 EILGNMNFVGSQATNYGEDLTRHDEL 328
Db 301 EILGNMNFVGSQATNYGEDLTRHDEL 328

RESULT 3

US-09-206-499-1
; Sequence 1, Application US/09206499
; Patent No. 6194385
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/206,499
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,242
; FILING DATE: 03/31/1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0261 US
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: CONUTUT01
;; CLONE: 2509570
US-09-206-499-1

Query Match 100.0%; Score 328; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 2.4e-299;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MMWRPSVLLLLLRHGAQCKSPDAGPHGQGRVHQAAPLSDAPHDDAHGNGFYDHEAFL 60
Db 1 MMWRPSVLLLLLRHGAQCKSPDAGPHGQGRVHQAAPLSDAPHDDAHGNGFYDHEAFL 60
Qy 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGGWVSLAELRAWIAHTQORHIRDSVSA 120
Db 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGGWVSLAELRAWIAHTQORHIRDSVSA 120
Qy 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADODGD 180
Db 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADODGD 180
Qy 181 SMATREELTAFLHPPEEFPHMRDVIATETLEDLRNKGYYQVVEEYIADLYSAEPGEEPA 240
Db 181 SMATREELTAFLHPPEEFPHMRDVIATETLEDLRNKGYYQVVEEYIADLYSAEPGEEPA 240
Qy 241 WYQTERQOFRDLNKGDLGSEVGHVWLPAPQDQPLVEANHLHESDTDKDGLSKA 300
Db 241 WYQTERQOFRDLNKGDLGSEVGHVWLPAPQDQPLVEANHLHESDTDKDGLSKA 300
Qy 301 EILGNWNVGVSQATNYGEDLTRHDEL 328
Db 301 EILGNWNVGVSQATNYGEDLTRHDEL 328

RESULT 4

US-09-270-270-1
; Sequence 1, Application US/09270270
; Patent No. 6235477
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/270,270
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/910,927
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0358 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166

;; TELEX:
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 328 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: RATRNOT02
;; CLONE: 922578
US-09-270-270-1

Query Match 100.0%; Score 328; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 2.4e-299;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MMWRPSVLLLLLRHGAQCKSPDAGPHGQGRVHQAAPLSDAPHDDAHGNGFYDHEAFL 60
Db 1 MMWRPSVLLLLLRHGAQCKSPDAGPHGQGRVHQAAPLSDAPHDDAHGNGFYDHEAFL 60
Qy 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGGWVSLAELRAWIAHTQORHIRDSVSA 120
Db 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGGWVSLAELRAWIAHTQORHIRDSVSA 120
Qy 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADODGD 180
Db 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADODGD 180
Qy 181 SMATREELTAFLHPPEEFPHMRDVIATETLEDLRNKGYYQVVEEYIADLYSAEPGEEPA 240
Db 181 SMATREELTAFLHPPEEFPHMRDVIATETLEDLRNKGYYQVVEEYIADLYSAEPGEEPA 240
Qy 241 WYQTERQOFRDLNKGDLGSEVGHVWLPAPQDQPLVEANHLHESDTDKDGLSKA 300
Db 241 WYQTERQOFRDLNKGDLGSEVGHVWLPAPQDQPLVEANHLHESDTDKDGLSKA 300
Qy 301 EILGNWNVGVSQATNYGEDLTRHDEL 328
Db 301 EILGNWNVGVSQATNYGEDLTRHDEL 328

RESULT 5

US-08-910-927B-6
; Sequence 6, Application US/08910927B
; Patent No. 5976801
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,927B
; FILING DATE: Hereewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

US-09-206-499-4
; Sequence 4, Application US/09206499
; Patent No. 6194385

LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: single
secondary: linear

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; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/206,499
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,242
; FILING DATE: 03/31/1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0261 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 220582
; US-09-206-499-4

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Query Match 5.5%; Score 18; DB 4; Length 325;
Best Local Similarity 100.0%; Pred. No. 4.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 305 NNNMFVGSQATNYGEDLT 322
DB 302 NNNMFVGSQATNYGEDLT 319

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RESULT 9
US-08-828-242-3
; Sequence 3, Application US/08828242
; Patent No. 5871970
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS

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; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,242
; FILING DATE: Filed Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0261 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 331 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1262329
; US-08-828-242-3

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Query Match 5.5%; Score 18; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 4.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 305 NNNMFVGSQATNYGEDLT 322
DB 308 NNNMFVGSQATNYGEDLT 325

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RESULT 10
US-08-910-927B-5
; Sequence 5, Application US/08910927B
; Patent No. 5976801
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,927B
; FILING DATE: Hereewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0358 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166

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;; TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
;; NUMBER OF SEQUENCES: 6
;; CORRESPONDENCE ADDRESSES:
;; ADDRESSEE: Incyte Pharmaceuticals, Inc.
;; STREET: 3174 Porter Drive
;; CITY: Palo Alto
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94304
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/910.927B
;; FILING DATE: Hereewith
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Billings, Lucy J.
;; REGISTRATION NUMBER: 36,749
;; REFERENCE/DOCKET NUMBER: PF-0358 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650-855-0555
;; TELEFAX: 650-845-4166
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 315 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: BLADNOT03
;; CLONE: 1601793
;; US-09-910-927B-3

Query Match 2.7%; Score 9; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 68 FDOTPEES 76
Db 61 FDOTPEES 69

RESULT 14
US-09-270-270-3
; Sequence 3, Application US/09270270
; Patent No. 6235477
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/270.270
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/910.927
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Billings, Lucy J.
;; REGISTRATION NUMBER: 36,749
;; REFERENCE/DOCKET NUMBER: PF-0358 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650-855-0555
;; TELEFAX: 650-845-4166
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 315 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: BLADNOT03
;; CLONE: 1601793
;; US-09-270-270-3

Query Match 2.7%; Score 9; DB 4; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 68 FDOTPEES 76
Db 61 FDOTPEES 69

RESULT 15
US-08-848-580-6
; Sequence 6, Application US/08848580
; Patent No. 6013619
; GENERAL INFORMATION:
; APPLICANT: Cochran, Charles G
; APPLICANT: Revak, Susan D
; TITLE OF INVENTION: NOVEL PULMONARY SURFACTANTS AND
; TITLE OF INVENTION: THERAPEUTIC USES, INCLUDING PULMONARY LAVAGE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
; STREET: 10550 No. 6013619th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/848.580
; FILING DATE: 28-APR-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/488,123
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/419,824
; FILING DATE: 11-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/060,833
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/715,397
; FILING DATE: 14-JUN-1991

us-09-768-840-1.oli.ra1

Tue May 20 14:43:20 2003

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; PRIOR APPLICATION DATA: US 07/293,201
; APPLICATION NUMBER:
; FILING DATE: 04-JAN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/141,200
; FILING DATE: 06-JAN-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 147.5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-784-2937
; TELEFAX: 619-784-9399
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-848-580-6
;
; Query Match 2.4%; Score 8; DB 3; Length 21;
; Best Local Similarity 100.0%; Pred. No. 0.98;
; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 8 LLLLLLL 15
; Db 3 LLLLLLL 10
;
; Search completed: May 14, 2003, 10:50:27
; Job time : 15 secs

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(without alignments)
1312.367 Million cell updates/sec

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Gapop 60.0 , Gapext 60.0

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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	328	100.0	328	9	US-09-902-853-221
3	328	100.0	328	9	US-09-907-824-221
4	328	100.0	328	9	US-09-907-841-221
5	328	100.0	328	9	US-09-904-011-221
6	328	100.0	328	9	US-10-028-072-364
7	328	100.0	328	9	US-09-906-742-221
8	328	100.0	328	9	US-10-121-045-364
9	328	100.0	328	9	US-10-123-904-364
10	328	100.0	328	9	US-10-140-470-364
11	328	100.0	328	9	US-09-906-838-221
12	328	100.0	328	9	US-09-907-613-221
13	328	100.0	328	9	US-09-907-942-221
14	328	100.0	328	9	US-10-175-746-364
15	328	100.0	328	9	US-10-176-918-364
16	328	100.0	328	9	US-10-176-921-364
17	328	100.0	328	9	US-10-137-865-364
18	328	100.0	328	9	US-10-140-474-364
19	328	100.0	328	9	US-09-904-820-221

20	328	100.0	328	9	US-09-904-859-221	Sequence 221, App
21	328	100.0	328	9	US-09-909-204-221	Sequence 221, App
22	328	100.0	328	9	US-10-142-431-364	Sequence 364, App
23	328	100.0	328	9	US-10-143-114-364	Sequence 364, App
24	328	100.0	328	9	US-09-904-786-221	Sequence 221, App
25	328	100.0	328	9	US-09-906-646-221	Sequence 221, App
26	328	100.0	328	9	US-09-906-700-221	Sequence 221, App
27	328	100.0	328	9	US-10-140-002-364	Sequence 364, App
28	328	100.0	328	9	US-09-902-903-221	Sequence 221, App
29	328	100.0	328	9	US-09-903-749A-221	Sequence 221, App
30	328	100.0	328	9	US-09-903-786-221	Sequence 221, App
31	328	100.0	328	9	US-10-142-419-364	Sequence 364, App
32	328	100.0	328	9	US-09-902-736-221	Sequence 221, App
33	328	100.0	328	9	US-09-904-119-221	Sequence 221, App
34	328	100.0	328	9	US-09-904-956-221	Sequence 221, App
35	328	100.0	328	9	US-09-907-794-221	Sequence 221, App
36	328	100.0	328	9	US-10-123-262-364	Sequence 364, App
37	328	100.0	328	9	US-10-142-423-364	Sequence 364, App
38	328	100.0	328	9	US-09-902-692-221	Sequence 221, App
39	328	100.0	328	9	US-09-903-520-221	Sequence 221, App
40	328	100.0	328	9	US-09-903-943-221	Sequence 221, App
41	328	100.0	328	9	US-09-904-462-221	Sequence 221, App
42	328	100.0	328	9	US-09-905-056-221	Sequence 221, App
43	328	100.0	328	9	US-09-907-925-221	Sequence 221, App
44	328	100.0	328	9	US-10-121-050-364	Sequence 364, App
45	328	100.0	328	9	US-10-141-755-364	Sequence 364, App

ALIGNMENTS

RESULT 1
US-09-905-291A-221
; Sequence 221, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,291A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222

Sequence 221, App

APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,853
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US/09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 221
LENGTH: 328
TYPE: PRT
ORGANISM: Homo Sapien
US-09-902-853-221

Query Match 100.0%; Score 328; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.1e-274;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLLRRGAGKSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60
DB 1 MMWRPSVLLLLLLRRGAGKSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60
QY 61 GREVAKEFQLTPEESQARLGRIVDRMDRAGDGVSVLAELRAWIAHTQQRHIRDSVSA 120
DB 61 GREVAKEFQLTPEESQARLGRIVDRMDRAGDGVSVLAELRAWIAHTQQRHIRDSVSA 120
QY 121 AWDTYDTRDGRVGVWELRNATYGHYAPGEEFHDVEDAETYYKKMLARDERRFVADODGD 180
DB 121 AWDTYDTRDGRVGVWELRNATYGHYAPGEEFHDVEDAETYYKKMLARDERRFVADODGD 180
QY 181 SMATREELTAFLHPEEPFPHMRDIVIAETLEDLDRNKDGVVQVEEYIADLYSAEPGEEPA 240
DB 181 SMATREELTAFLHPEEPFPHMRDIVIAETLEDLDRNKDGVVQVEEYIADLYSAEPGEEPA 240
QY 241 WVQTERQQFRDLNKGDLGDSYGVHWYLPAPQDQPLVEANHLHESDTRKDGRLSKA 300
DB 241 WVQTERQQFRDLNKGDLGDSYGVHWYLPAPQDQPLVEANHLHESDTRKDGRLSKA 300
QY 301 EILGNWNNFVGSQATNYGDLTRHDEL 328
DB 301 EILGNWNNFVGSQATNYGDLTRHDEL 328

RESULT 2
US-09-902-853-221
Sequence 221, Application US/09902853
Publication No. US20020192659A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.

Qy 61 GREVAKEFDQLTPEESQARLGRIVDMDRAGDGGWVSLAELRAWIAHTQQRHIRDSYSA 120
Db 61 GREVAKEFDQLTPEESQARLGRIVDMDRAGDGGWVSLAELRAWIAHTQQRHIRDSYSA 120
Qy 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEADATYKKMLARDERRFRVADQDGD 180
Db 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEADATYKKMLARDERRFRVADQDGD 180
Qy 181 SMATREELTAFLHPEEPHMRDVIATLEDDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
Db 181 SMATREELTAFLHPEEPHMRDVIATLEDDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
Qy 241 WQTERQOQFRDRLNKGHLGDSVGHVWLPAPQDQPLVEANHLHESDTDKDGRLSKA 300
Db 241 WQTERQOQFRDRLNKGHLGDSVGHVWLPAPQDQPLVEANHLHESDTDKDGRLSKA 300
Qy 301 EILGNWNNFVGSQATNYGDELTRHDEL 328
Db 301 EILGNWNNFVGSQATNYGDELTRHDEL 328

RESULT 3

US-09-907-824-221
; Sequence 221, Application US/09907824
; Publication No. US20020197671A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,824
; PRIOR FILING DATE: 2001-07-17
; PRIOR FILING DATE: 2000-09-18
; PRIOR FILING DATE: 2000-02-22
; PRIOR FILING DATE: 1999-07-07
; PRIOR FILING DATE: 1999-07-26
; PRIOR FILING DATE: 1999-07-26
; PRIOR FILING DATE: 1999-07-28
; PRIOR FILING DATE: 1999-07-28
; PRIOR FILING DATE: 1999-09-08
; PRIOR FILING DATE: 1999-09-13
; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 221
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-907-824-221

Query Match 100.0%; Score 328; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.1e-274;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMWRPSVLLLLLRHGAQKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFL 60
Db 1 MMWRPSVLLLLLRHGAQKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFL 60
Qy 61 GREVAKEFDQLTPEESQARLGRIVDMDRAGDGGWVSLAELRAWIAHTQQRHIRDSYSA 120
Db 61 GREVAKEFDQLTPEESQARLGRIVDMDRAGDGGWVSLAELRAWIAHTQQRHIRDSYSA 120
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Db 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEADATYKKMLARDERRFRVADQDGD 180
Qy 181 SMATREELTAFLHPEEPHMRDVIATLEDDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
Db 181 SMATREELTAFLHPEEPHMRDVIATLEDDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
Qy 241 WQTERQOQFRDRLNKGHLGDSVGHVWLPAPQDQPLVEANHLHESDTDKDGRLSKA 300
Db 241 WQTERQOQFRDRLNKGHLGDSVGHVWLPAPQDQPLVEANHLHESDTDKDGRLSKA 300
Qy 301 EILGNWNNFVGSQATNYGDELTRHDEL 328
Db 301 EILGNWNNFVGSQATNYGDELTRHDEL 328

RESULT 4

US-09-907-841-221
; Sequence 221, Application US/09907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.

us-09-768-840-1.oli.rapb

Tue May 20 14:43:21 2003

```

; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,841
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05

RESULT 5
US-09-904-011-221
; Sequence 221, Application US/09904011
; Publication No. US20030003530A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,011
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
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; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05

Query Match 100.0%; Score 328; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.1e-274; Indels 0; Gaps 0;
Matches 328; Conservative 0; Mismatches 0;

QY 1 MMWRPSVLLLLLRHCAQKSPDAGPHGQGRVHQAAPLSDAPHDHDAHGNGFYDHEAFL 60
DB 1 MMWRPSVLLLLLRHCAQKSPDAGPHGQGRVHQAAPLSDAPHDHDAHGNGFYDHEAFL 60
QY 61 GREVAKFEDQLTPESQARLGRIVDRMDRAGDGGWVSLAELRANIHTQQRHSDSYSA 120
DB 61 GREVAKFEDQLTPESQARLGRIVDRMDRAGDGGWVSLAELRANIHTQQRHSDSYSA 120
QY 121 AWDYTDROGRVGEWELRNATYGHVAPGEFHDVEDATYKKMLARDERFRFVADQDGD 180
DB 121 AWDYTDROGRVGEWELRNATYGHVAPGEFHDVEDATYKKMLARDERFRFVADQDGD 180
QY 181 SMATREELTALHPPEEPHMRDIVIAETLEDLRNKDGYVQVEYIADLYSAEPGEEPA 240
DB 181 SMATREELTALHPPEEPHMRDIVIAETLEDLRNKDGYVQVEYIADLYSAEPGEEPA 240
QY 241 WYQTERQOFRDLNKGHLDGSEVGHVWLPAAQDQPLVEANHLHESDTRDKGRLSKA 300
DB 241 WYQTERQOFRDLNKGHLDGSEVGHVWLPAAQDQPLVEANHLHESDTRDKGRLSKA 300
QY 301 EILGNWNNFVGSQATNYGDELTRHDEL 328
DB 301 EILGNWNNFVGSQATNYGDELTRHDEL 328
US-09-907-841-221
; QUERY MATCH
; BEST LOCAL SIMILARITY
; MATCHES
; TYPE: PRT
; LENGTH: 328
; ORGANISM: Homo sapiens
; US-09-907-841-221
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; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 221
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-011-221

Query Match      100.0%; Score 328; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.le-274;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLRHGAQCKSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAPL 60
   |||||||
Db 1 MMWRPSVLLLLLRHGAQCKSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAPL 60
   |||||||
QY 61 GREVAKFQDLTPESQARLGRVDRMDRAGDGDGHSVLAELRAMTAHTQQRHIRDSVSA 120
   |||||||
Db 61 GREVAKFQDLTPESQARLGRVDRMDRAGDGDGHSVLAELRAMTAHTQQRHIRDSVSA 120
   |||||||
QY 121 AWDTYDTRDGRVGEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQGD 180
   |||||||
Db 121 AWDTYDTRDGRVGEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQGD 180
   |||||||
QY 181 SMATRELTAFLLHPEEFPHMRDIVTAETLEDLDRNKDGVVQVEEYIADLYSAEPGEERPA 240
   |||||||
Db 181 SMATRELTAFLLHPEEFPHMRDIVTAETLEDLDRNKDGVVQVEEYIADLYSAEPGEERPA 240
   |||||||
QY 241 WYOTERQOQFRDLNKGHLDSGVGHVLPAPQDQPLVEANHLHESDTRDKGRLSKA 300
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Db 241 WYOTERQOQFRDLNKGHLDSGVGHVLPAPQDQPLVEANHLHESDTRDKGRLSKA 300
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QY 301 EILGNWNVFVGSQATNYGEDLTRHHDEL 328
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Db 301 EILGNWNVFVGSQATNYGEDLTRHHDEL 328
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RESULT 6
US-10-028-072-364
; Sequence 364, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/028,072
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
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; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: 60/063550
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063561
; PRIOR FILING DATE: 1997-10-28
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; PRIOR APPLICATION NUMBER: 60/069334
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069694
; PRIOR FILING DATE: 1997-12-16
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; PRIOR FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: 60/073612
; PRIOR FILING DATE: 1998-02-04
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Tue May 20 14:43:21 2003

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;; PRIOR FILING DATE: 1998-02-09
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;; PRIOR APPLICATION NUMBER: 60/079294
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;; PRIOR APPLICATION NUMBER: 60/088858
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/089532
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089599
;; PRIOR FILING DATE: 1998-06-17
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;; PRIOR APPLICATION NUMBER: 60/090538
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;;
Query Match 100.0%; Score 328; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.le-274;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMWRPSVLLLLLLRHGAQKQSPDAGPHGQGRVHOAAPLSDAPHDDAHGNFYDHEAFL 60
DB 1 MMWRPSVLLLLLLRHGAQKQSPDAGPHGQGRVHOAAPLSDAPHDDAHGNFYDHEAFL 60
QY 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWYSLAELRAWTQQRHRSVSA 120
DB 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWYSLAELRAWTQQRHRSVSA 120
QY 121 AWDTYTDTRDGRVGVWEELRNATYGHYAPGEEFHDVEDAEYKKMLARDERRFRVADQGD 180
DB 121 AWDTYTDTRDGRVGVWEELRNATYGHYAPGEEFHDVEDAEYKKMLARDERRFRVADQGD 180
QY 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
DB 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
QY 241 WVQTERQQFRDRLNKDGLDGSVEGHVLPAPQDQPLVEANHLHESDTDKDGRLSKA 300
DB 241 WVQTERQQFRDRLNKDGLDGSVEGHVLPAPQDQPLVEANHLHESDTDKDGRLSKA 300
QY 301 EILGNMFMVGSQATNYCEDLTRHDEL 328
DB 301 EILGNMFMVGSQATNYCEDLTRHDEL 328
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RESULT 7
US-09-768-840-1.oli.rapb
;; Sequence 221, Application US/09906742
;; Publication No. US20030023054A1
;; GENERAL INFORMATION:
;; APPLICANT: Genentech, Inc.
;; APPLICANT: Ashkenazi, Avi
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, A.
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, Christine J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth, J.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Mather, Jennie P.
;; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William, I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: 10466-14
 ; CURRENT APPLICATION NUMBER: US/09/906,742
 ; CURRENT FILING DATE: 2001-07-16
 ; PRIOR APPLICATION NUMBER: 09/665,350
 ; PRIOR FILING DATE: 2000-09-18
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414
 ; PRIOR FILING DATE: 2000-02-22
 ; PRIOR APPLICATION NUMBER: US 60/143,048
 ; PRIOR FILING DATE: 1999-07-07
 ; PRIOR APPLICATION NUMBER: US 60/145,698
 ; PRIOR FILING DATE: 1999-07-26
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 ; PRIOR FILING DATE: 1999-07-28
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 ; PRIOR FILING DATE: 1999-09-15
 ; PRIOR APPLICATION NUMBER: PCT/US99/21547
 ; PRIOR FILING DATE: 1999-09-15
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 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: PCT/US99/30911
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US99/30999
 ; PRIOR FILING DATE: 1999-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US00/00219
 ; PRIOR FILING DATE: 2000-01-05
 ; NUMBER OF SEQ ID NOS: 423
 ; SEQ ID NO 221
 ; LENGTH: 328
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-09-906-742-221

Query Match 100.0%; Score 328; DB 9; Length 328;
 Best Local Similarity 100.0%; Pred. No. 1.1e-274;
 Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMWRPSVLLLLLRHGAQCKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNGFYDHEAFL 60
 DB 1 MMWRPSVLLLLLRHGAQCKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNGFYDHEAFL 60
 QY 61 GREVAKFEDQLTPESQARLGRIVDRMDRAGDGGVSWLAELRAWIAHTQQRHSDVSA 120
 DB 61 GREVAKFEDQLTPESQARLGRIVDRMDRAGDGGVSWLAELRAWIAHTQQRHSDVSA 120
 QY 121 AWDTYDTRDGRGVGWEELRNATYGHVAPGEEFHDVEDAETYYKKMLARDERRFRVADQGD 180
 DB 121 AWDTYDTRDGRGVGWEELRNATYGHVAPGEEFHDVEDAETYYKKMLARDERRFRVADQGD 180
 QY 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKGDLGSEVGHVWLPQAQDQPLVEANHLHSDTDKDGRLSKA 240
 DB 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKGDLGSEVGHVWLPQAQDQPLVEANHLHSDTDKDGRLSKA 240
 QY 301 EILGNMNFVGSQATNYGDELTRHDEL 328
 DB 301 EILGNMNFVGSQATNYGDELTRHDEL 328

QY 241 WVQTERQQFRDRLNKGDLGSEVGHVWLPQAQDQPLVEANHLHSDTDKDGRLSKA 300
 DB 241 WVQTERQQFRDRLNKGDLGSEVGHVWLPQAQDQPLVEANHLHSDTDKDGRLSKA 300
 QY 301 EILGNMNFVGSQATNYGDELTRHDEL 328
 DB 301 EILGNMNFVGSQATNYGDELTRHDEL 328

RESULT 8

US-10-121-049-364
 ; Sequence 364, Application US/10121049
 ; Publication No. US20030022239A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3330R1C17
 ; CURRENT APPLICATION NUMBER: US/10/121,049
 ; CURRENT FILING DATE: 2002-04-12
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 364
 ; LENGTH: 328
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-121-049-364

Query Match 100.0%; Score 328; DB 9; Length 328;
 Best Local Similarity 100.0%; Pred. No. 1.1e-274;
 Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMWRPSVLLLLLRHGAQCKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNGFYDHEAFL 60
 DB 1 MMWRPSVLLLLLRHGAQCKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNGFYDHEAFL 60
 QY 61 GREVAKFEDQLTPESQARLGRIVDRMDRAGDGGVSWLAELRAWIAHTQQRHSDVSA 120
 DB 61 GREVAKFEDQLTPESQARLGRIVDRMDRAGDGGVSWLAELRAWIAHTQQRHSDVSA 120
 QY 121 AWDTYDTRDGRGVGWEELRNATYGHVAPGEEFHDVEDAETYYKKMLARDERRFRVADQGD 180
 DB 121 AWDTYDTRDGRGVGWEELRNATYGHVAPGEEFHDVEDAETYYKKMLARDERRFRVADQGD 180
 QY 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKGDLGSEVGHVWLPQAQDQPLVEANHLHSDTDKDGRLSKA 240
 DB 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKGDLGSEVGHVWLPQAQDQPLVEANHLHSDTDKDGRLSKA 240
 QY 241 WVQTERQQFRDRLNKGDLGSEVGHVWLPQAQDQPLVEANHLHSDTDKDGRLSKA 300
 DB 241 WVQTERQQFRDRLNKGDLGSEVGHVWLPQAQDQPLVEANHLHSDTDKDGRLSKA 300
 QY 301 EILGNMNFVGSQATNYGDELTRHDEL 328
 DB 301 EILGNMNFVGSQATNYGDELTRHDEL 328

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APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C160
CURRENT APPLICATION NUMBER: US/10/140,470
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See: Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 364
LENGTH: 328
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-470-364

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Query Match	100.0%	Score 328;	DB 9;	Length 328;
Best Local Similarity	100.0%;	Pred. No. 1.1e-274;		
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Db	1	MMWRPSVLLLLLLRRGAACKSPDAGPHGQGRVHQAAPLSDAPHDDAHGNYDHEAFL	60	
QY	61	GREVAKFEDQITPEESQARLGRIVRMDRAGDGDGWSVLAELRAWIAHTQQRHIRDSVSA	120	
Db	61	GREVAKFEDQITPEESQARLGRIVRMDRAGDGDGWSVLAELRAWIAHTQQRHIRDSVSA	120	
QY	121	AWDYITDTRDGRVGEWEELRNATGYAPGEEFHDVEDAETYYKKMLARDERRFVADODGD	180	
Db	121	AWDYITDTRDGRVGEWEELRNATGYAPGEEFHDVEDAETYYKKMLARDERRFVADODGD	180	
QY	181	SMATREELTAFLHPPEEPHMRDIIAETLEDLDRNKDGYVQVEEYIADLYSAPGEEEPA	240	
Db	181	SMATREELTAFLHPPEEPHMRDIIAETLEDLDRNKDGYVQVEEYIADLYSAPGEEEPA	240	
QY	241	WYQTERQGRFRDLNKGHDGSDGSEVGHWVLPQAQDQPLVEANHLLHESDTDKDGRLSKA	300	
Db	241	WYQTERQGRFRDLNKGHDGSDGSEVGHWVLPQAQDQPLVEANHLLHESDTDKDGRLSKA	300	
QY	301	ETLGNMNMFGVSQATNYGEDLTRHDEL	328	
Db	301	ETLGNMNMFGVSQATNYGEDLTRHDEL	328	

RESULT 11
US-09-906-838-221
; Sequence 221, Application US/09906838
; Publication No. US20030027143A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.

RESULT 9
 US-10-123-904-364
 ; Sequence 364, Application US/10123904
 ; Publication No. US20030022326A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME

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; FILE REFERENCE: P3330RIC54
; CURRENT APPLICATION NUMBER: US/10/123,904
; CURRENT FILING DATE: 2002-04-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 364
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-123-904-364

Query Match 100.0%; Score 328; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.1e-274;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRFSVLLLLLRRHGAGQKPSDAGPHGGQGRVHQAAPLSDAPHDHAGNFQYDHEAFL 60
D 1 MMWRFSVLLLLLRRHGAGQKPSDAGPHGGQGRVHQAAPLSDAPHDHAGNFQYDHEAFL 60
QY 61 GREVAKFQDLTPESQARLGRIVDRMDRAGDGCWGSIAELRAWIAHTQQRHIRDSVSA 120
D 61 GREVAKFQDLTPESQARLGRIVDRMDRAGDGCWGSIAELRAWIAHTQQRHIRDSVSA 120
QY 121 ANDTYTDTRDGRGVGWEELRNATYGHVAPCEEFHDVEDAETYYKKMLARDERRFVADQGD 180
D 121 ANDTYTDTRDGRGVGWEELRNATYGHVAPCEEFHDVEDAETYYKKMLARDERRFVADQGD 180

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DB 181 SMATREELTAF LNP EEF FERRA V ARL 300
QY 241 WVQTERQQFDRFDRLNKDGLDGESEGVHWVLPQAQDQPLVEANHLLHESDTDKDGRLSKA 300
Db 241 WVQTERQQFDRFDRLNKDGLDGESEGVHWVLPQAQDQPLVEANHLLHESDTDKDGRLSKA 300
QY 301 EILGNMNMFGVSQATNYGEDLTRHDEL 328
Db 301 EILGNMNMFGVSQATNYGEDLTRHDEL 328

RESULT 10
US-10-140-470-364
; Sequence 364, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen

APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,838
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 221
LENGTH: 328
TYPE: PRT
ORGANISM: Homo Sapien
US-09-906-838-221

Query Match 100.0%; Score 328; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 1,1e-274;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MMWRPSVLLLLLRHCAQCKPSDAGPHGQGRVHQAAPLSDAPHDHAGNFQYDHEAPL 60
QY 61 GREVAKEFDQLTPEESQARLGRIIVDRMDRAGDGDGWSLAELRAWHTAHTQQRHDSVSA 120
DB 61 GREVAKEFDQLTPEESQARLGRIIVDRMDRAGDGDGWSLAELRAWHTAHTQQRHDSVSA 120

QY 121 AWDTYDTRDGRVGEELRNATYGHYAPGEFHDVEDAETKKMLARDERRFRVADQGD 180
DB 121 AWDTYDTRDGRVGEELRNATYGHYAPGEFHDVEDAETKKMLARDERRFRVADQGD 180
QY 181 SMATREELTAFLHPEEFPHMRDIVIAETLEDLRNKDGYVQVEEYIADLYSAEPGEPEA 240
DB 181 SMATREELTAFLHPEEFPHMRDIVIAETLEDLRNKDGYVQVEEYIADLYSAEPGEPEA 240
QY 241 WVQTERQQFRDLNKDGLDGSVGHVWLPAPADQPLVEANHLHESDTRDKDRLSKA 300
DB 241 WVQTERQQFRDLNKDGLDGSVGHVWLPAPADQPLVEANHLHESDTRDKDRLSKA 300
QY 301 EILGNMNFVGSQATNYGDLTRHDEL 328
DB 301 EILGNMNFVGSQATNYGDLTRHDEL 328
RESULT 12
US-09-907-613-221
Sequence 221, Application US/09907613
Publication No. US20030027145A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,613
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 221
LENGTH: 328
TYPE: PRT
ORGANISM: Homo sapiens
US-09-907-613-221

Query Match 100.0%; Score 328; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.le-274;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLLRHGAQKPSDPAGPHGQGRVHQAAPLSDAPHDDAHGNGFYDHEAFL 60
DB 1 MMWRPSVLLLLLLRHGAQKPSDPAGPHGQGRVHQAAPLSDAPHDDAHGNGFYDHEAFL 60
QY 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSA 120
DB 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSA 120
QY 121 AWDYTDTRDGRVGVWEELRNATYGHVAPGEEFHDVEDAETYYKKMLARDERRFRVADQDGD 180
DB 121 AWDYTDTRDGRVGVWEELRNATYGHVAPGEEFHDVEDAETYYKKMLARDERRFRVADQDGD 180
QY 181 SMATREELTAFLHPEEPFPHMRDIIAETLEDLRNKDGYVQVEEYIADLYSAEPGEEPA 240
DB 181 SMATREELTAFLHPEEPFPHMRDIIAETLEDLRNKDGYVQVEEYIADLYSAEPGEEPA 240
QY 241 WVOTERQOQFRDLNKGDLGSEVGHVWVLPQAQDQPLVEANHLLHESDTDKDGRLSKA 300
DB 241 WVOTERQOQFRDLNKGDLGSEVGHVWVLPQAQDQPLVEANHLLHESDTDKDGRLSKA 300
QY 301 EILGNMNFVGSQATNYGDLTRHDEL 328
DB 301 EILGNMNFVGSQATNYGDLTRHDEL 328

RESULT 13
US-09-907-942-221
Sequence 221, Application US/09907942
Publication No. US20030027146A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,942
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 221
LENGTH: 328
TYPE: PRT
ORGANISM: Homo sapiens
US-09-907-942-221

Query Match 100.0%; Score 328; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.le-274;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLLRHGAQKPSDPAGPHGQGRVHQAAPLSDAPHDDAHGNGFYDHEAFL 60
DB 1 MMWRPSVLLLLLLRHGAQKPSDPAGPHGQGRVHQAAPLSDAPHDDAHGNGFYDHEAFL 60
QY 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSA 120
DB 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSA 120
QY 121 AWDYTDTRDGRVGVWEELRNATYGHVAPGEEFHDVEDAETYYKKMLARDERRFRVADQDGD 180
DB 121 AWDYTDTRDGRVGVWEELRNATYGHVAPGEEFHDVEDAETYYKKMLARDERRFRVADQDGD 180
QY 181 SMATREELTAFLHPEEPFPHMRDIIAETLEDLRNKDGYVQVEEYIADLYSAEPGEEPA 240
DB 181 SMATREELTAFLHPEEPFPHMRDIIAETLEDLRNKDGYVQVEEYIADLYSAEPGEEPA 240
QY 241 WVOTERQOQFRDLNKGDLGSEVGHVWVLPQAQDQPLVEANHLLHESDTDKDGRLSKA 300

Db 241 WYQTERQOFRDLNKGDLGSEVGHVLPAPQDQPLVEANHLHESDTDKDGRLSKA 300
Qy 301 EILGNMNFVGSQATNYGDELTRHDEL 328
Db 301 EILGNMNFVGSQATNYGDELTRHDEL 328

RESULT 14

US-10-175-746-364
; Sequence 364, Application US/10175746
; Publication No. US20030027270A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C353
; CURRENT APPLICATION NUMBER: US/10/175,746
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 364
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-746-364

Query Match 100.0%; Score 328; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.le-274;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMWRPSVLLLLLLLRHGAQKPSDPAGPHGQGRVHQAPLSDAPHDDAHGNFYDHEAFL 60
Db 1 MMWRPSVLLLLLLLRHGAQKPSDPAGPHGQGRVHQAPLSDAPHDDAHGNFYDHEAFL 60
Qy 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWSLAEALRAWIAHTQQRHIRDSVSA 120
Db 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWSLAEALRAWIAHTQQRHIRDSVSA 120
Qy 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQDGD 180
Db 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQDGD 180
Qy 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
Db 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
Qy 241 WYQTERQOFRDLNKGDLGSEVGHVLPAPQDQPLVEANHLHESDTDKDGRLSKA 300
Db 241 WYQTERQOFRDLNKGDLGSEVGHVLPAPQDQPLVEANHLHESDTDKDGRLSKA 300
Qy 301 EILGNMNFVGSQATNYGDELTRHDEL 328
Db 301 EILGNMNFVGSQATNYGDELTRHDEL 328

RESULT 15

Search completed: May 14, 2003, 10:50:56
Job time : 24 secs

US-10-176-918-364
; Sequence 364, Application US/10176918
; Publication No. US20030027275A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C382
; CURRENT APPLICATION NUMBER: US/10/176,918
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 364
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-918-364

Query Match 100.0%; Score 328; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.le-274;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMWRPSVLLLLLLLRHGAQKPSDPAGPHGQGRVHQAPLSDAPHDDAHGNFYDHEAFL 60
Db 1 MMWRPSVLLLLLLLRHGAQKPSDPAGPHGQGRVHQAPLSDAPHDDAHGNFYDHEAFL 60
Qy 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWSLAEALRAWIAHTQQRHIRDSVSA 120
Db 61 GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWSLAEALRAWIAHTQQRHIRDSVSA 120
Qy 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQDGD 180
Db 121 AWDYTDTRDGRGVGWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQDGD 180
Qy 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
Db 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA 240
Qy 241 WYQTERQOFRDLNKGDLGSEVGHVLPAPQDQPLVEANHLHESDTDKDGRLSKA 300
Db 241 WYQTERQOFRDLNKGDLGSEVGHVLPAPQDQPLVEANHLHESDTDKDGRLSKA 300
Qy 301 EILGNMNFVGSQATNYGDELTRHDEL 328
Db 301 EILGNMNFVGSQATNYGDELTRHDEL 328

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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 19, 2003, 22:09:52 ; Search time 3346 Seconds
(without alignments)
2852.875 Million cell updates/sec

Title: US-09-768-840-1

Perfect score: 328

Sequence: 1 MMWRPSVLLLLLLRHGAQG.....FVGSQATNYGDELTRHHDEL 328

Scoring table: OLIGO

Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Word size: 1

Total number of hits satisfying chosen parameters: 4106487

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n_model -DEV=xlh
-O=/cgn2_1/USPTO_spool/US09768840/runat_14052003_095832_17363/app_query.fasta.1.519
-DB=GenEmbl -QMT=fastcap -SUFFIX=olip2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09768840 -ECGN_1_1_2496_@runat_14052003_095832_17363 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

GenEmbl :
1: gb_ba : *
2: gb_htg : *
3: gb_in : *
4: gb_lm : *
5: gb_ov : *
6: gb_pat : *
7: gb_ph : *
8: gb_pl : *
9: gb_pr : *
10: gb_ro : *
11: gb_sts : *
12: gb_sy : *
13: gb_un : *
14: gb_vi : *
15: em_ba : *
16: em_fun : *
17: em_hum : *
18: em_in : *
19: em_mu : *
20: em_om : *
21: em_or : *
22: em_ov : *
23: em_pat : *
24: em_ph : *
25: em_pi : *
26: em_ro : *
27: em_sts : *
28: em_un : *

29: em_vl : *
30: em_htg_hum : *
31: em_htg_inv : *
32: em_htg_other : *
33: em_htg_mus : *
34: em_htg_pln : *
35: em_htg_rdd : *
36: em_htg_mam : *
37: em_htg_vrt : *
38: em_sy : *
39: em_htgo_hum : *
40: em_htgo_mus : *
41: em_htgo_other : *

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	328	100.0	1055	6	AR035969	Sequence
2	328	100.0	1055	6	AR135029	Sequence
3	328	100.0	1463	6	AR083085	Sequence
4	328	100.0	1463	6	AR152960	Sequence
5	328	100.0	1470	9	BC011346	Homo sapi
6	328	100.0	1503	6	AX464230	Sequence
7	300	91.5	1507	6	AX354366	Sequence
8	300	91.5	1507	6	AX354369	Sequence
9	235	71.6	1454	9	AF183423	Sequence
10	81	24.7	179394	9	AC010619	Homo sapi
11	65	19.8	658	6	AX354365	Sequence
12	57	17.4	1414	10	BC005487	Sequence
13	57	17.4	1421	10	BC025602	Sequence
14	57	17.4	110000	2	AC073763	0
15	57	17.4	161995	2	AC099450	Rattus no
16	57	17.4	186243	2	AC073740	Mus muscu
17	57	17.4	191713	2	AC126256	Mus muscu
18	25	7.6	294	10	RAT0RF	L1683 Rattus norv
19	20	6.1	110000	2	AC073763_2	Continuation (3 of
20	19	5.8	45565	5	FR151J19	AL021531 Fugu rubr
21	18	5.5	408	6	AX351308	Sequence
22	18	5.5	411	6	AX341934	Sequence
23	18	5.5	501	6	AX331573	Sequence
24	18	5.5	1454	9	BC010120	Homo sapi
25	18	5.5	1998	10	MUSRCAL	D13003 Mus musculu
26	18	5.5	2104	6	AX330466	Sequence
27	18	5.5	2104	9	HUMSCN	D42073 Human mRNA
28	18	5.5	2416	9	AK094360	Sequence
29	18	5.5	2557	10	MUSRET15	AK094360 Homo sapi
30	18	5.5	44882	2	AC020850_4	D43956 Mouse gene
31	18	5.5	79018	9	AL627107	Continuation (5 of
32	18	5.5	94497	9	HSJG65P5	AL627107 Human DNA
33	18	5.5	110000	2	AC020850_2	AL078612 Human DNA
34	18	5.5	176708	2	AC027548	Continuation (3 of
35	18	5.5	182482	2	AL512583	AC027548 Homo sapi
36	18	5.5	213666	2	AC020837	AL512583 Mus muscu
37	17	5.2	74	6	AX193367	Sequence
38	13	4.0	140374	2	AC113655	AX193367 Rattus no
39	13	4.0	152260	2	AC125901	AC113655 Rattus no
40	13	4.0	155611	2	AC118188	AC125901 Rattus no
41	13	4.0	164378	2	AC109856	AC118188 Rattus no
42	13	4.0	208146	2	AC129665	AC109856 Rattus no
43	13	4.0	250213	2	AC114695	AC129665 Rattus no
44	12	3.7	112797	2	AC111827	AC114695 Rattus no
45	12	3.7	162420	2	AC120909	AC111827 Rattus no

ALIGNMENTS

RESULT 1

AR035969	AR035969	Sequence 2 from patent US 5871970.	1055 bp	DNA	linear	PAT 29-SEP-1999
LOCUS						
DEFINITION	Sequence 2 from patent US 5871970.					
ACCESSION	AR035969					
VERSION	AR035969.1	GI:5952637				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	Unclassified.					
AUTHORS	Hillman,J.L. and Goli,S.K.					
TITLE	Calcium-binding protein					
JOURNAL	Patent: US 5871970-A 2 16-FEB-1999;					
FEATURES	Location/Qualifiers					
source	1..1055					
BASE COUNT	225 a 300 c 375 g 151 t					
ORIGIN	/organism="unknown"					
Alignment Scores:						
Pred. No.:	0	Length:	1055			
Score:	328.00	Matches:	328			
Percent Similarity:	100.00%	Conservative:	0			
Best Local Similarity:	100.00%	Mismatches:	0			
Query Match:	100.00%	Indels:	0			
DB:	6	Gaps:	0			
US-09-768-840-1 (1-328) x AR035969 (1-1055)						
Qy 1 MetMetTrpArgProSerValLeuLeuLeuLeuLeuLeuLeuAArgHisGlyAlaGlnGly 20						
Db 34 ATGATGTGGCGACCATTAGTTCTGCTTCTGTTGCTACTGAGGCACGGGCCCGG 93						
Qy 21 LysProSerProAspAlaGlyProHisGlyGlnGlyArgValHisGlnAlaAlaProLeu 40						
Db 94 AAGCCATCCCCAGACGCGAGGCCCTCATGGCAGGGAGGGTGCAACGSGCGSCCCCCTG 153						
Qy 41 SerAspAlaProHisAspAspAlaHisGlyAsnPheGlnTyrAspHisGluAlaPheLeu 60						
Db 154 AGCGACGCTCCCATCATGATGACGCCACGGGAATTCACAGTAGCACATGAGCTTTCCTG 213						
Qy 61 GlyArgGluValAlaIysGluPheAspGlnLeuThrProGluGluSerGlnAlaArgLeu 80						
Db 214 GGACGGGAAGTGGCCAGAAGATTCACCAACTCACCCAGAGAAAGCCAGCCCGCTCTG 273						
Qy 81 GlyArgIleValAspArgMetAspArgAlaGlyAspGlyAspGlyTrpValSerLeuAla 100						
Db 274 GSGCGATCGTGACCGCATGACCGCGGGGGAGCGCGGTGGTGTGCTGGTGGCC 333						
Qy 101 GluLeuArgAlaTrpIleAlaHisThrGlnGlnArgHisIleArgAspSerValSerAla 120						
Db 334 GAGCTCGCGCTGGATCCGCACACGACGACGCGGCACATACGGGACTCGGTGACGCG 393						
Qy 121 AlaTrpAspThrTyrAspThrAspArgaspGlyArqValcIlyTrpGluGluLeuArgasn 140						
Db 394 GCCTGGACACGTACGACACGACGCCGCGGTGTGGTGGAGGAGCTGGCGAAC 453						
Qy 141 AlaThrTyrGlyHisTyrAlaProGlyGluGluPheHisAspValGluAspAlaGluThr 160						
Db 454 GCCACCTATGGCCACTACGCGCGCGGTGAAGAATTTTCATGAGCTGGAGGATGCAGAGAC 513						
Qy 161 TyrLysLysMetLeuAlaArgAspGluArgArgPheArgValAlaAspGlnAspGlyAsp 180						
Db 514 TACAANAAGATCTGCTCGGACGACGCGGCTTCCGGGTGGCCACGAGATGGGGAC 573						
Qy 181 SerMetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMet 200						
Db 574 TCGATGGCCACTCGAGAGGAGCTGACAGCCTTCTGCACCCCGAGGAGTTCCTCATG 633						
Qy 201 ArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysaspGlyTyVal 220						
Db 634 CGGGACATCGTATTGCTGAACCTTGGAGGACCTGGACAGAAACAAAGATGCTATGTC 693						

[illegible]

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31..1017
/codon_start=1
/product="hypothetical protein LOC57333"
/protein_id="AAH13436.1"
/db_xref="GT:15488595"

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BASE COUNT	332 a	454 c	470 q	214 f
QPLVEANHLHESD	TDK	DGRLSKAEILL		

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Alignment Scores:
Pred. No.:          0      Length:      1470
Score:             328.00   Matches:      328
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match:      100.00%   Indels:      0
DB:                9      Gaps:        0

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US-09-768-840-1 (1-328) x BC013436 (1-1470)

[illegible]

Qy	241	TrpValGlnThrGluArgGlnGlnPheArgAspPheArgAspLeuAsnLysAspGlyHis	260
Db	751	TGGGTGCACAGCAGAGCAGCAGTCCGGGACTTCGGGATCTGAACAGGATGGGCAC	810
Qy	261	LeuAspGlySerGluValGlyHisTrpValLeuProAlaGlnAspGlnProLeuVal	280
Db	811	CTGGATGGGAGTCAGTGGGCCACTTGGGTGCTGCCCCCTGCCACGACCAAGCCCTTGGTG	870
Qy	281	GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla	300
Db	871	GAAGCCCAACACCTGCTGCACGAGACGACACGACAAGGATGGCGGCTGACCAAGCG	930
Qy	301	GluIleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTrpGlyGluAsp	320
Db	931	GAATCCTGGGTAAATTGGACATGTTTGTGGGCAGTCAGGCCCAACCACTATGCGCAGGAC	990
Qy	321	LeuThrArgHisHisAspGluLeu	328
Db	991	CTGACCCGGCACCCACGATGAGCTG	1014

RESULT 6

LOCUS

ACCESSION
VERSION
KEYWORDS
SOURCE

STAYERS

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

sour

ORIGIN

Alignment

Pred. No.

Percent S.

Query Matrix

OB:

JS-09-768

 $\frac{1}{2}y$

35.

21

95

...

1

224

Yi
T9

215

Db	534	TACAAAAGATGCTGGCTCGGACGAGCGCGCTTTCCGGGTGCGCAGCAGGATGGGCAC	593
Qy	181	SerMetAlaThrArgGluGluLeuLeuThrAlaPheLeuHisProGluGluPheProHisMet	200
Db	594	TCGATGCCACTCGACGAGCGTACAGCCCTTCCTGCACCCGAGGATTCCTCCATCATG	653
Qy	201	ArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrVal	220
Db	654	CGGACATCGTGATTCTGAAACCCCTGCAGACCTGCGAGCACTCCGGATCTGAACAGGATGGCTATGTC	713
Qy	221	GlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGluGluProAla	240
Db	714	CAGGTGAGGAGTACATCCGGATCTGTACTCAGCCGAGGCTCGGAGGAGCGCGCG	773
Qy	241	TrpValGlnThrGluArgGlnGlnPheArgAspPheArgAspLeuAsnLysAspGlyHis	260
Db	774	TGGGTGCAGACGAGAGCGACGACTCCGGAGCTCCGGATCTGAACAGGATGGGCAC	833
Qy	261	LeuAspGlySerGluValGlyHisTrpValLeuProProAlaGlnAspGlnProLeuVal	280
Db	834	CTGGATGGGATGAGTGGGCGCACTGGGTCTGCCCTGCCAGACCCAGCCCTGGTG	893
Qy	281	GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla	300
Db	894	GAAGCAACCACTGCTGCACGARAGCGACGACGACGATGGCGGCTGAGCAAGCG	953
Qy	301	Glu-TleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAs	320
Db	954	SA-AATCTGGGTAAATGGAAACATGTTGTGGCAGTCAGGCCACCACTATGCGAGGA	1012
Qy	320	PleuThrArgHisHisAspGluLeu	328
Db	1013	CCTGACCCGCGACCATGATGAGCTG	1037
RESULT	9		
AF183423			
LOCUS	AF183423	1454 bp	linear
DEFINITION	Homo sapiens reticulocabin precursor mRNA, complete cds.		
ACCESSION	AF183423		
VERSION	AF183423.1	GI:9963784	
KEYWORDS			
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens.		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	Peng, Y., Gu, Y., Huang, C., Xu, S., Han, Z., Fu, G. and Chen, Z.		
JOURNAL	A novel gene expressed in human hypothalamus		
REFERENCE	Unpublished		
AUTHORS	2 (bases 1 to 1454)		
TITLE	Peng, Y., Gu, W., Huang, C., Xu, S., Han, Z., Fu, G. and Chen, Z.		
JOURNAL	Direct Submission		
FEATURES	Submitted (03-SEP-1999) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong Shanghai 201203, P. R. China		
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	/evidence=not experimental		
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	RAWIAHTQQRHTRDSVSAWDTYDTRDGRVGHLEELRNATYGHYAPGEEFHVDA		
	YKKMLARDERFRVADQDSMATRELTAFHPPEEFPHMRDVIATETLELDLRNKI		
	YVQVEEYIADLYSAPEEPEAPVQTRERQQQFRDLRDLNKDLGDSGEVHWVLPPLA		

[illegible]

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Db 115824 GGACGGAGTGCACCAAGTTCGACCAACTCACCCAGAGGAAGCCAGCCGCTCTG 115883
Qy 81 Gly 81
Db 115884 GGG 115886
RESULT 11
LOCUS AX354365
DEFINITION Sequence 11 from Patent WO0196523.
ACCESSION AX354365
VERSION AX354365.1 GI:18619207
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1
AUTHORS Kennedy,G.C., Kang,S., Reinhard,C. and Jefferson,A.B.
TITLE Polynucleotides related to colon cancer
JOURNAL Patent: WO 0196523-A 11 20-DEC-2001;
CHIRON CORPORATION (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 134 a 240 c 184 g 100 t
ORIGIN
Alignment Scores:
Pred. No.: 8,246-60 Length: 658
Score: 65.00 Matches: 65
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 19.82% Indels: 0
DB: 6 Gaps: 0
US-09-768-840-1 (1-328) x AX354365 (1-658)
Qy 264 SerGluValGlyHisTrpValLeuProProAlaGlnAspGlnProLeuValGluAlaAsn 283
Db 36 AGTAGAGTGGCCACTGGGTCTGCCCTGCCAGGACCCCTGGTGGAGCAAC 95
Qy 284 HisLeuLeuHisGluSerAspThrAspGlyArgLeuSerLysAlaGluLeuLeu 303
Db 96 CACCTGCTGCACGAGCGACGACGAGCGGCGCTGAGCAACCGGAATCCTG 155
Qy 304 GlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAspLeuThrArg 323
Db 156 GGTAAATGGACATGTTTGGCGCATCGCCACCACTATGTTGAGGACCTGACCCGG 215
Qy 324 HisHisAspGluLeu 328
Db 216 CACCACATGAGCTG 230
RESULT 12
LOCUS BC005487
DEFINITION 1414 bp mRNA linear ROD 07-AUG-2002
ACCESSION IMAGE:3486146, mRNA, partial cds.
VERSION BC005487.1 GI:13529538
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1414)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (27-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer

```

```

REMARK
COMMENT
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcdépa@stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 7 Row: h Column: 5
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis.
FEATURES
source Location/Qualifiers
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/organism="Mus musculus"
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/map="CS7BL/6J"
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old, gross tissue."
/clone_lib="NCI_CGAP_Mam5"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
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VADQDSDMATREELTALHPEEFPHMRDIVVAETLEDKNDGYVQVEYVADLYS
EPPGEEPAWQTERQQFREFRDNLKQDQSDGSEVGYWVLPSPDQPLVEANILHES
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BASE COUNT 422 a 384 c 392 g 216 t
ORIGIN

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Alignment Scores:
Pred. No.: 6,246-51 Length: 1414
Score: 57.00 Matches: 57
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 17.38% Indels: 0
DB: 10 Gaps: 0
US-09-768-840-1 (1-328) x BC005487 (1-1414)

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Qy 148 ProGlyGluGluPheHisAspValGluAspAlaGluThrTyrLysLysMetLeuAlaArg 167
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Qy 168 AspGluArgArgPheArgValAlaAspGlnAspGlyAspSerMetAlaThrArgGluGlu 187
Db 463 GATGAGCGCGATTTCGGGTAGCCGACCAAGATGGGACTCCATGCTACTCGGGAAGAG 522
Qy 188 LeuThrAlaPheLeuHisProGluGluPheProHisMetArgAspIleVal 204
Db 523 CTGACGCGCTTCTGCATCCGAGGAGTTCCTCTACATCGGAGACATCGT 573
RESULT 13
LOCUS BC025602
DEFINITION 1421 bp mRNA linear ROD 07-AUG-2002
Mus musculus, Similar to hypothetical protein LOC57333, clone
MGC:36253 IMAGE:5250505, mRNA, complete cds.

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us-09-768-840-1.0lip2n.rge

Tue May 20 14:43:22 2003

```

ACCESSION BC025602.1 GI:19343897
VERSION BC025602.1
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE Strausberg, R.
AUTHORS Direct Submission
TITLE National Institutes of Health, Mammalian
JOURNAL Submitted (06-MAR-2002) National Institutes of Health, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: gcaps-r@mail.nih.gov
Tissue Procurement: Lohar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nih.gov
Akhter, N., Ayala, R., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Mastello, C., Masker, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 56 Row: 5 Column: 12
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, GenomeScan gene prediction, similarity but not identity
to protein.
FEATURES
Location/Qualifiers
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/organism="Mus musculus"
/db_xref="taxon:10090"
/map="C57BL/6J"
/clone="MGC:36253 IMAGE:5250505"
/tissue_type="Mammary tumor. WAP-TGF alpha model. 7 months
old gross tissue."
/clone_lib="NCI_CGAP_Mam5"
/lab_host="DH10B"
/Note="Vector: pCMV-SPORT6"
76..1062
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YKMLARDERFRVADQGDSDMAPEELTAFLPEEPHMRDVIYVAETLELDKNDKG
YVQVEYIADLYSEEPGEFPANVGTQRFREFDLNKGQDGLDSEGVYWLPPSQD
QPIVEANHLHESDTRKDKSAELNNWNNFVGSQATNYGDLTRHDEL"
BASE COUNT 335 a 414 c 427 g 245 t
ORIGIN
Alignment Scores: 6.27e-51 Length: 1421
Pred. No.: 57 Matches: 57
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 17.38% Indels: 0
Query Match: 10 Gaps: 0
DB:
US-09-768-840-1 (1-328) x BC025602 (1-1421)
QY 148 ProGlyGluGluPheHisAspValGluaspAlaGluThrTyrLysMetLeuAlaarg 167
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517 CCGGAGAGAGAGTTTCATGATGCGGAGATCCGAGACCTACAGAACATGCTGCTGG 576
|||||
168 AspGluArgArgPheArgValAlaAspGlnAspGlyAspSerMetAlaThrArgGluGlu 187
|||||
577 GATGAGCGCGATTCGGGTAGCCGACCAAGATGGCGACTCCATCGCTACTCGGAAGAG 636
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188 LeuThrAlaPheLeuHisProGluGluPheProHisMetArgAspIleVal 204
|||||
637 CTGACGCGCTTCTGATCCGAGGAGATTCCCTCACATCGGGACATCGTG 687
|||||
RESULT 14
AC073763_0
WPCOMMENT
Sequence split into 4 fragments LOCUS AC073763 Accession AC073763
Fragment Name Begin End
AC073763_0 1 110000
AC073763_1 100001 210000
AC073763_2 200001 310000
AC073763_3 300001 409770
LOCUS AC073763 409770 bp DNA linear HTG 29-JUN-2000
DEFINITION Mus musculus clone RP23-343P5, WORKING DRAFT SEQUENCE, 63 unordered
pieces.
ACCESSION AC073763
VERSION AC073763.1 GI:8810380
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Mus musculus.
ORGANISM Mus musculus;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 409770)
DOE Joint Genome Institute.
TITLE Sequencing of Mouse
JOURNAL Unpublished
2 (bases 1 to 409770)
DOE Joint Genome Institute.
REFERENCE Direct Submission
AUTHORS Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 1868949
Center clone name: RPCI-23_343P5
-----
Summary Statistics
Consensus quality: 353352 bases at least Q40
Consensus quality: 382147 bases at least Q30
Consensus quality: 388243 bases at least Q20
Estimated insert size: 217190; agarose-fp estimation
Estimated insert size: 403570; sum-of-contigs estimation
Quality coverage: 8.5 in Q20 bases; agarose-fp estimation
Quality coverage: 4.57 in Q20 bases; sum-of-contigs estimation
NOTE: This is a 'working draft' sequence. It currently
* consists of 63 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1003: contig of 1003 bp in length
* * 1104: gap of unknown length
* * 2382: contig of 1279 bp in length
* * 2483: gap of unknown length
* * 3614: contig of 1132 bp in length

```

```

* 3615 3714: gap of unknown length
* 3715 4723: contig of 1009 bp in length
* 4724 4823: gap of unknown length
* 4824 6292: contig of 1469 bp in length
* 6293 6392: gap of unknown length
* 6393 7431: contig of 1039 bp in length
* 7432 7531: gap of unknown length
* 7532 8859: contig of 1338 bp in length
* 8860 8959: gap of unknown length
* 8960 10066: contig of 1097 bp in length
* 10067 10166: gap of unknown length
* 10167 11248: contig of 1082 bp in length
* 11249 13349: gap of unknown length
* 13349 13441: contig of 1993 bp in length
* 13442 14589: contig of 1148 bp in length
* 14590 14689: gap of unknown length
* 14690 15797: contig of 1108 bp in length
* 15798 15897: gap of unknown length
* 15898 16915: contig of 1018 bp in length
* 16916 18367: contig of 1352 bp in length
* 18368 18468: gap of unknown length
* 18469 19731: contig of 1264 bp in length
* 19732 19831: gap of unknown length
* 19832 20934: contig of 1103 bp in length
* 20935 22011: contig of 1767 bp in length
* 22012 22901: gap of unknown length
* 22902 24723: contig of 1822 bp in length
* 24724 24823: gap of unknown length
* 24824 26095: contig of 1272 bp in length
* 26096 26195: gap of unknown length
* 26196 27347: contig of 1152 bp in length
* 27348 27447: gap of unknown length
* 27448 29537: contig of 2090 bp in length
* 29538 29637: gap of unknown length
* 29638 31063: contig of 1426 bp in length
* 31064 31164: gap of unknown length
* 31165 33463: contig of 2200 bp in length
* 33464 36040: contig of 2577 bp in length
* 36041 36141: gap of unknown length
* 36142 38979: contig of 2839 bp in length
* 38980 42211: gap of unknown length
* 42212 42317: gap of unknown length
* 42318 44053: contig of 1736 bp in length
* 44054 44154: gap of unknown length
* 44155 45760: contig of 1607 bp in length
* 45761 45860: gap of unknown length
* 45861 48398: contig of 2538 bp in length
* 48399 52535: gap of unknown length
* 52536 52635: contig of 4037 bp in length
* 52636 56329: gap of unknown length
* 56330 56429: contig of 3694 bp in length
* 56430 60257: gap of unknown length
* 60258 60357: gap of unknown length
* 60358 63458: contig of 3101 bp in length
* 63459 63558: gap of unknown length
* 63559 66742: contig of 3184 bp in length
* 66743 66842: gap of unknown length
* 66843 69475: contig of 2633 bp in length
* 69476 69575: gap of unknown length
* 69576 73406: contig of 3831 bp in length
* 73407 73506: gap of unknown length
* 73507 77765: contig of 4259 bp in length
* 77766 77865: gap of unknown length
* 77866 82516: contig of 4651 bp in length
* 82517 82617: gap of unknown length
* 82618 88124 88223: gap of unknown length

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* 88224 93473: contig of 5250 bp in length
* 93474 95573: gap of unknown length
* 95574 98553: contig of 5080 bp in length
* 98554 98753: gap of unknown length
* 98754 103469: contig of 4716 bp in length
* 103470 103569: gap of unknown length
* 103570 109147: contig of 5578 bp in length
* 109148 109247: gap of unknown length
* 109248 116537: contig of 7290 bp in length
* 116538 124186: contig of 7549 bp in length
* 124187 124286: gap of unknown length
* 124287 132204: contig of 7918 bp in length
* 132205 132304: gap of unknown length
* 132305 140886: contig of 8582 bp in length
* 140887 140986: gap of unknown length
* 140987 151061: contig of 10075 bp in length
* 151062 151161: gap of unknown length
* 151162 159241: contig of 8080 bp in length
* 159242 159341: gap of unknown length
* 159342 167120: contig of 7779 bp in length
* 167121 167220: gap of unknown length
* 167221 178631: contig of 11411 bp in length
* 178632 178731: gap of unknown length
* 178732 190111: contig of 11380 bp in length
* 190112 190211: gap of unknown length
* 190212 201488: contig of 11277 bp in length
* 201489 212958: contig of 11370 bp in length
* 212959 213058: gap of unknown length
* 213059 227047: contig of 13989 bp in length
* 227048 227147: gap of unknown length
* 227148 241205: contig of 14058 bp in length
* 241206 241305: gap of unknown length
* 241306 258822: contig of 17517 bp in length
* 258823 258922: gap of unknown length
* 258923 277362: contig of 18340 bp in length
* 277363 277462: gap of unknown length
* 277463 299258: contig of 21896 bp in length
* 299259 299358: gap of unknown length
* 299359 321207: contig of 21849 bp in length
* 321208 321307: gap of unknown length
* 321308 342521: contig of 21214 bp in length
* 342522 342621: gap of unknown length
* 342622 374406: contig of 31785 bp in length
* 374407 374506: gap of unknown length
* 374507 409770: contig of 35264 bp in length.

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FEATURES

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1. 409770
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-343P5"
/culture_lib="RPECI mouse BAC library 23"

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BASE COUNT 98446 a 106220 c 104553 g 94328 t 6223 others
ORIGIN

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Alignment Scores:

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Pred. No.: 3 76e-49 Length: 110000
Score: 57.00 Matches: 57
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 17.38% Indels: 0
DB: 2 Gaps: 0

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US-09-768-840-1 (1-328) x AC073763_0 (1-110000)

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Qy 148 ProGlyGluGluPheHisAspValGluAspAlaGluThrTyrLysLysMetLeuAlaArg 167
Db 73051 CCAGGAGAGGAGTTTCATGATGTGGAGATGCCGAGACCTACAGAGAGATGCTGGCTCGG 73110
Qy 168 AspGluArgArgPheArgValAlaAspGlnAspGlyAspSerMetAlaThrArgGluGlu 187
Db 73111 GATGAGCGCGGATTCGGGTAGCCGACCAAGATGGCGACTCCATGGCTACTCGGGAAGAG 73170

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Tue May 20 14:43:22 2003

COMMENT

On Jul 11, 2002 this sequence version replaced gi:17973707.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: G1A
Center clone name: CH230-58K9
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; Version 0.990329
Consensus quality: 72324 bases at least Q40
Consensus quality: 75885 bases at least Q30
Consensus quality: 78825 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 76 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1262: contig of 1262 bp in length
1362: gap of unknown length
2553: contig of 1191 bp in length
2653: gap of unknown length
3757: contig of 1104 bp in length
3857: gap of unknown length
4985: contig of 1128 bp in length
5085: gap of unknown length
5664: contig of 1379 bp in length
6465: gap of unknown length
7627: contig of 1063 bp in length
7727: gap of unknown length
9254: contig of 1527 bp in length
9354: gap of unknown length
10426: contig of 1072 bp in length
10526: gap of unknown length
12189: contig of 1663 bp in length
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13535: contig of 1246 bp in length
13635: gap of unknown length
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14981: gap of unknown length
16019: contig of 1038 bp in length
16119: gap of unknown length
17874: contig of 1755 bp in length
17974: gap of unknown length
19443: contig of 1469 bp in length
19543: gap of unknown length
20718: contig of 1175 bp in length
20818: gap of unknown length
21845: contig of 1027 bp in length
21945: gap of unknown length
23218: contig of 1273 bp in length
23318: gap of unknown length
24738: contig of 1420 bp in length
24739: gap of unknown length
24838: gap of unknown length
25907: contig of 1069 bp in length
26007: gap of unknown length
27565: contig of 1558 bp in length
27665: gap of unknown length
29113: contig of 1448 bp in length
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30466: contig of 1253 bp in length
30567: gap of unknown length
31810: contig of 1244 bp in length
31910: gap of unknown length

Qy 188 LeuThralAlphaLeuHisProGluCluPheProHisMetargAspIleVal 204
|||||
Db 73171 CTGACGGCCTTTCGATCCGAGGAGTTCCTCACATCGGAGCAGTCG 73221

RESULT 15
AC099450 161995 bp DNA linear HTG 12-JUL-2002
LOCUS Rattus norvegicus clone CH230-58K9, *** SEQUENCING IN PROGRESS ***,
DEFINITION 76 unordered pieces.
AC099450
AC099450.3 GI:21729730
VERSION HTG; HTGS_PHASE1.
KEYWORDS Norway rat.
SOURCE Rattus norvegicus

ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

1 (bases 1 to 161995)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Albrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbata,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brleva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.B., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,K., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Douthey,K.R., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hogue,M., Holloway,C., Hollins,B.,
Homs,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlovic,J., Kureishi,A., Landry,N., Leal,B., Lewis,L., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieut,C., Liu,J., Liu,W., Louised,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Martindale,A., Martinez,E.,
Maheshwari,M., Mapua,P., Martin,R., Meador,M., Mel,G., Metzker,M.,
Massey,E., Mawhiney,E., McLeod,M.P., Morgan,M., Morris,S.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Nguyen,N.,
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Ogih,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savory,G.,
Scherer,S., Scott,G., Shen,H., Shoostari,N., Sisson,I.,
Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Umani,K., Vasquez,L., Vera,V., Villalobos,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczyk,R., Woodson,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 161995)
Worley,K.C.
Direct Submission
Submitted (15-NOV-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 161995)
Worley,K.C.
Direct Submission
Submitted (12-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

* 31911	33117: contig of 1207 bp in length
* 33118	33217: gap of unknown length
* 33218	34746: contig of 1529 bp in length
* 34747	34846: gap of unknown length
* 34847	35894: contig of 1048 bp in length
* 35895	35994: gap of unknown length
* 35995	37035: contig of 1041 bp in length
* 37036	37135: gap of unknown length
* 37136	38560: contig of 1425 bp in length
* 38561	38660: gap of unknown length
* 38661	40269: contig of 1609 bp in length
* 40270	40369: gap of unknown length
* 40370	41831: contig of 1462 bp in length
* 41832	41931: gap of unknown length
* 41932	43245: contig of 1314 bp in length
* 43246	43345: gap of unknown length
* 43346	44723: contig of 1378 bp in length
* 44724	44823: gap of unknown length
* 44824	45957: contig of 1134 bp in length
* 45958	46057: gap of unknown length
* 46058	47129: contig of 1072 bp in length
* 47130	47229: gap of unknown length
* 47230	48635: contig of 1406 bp in length
* 48636	48735: gap of unknown length
* 48736	50416: contig of 1681 bp in length
* 50417	50516: gap of unknown length
* 50517	51629: contig of 1113 bp in length
* 51630	51729: gap of unknown length
* 51730	53142: contig of 1413 bp in length
* 53143	53242: gap of unknown length
* 53243	54385: contig of 1153 bp in length
* 54396	54495: gap of unknown length
* 54496	56434: contig of 1939 bp in length
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* 57598	57697: gap of unknown length
* 57698	59050: contig of 1353 bp in length
* 59051	59150: gap of unknown length
* 59151	60201: contig of 1051 bp in length
* 60202	60301: gap of unknown length
* 60302	61686: contig of 1385 bp in length
* 61687	61786: gap of unknown length
* 61787	63721: contig of 1935 bp in length
* 63722	63821: gap of unknown length
* 63822	65638: contig of 1817 bp in length
* 65639	65738: gap of unknown length
* 65739	67435: contig of 1697 bp in length
* 67436	67535: gap of unknown length
* 67536	69342: contig of 1807 bp in length
* 69343	69442: gap of unknown length
* 69443	71340: contig of 1898 bp in length
* 71341	71440: gap of unknown length
* 71441	72903: contig of 1463 bp in length
* 72904	73003: gap of unknown length
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* 74448	74547: gap of unknown length
* 74548	77270: contig of 2723 bp in length
* 77271	77370: gap of unknown length
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* 79579	79778: gap of unknown length
* 79779	82673: contig of 2895 bp in length

Alignment Scores:

Pred. No.:	5,41e-49	Length:	161995
Score:	57.00	Matches:	57
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	17.38%	Indels:	0
DB:	2	Gaps:	0

US-09-768-840-1 (1-328) x AC099450 (1-161995)

Qy 148 ProGlyGluGluPheHisAspValGluAlaGluThrTyLysLysMetLeuAlaArg 167

Db 22144	CCAGGGGAGGANTTTCATGATGTGGAGGATGCCGAGACTTACAGAAGATGCTGGCTCGG	22203
Qy 168	AspGluArgArgPheArgValAlaAspGlnAspGlyAspSerMetAlaThrArgGluGlu	187
Db 22204	GATCAGCGCGGATTCGGGTAGCTGACCAAGATGGGGACTCCATGGCTACTCGGGAAGAG	22263
Qy 188	LeuThrAlaPheLeuHisProGluGluPheProHisMetArgAspIleVal	204
Db 22264	CTACGGCCCTTCTGCATCCTGAGGAGTTCCCTCACAATCGGGACATCGTG	22314

Search completed: May 20, 2003, 08:33:08
Job time : 3556 secs

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GenCore version 5.1.4.p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 19, 2003, 22:09:52 ; Search time 293 seconds
(without alignments)
2521.008 Million cell updates/sec

Title: US-09-768-840-1
Perfect score: 328
Sequence: 1 MWRPVSLLLLLLRHCAQG.....FVGSQATNYGDLTRHDEL 328

Scoring table: OLIGO

Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 112599159 residues

Word size: 1

Total number of hits satisfying chosen parameters: 4368709

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters: -DEV-xlh

-Q/cgn2.1/USPTO.spool/US09768840/runat_14052003_095831_17355/app_query.fasta_1.519
-DB-N_Geneseq_101002 -QFWT-fastap -SUFFIX-olip2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=plc -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER-US09768840.ecgn_1.1.263/runat_14052003_095831_17355 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGESQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : N_Geneseq_101002.*

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2: /SID52/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
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23: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SID52/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	328	100.0	1055	19	Human calcium-bind
2	328	100.0	1055	22	Human calcium-bind
3	328	100.0	1463	20	Human reticulocalb
4	328	100.0	1503	20	Protein PRO272 cDN
5	328	100.0	1503	21	Human PRO272 prote
6	328	100.0	1503	22	Human cDNA sequenc
7	328	100.0	1503	22	Human PRO272 cDNA
8	328	100.0	1503	22	Human anglogenesis
9	328	100.0	1542	21	cDNA encoding a bo
10	300	91.5	1507	20	Human secreted pro
11	300	91.5	1507	24	Human colon cancer
12	300	91.5	1507	24	Human colon cancer
13	249	75.9	1480	22	Human polynucleoti
14	249	75.9	1480	22	Human polynucleoti
15	249	75.9	1480	22	Human polynucleoti
16	180	54.9	1487	22	DNA encoding nove
17	140	42.7	586	20	Human colon cancer
18	99	30.2	300	20	Human secreted pro
19	89	27.1	352	20	Human gene express
20	65	19.8	431	24	Human secreted pro
21	65	19.8	658	24	Human ovarian canc
22	37	11.3	448	24	Human colon cancer
23	26	7.9	140	20	Human ovarian canc
24	21	6.4	65	24	Human secreted pro
25	19	5.8	60	24	Rat spliced transc
26	18	5.5	408	24	Human spliced tran
27	18	5.5	411	24	Human colon cancer
28	18	5.5	501	24	Human colon tumour
29	18	5.5	2055	24	Breast cancer rela
30	18	5.5	2104	24	Human ovarian anti
31	18	5.5	2104	24	Human benign prost
32	18	5.5	2358	22	Human adenocarcino
33	17	5.2	74	22	Human cervical can
34	11	3.4	373	22	Colon tumour relat
35	11	3.4	374	22	Novel human polynu
36	10	3.0	331	22	Human secreted pro
37	10	3.0	399	21	Human secreted pro
38	10	3.0	399	21	Human 5' EST isola
39	10	3.0	550	22	Human EST-derived
40	10	3.0	569	24	Oligonucleotide fo
41	10	3.0	569	24	Oligonucleotide fo
42	10	3.0	651	19	Nucleotide sequenc
43	10	3.0	878	22	Primer specific fo
44	10	3.0	1401	19	Human T1 receptor-
45	10	3.0	1408	19	Nucleotide sequenc

ALIGNMENTS

RESULT 1
AAV57600
ID AAV57600 standard; cDNA; 1055 BP.

XX AAV57600;

AC AAV57600;

DT 15-DEC-1998 (first entry)

XX Human calcium-binding protein encoding cDNA.

DE Human; calcium-binding protein; reticulocalbin; sickle cell anaemia;
KW HCBP; beta thalassaemia; cell proliferation; cancer; adenocarcinoma;
KW Leukemia; lymphoma; melanoma; sarcoma; ss.

XX Homo sapiens.

OS Homo sapiens.

XX Key

FT CDS

Location/Qualifiers
34..1020

101	Qy	GluLeuArgAlaTrrpIleAlaHisThrGlnGlnArgHisIleArgAspSerValSerAla	120
102			
103			
104			
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121	Qy	AlaTrpAspThrTyrAspThrAspArgAspGlyValArgValGlyTrpGluGluLeuArgAsn	140
122			
123			
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141	Qy	AlaThrTyrGlyHisTyrAlaProGlyGluGluPheHisAspValGluAspAlaGluThr	160
142			
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160			
161	Qy	TyrLysLysMetLeuAlaArgAspGluArgPheArgValalaAspGlnAspGlyAsp	180
162			
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177			
178			
179			
180			
181	Qy	SerMetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMet	200
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201	Qy	ArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrVal	220
202			
203			
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205			
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217			
218			
219			
220			
221	Qy	GlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGluGluProAla	240
222			
223			
224			
225			
226			
227			
228			
229			
230			
231			
232			

mumps, rhinovirus, poliovirus, coxsackie-virus, smallpox, Colorado tick fever, HIV, rabies, gastroenteritis, and rubella, encephalitis, and bacterial, fungal, parasitic, protozoal, or helminthic infections. Development disorders include e.g. renal tubular acidosis, anaemia, Cushing's syndrome, achondroplastic dwarfism, epilepsy, gonadal dysgenesis, hereditary neuropathies such as Charcot-Marie-Tooth disease, and neurofibromatosis, hypothyroidism, hydrocephalus, seizure disorders such as Sydenham's chorea and cerebral palsy, spinal bifida, and congenital glaucoma, cataract, or sensorineural hearing loss. Neoplastic disorders include e.g. adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma and teratocarcinoma. Overexpression of reticulocalbin mRNA has been associated with increased matrix invasive properties of human breast cancer lines.

XX 210 A. 159 C. 478 G. 215 T; 1 other;
XX 210 A. 159 C. 478 G. 215 T; 1 other;

Alignment Scores:	8,46e-290	Length:	1463
Pred. No.:	328.00	Matches:	328
Score:	100.00%	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	20	Gaps:	0
DB			

--- 22 550 840-1 /1-328) x AAX27229 (1-1463)

[illegible]

QY	241	TtpValGlnThrGluArgGlnInPnearGasPrmenTg	
Dd	769	TGGGTGCAGACGAGCAGCTCCGGGACTTCGGGATCTGAACRAGGATGGGCAC	828
QY	261	LeuAspGlySerGluValGlyHisTrpValLeuProAlaGlnAspGlnProLeuVal	280
Dd	829	CTGGATGGGAGTGAGTTGGGCCACTGGTGTGCCCCCTGCCCAGGACCAGCCCCTGGTG	888
QY	281	GluAlaAsnHisLeuLeuHisGlusErAspThrAspLysAspGlyArqLeuSerLysAla	300
Dd	889	GAAGCAACACCCCTGCTGCACGAGACGACCGAACAAGGATGGCGCTGACGAAAGCG	948
QY	301	GluIleuGluValAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrglyGluAsp	320
Dd	949	GAATCTCTGGGTAAATTGGACATGTTTGTGGCAGTCTCAGGCCACCACTATGGCGAGGAC	1008
QY	321	LeuThrArgHisHisaspGluLeu	328
Dd	1009	CTGACCCGGCACCAACCATGAGCTG	1032
RESULT 4			
ID	AAx52253	standard; DNA; 1503 BP.	
XX	AAx52253;		
XX		(first entry)	
DE	Protein PR0272	CDNA clone DNA040620-1183.	
KW	Secreted protein; transmembrane protein; human; enterocolitis;		
KW	Zollinger-Ellison syndrome; gastrointestinal ulceration;		
KW	congenital microvillus atrophy; skin disease; cell growth;		
KW	abnormal keratinocyte differentiation; psoriasis; epithelial cancer;		
KW	Parkinson's disease; Alzheimer's disease; ALS; neuropathy;		
KW	fibrinomodulin; dermal scarring; Usher Syndrome; Atrophia areata;		
KW	anti-thrombotic; wound healing; tissue repair; ss.		
OS	Homo sapiens.		
PN	WO9914328-A2.		
PD	25-MAR-1999.		
PF	16-SEP-1998;	98WO-US19330.	
PR	25-NOV-1997;	97US-0066840.	
PR	17-SEP-1997;	97US-0059113.	
PR	17-SEP-1997;	97US-0059115.	
PR	17-SEP-1997;	97US-0059117.	
PR	17-SEP-1997;	97US-0059119.	
PR	17-SEP-1997;	97US-0059121.	
PR	17-SEP-1997;	97US-0059122.	
PR	17-SEP-1997;	97US-0059124.	
PR	18-SEP-1997;	97US-0059263.	
PR	15-OCT-1997;	97US-0062125.	
PR	17-OCT-1997;	97US-0062285.	
PR	21-OCT-1997;	97US-0063486.	
PR	24-OCT-1997;	97US-0082814.	
PR	24-OCT-1997;	97US-0082816.	
PR	24-OCT-1997;	97US-0083045.	
PR	24-OCT-1997;	97US-0063120.	
PR	24-OCT-1997;	97US-0063121.	
PR	24-OCT-1997;	97US-0063127.	
PR	24-OCT-1997;	97US-0063128.	
PR	27-OCT-1997;	97US-0063329.	
PR	27-OCT-1997;	97US-0063327.	
PR	28-OCT-1997;	97US-0063541.	
PR	28-OCT-1997;	97US-0063542.	
PR	28-OCT-1997;	97US-0063544.	

XX	Homo sapiens.
OS	WO200104311-AI.
PN	18-JAN-2001.
XX	
PD	
XX	
PF	22-FEB-2000; 2000WO-US04414.
XX	
PR	07-JUL-1999; 99US-0143048.
XX	26-JUL-1999; 99US-0145698.
PR	28-JUL-1999; 99US-0146222.
PR	08-SEP-1999; 99WO-US20594.
PR	13-SEP-1999; 99WO-US20944.
PR	15-SEP-1999; 99WO-US21090.
PR	15-SEP-1999; 99WO-US21547.
PR	05-OCT-1999; 99WO-US23089.
PR	29-NOV-1999; 99WO-US28214.
PR	30-NOV-1999; 99WO-US28313.
PR	16-DEC-1999; 99WO-US30911.
PR	20-DEC-1999; 99WO-US30915.
PR	20-DEC-1999; 99WO-US30999.
PR	05-JAN-2000; 99WO-US00219.
XX	(GETH) GENENTECH INC.
PA	Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI	Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI	Gadowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin LJ;
PI	Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI	Williams PM, Wood WI;
XX	WPI: 2001-081051/09.
DR	P-PSDB; AAB80250.
XX	Sixty one nucleic acids encoding PRO polypeptides which are useful in the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's disease).
PT	Claim 2; Fig 79; 393pp; English.
XX	The present sequence is one of sixty one nucleic acids encoding novel secreted and transmembrane PRO polypeptides. The PRO polypeptides are useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders (e.g. enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair, cardiovascular disorders (e.g. endometrial bleeding angiogenesis, ischaemias such as coronary C C ischaemia, atherosclerosis), inflammatory disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis), infertility, AIDS and C C diabetes and retinal disorders such as retinitis pigmentosa.
CC	The PRO nucleic acids have applications in molecular biology, including C C use as hybridization probes, and in chromosome and gene mapping.
XX	Sequence 1503 BP; 357 A; 456 C; 474 G; 216 T; 0 other;
SQ	
Alignment Scores:	
Pred. No.:	8,67e-290 Length: 1503
Score:	328.00 Matches: 328
Percent Similarity:	100.00% Conservative: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	100.00% Indels: 0
DB:	22 Gaps: 0
US-09-768-840-1 (1-328) x AAF72411 (1-1503)	
Qy	1 MetMetTrrPargProSerValLeuLeuLeuLeuLeuLeuAArgHisGlyAlaGlnGly 20
Db	35 ATGATGGGGACCATCAGTTCTGCTTCCTGTACTGTAGGCACGCCCGAGGG 94
Oy	21 LysProSerProAspAlaGlyProHisGlyClnGlyArgValHisGlnAlaLaProLeu 40

QY	281	GIuAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla	300
Db	875	GRAGCCACCACCTGCTGTCACGAGAGCGACACGGACAAGATGGCGCTGAGCAAAAGCG	934
QY	301	GIuIleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAsp	320
			994

Alignment Scores:

Qy	321	LeuThrArgHisHisAspGluLeu	328
Db	995	CTGACCCGGCACCATGATGCTG	1018
RESULT 9			
AAZ36246			
IN AAZ36246 standard; CDNA; 1542 BP.			

AA236246;
22-FEB-2000 (first entry)
... secreting protein designated BMS37.

XX	22-FEB-2000 (first entry)	
DT		
XX		
XX		
DE		
XX		
XX		
KW	CDNA encoding a bone marrow secreted protein designated BMS37.	
KW		
KW	Bone marrow secreted protein; bone marrow stromal cell; cytokine;	
KW	cell proliferation; cell differentiation; hematopoiesis; anaemia;	
KW	myeloid cell deficiency; lymphoid cell deficiency; myeloid cell;	
KW	erythroid progenitor cell; colony stimulating factor; granulocyte;	
KW	monocyte; macrophage; myelo-suppression; megakaryocyte; platelet;	
KW	platelet disorder; thrombocytopenia; hematopoietic stem cell;	
KW	stem cell disorder; aplastic anaemia; bone differentiation;	
KW	paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon;	
KW	ligament; nerve; wound healing; tissue repair; burn; incision; ulcer;	
KW	bone fracture; cartilage damage; artificial joint; ss.	
XX		
OS	Homo sapiens.	
XX		
XX		
FH	Location/Qualifiers	
DE	121..1107	
FT	/*tag= a	
FT	/product= "bone marrow secreted protein"	
FT	121..180	
FT	/tag= b	
FT	polyA_signal	
FT	1508..1513	
FT	/tag= c	
XX		
PN	W09333979-A2.	
XX		
XX		
PD	08-JUL-1999.	
XX		
XX	18-DEC-1998; 98WO-US27008.	
XX		
XX	30-DEC-1997; 97US-0068958.	
PR	24-SEP-1998; 98US-0101603.	
PR	30-SEP-1998; 98US-0102540.	
XX		
XX	(CHIR) CHIRON CORP.	
PA		
XX		
PI	Lin H, Cao L;	
XX		
XX	WPI; 2000-038344/03.	
DR	P-PSDB; AAY3640.	
DR		
XX		
XX	New isolated human polynucleotide and secreted proteins can induce	
PT	production of other cytokines in certain cell populations -	
XX		
XX	Claim 11; Page 112-113; 120pp; English.	
XX		
XX	AAZ36228-49 encode bone marrow secreted proteins of human bone marrow	
CC	stromal cells. The proteins can exhibit cytokine, cell proliferation, or	
CC	cell differentiation activity (either inducing or inhibiting). They can	
CC	be used to support colony forming cells or factor-dependent cell lines,	
CC	to regulate hematopoiesis, and to treat myeloid or lymphoid cell	
CC	deficiencies. In addition, they may be used to support the growth and	

proliferation of erythroid progenitor cells, and to treat various anemias. They can have colony stimulating factor (CSF) activity and can be used to support the growth and proliferation of myeloid cells such as granulocytes, monocytes or macrophages, to prevent or treat myelo-suppression, to support the growth and proliferation of megakaryocytes and platelets, thereby allowing prevention of platelet disorders such as thrombocytopenia, and to support the growth and proliferation of hematopoietic stem cells, to support the growth in conjunction with platelet transfusions to treat stem cell disorders, such as aplastic anemia and paroxysmal nocturnal hemoglobinuria, or to repopulate the stem cell compartment after irradiation or chemotherapy. They can be used for growth or differentiation of bone, cartilage, tendon, ligament, or nerve tissue, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers, to induce cartilage and/or bone growth in circumstances where bone is not normally formed and thus have an application in healing bone fractures and cartilage damage or defects, prophylactic use in fracture reduction and also in the improved fixation of artificial joints.

Sequence 1542 BP; 321 A; 506 C; 475 G; 240 T; 0 other;

Alignment Scores:

Pred. No.:	8,886-290	Length:	1542
Score:	328.00	Matches:	328
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	21	Gaps:	0

JS-09-768-840-1 (1-328) x AA236246 (1-1542)

[illegible]

Db	721	CGGGACATCGGTGATTGCTGAACACCTGGAGCACTGGACAGAACAAGATGGCTATGTC	780
Qy	221	GlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGluGluProAla	240
Db	781	CAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGAGGAGGAGCGGCG	840
Qy	241	TrpValGlnThrGluArgGlnGlnPheArgAspPheArgAspLeuAsnLysAspGlyHis	260
Db	841	TGGGTGCAGACGGAGAGCGACAGTTCGCGGACTTCGCGGATCTGCACAGGATGGGCAC	900
Qy	261	LeuAspGlySerGluValGlyHisTyrValLeuProProAlaGlnAspClnProLeuVal	280
Db	901	CTGGATGGGAGTGGAGTGGGCCACTGGGTGCTGCCCCCTGCCAGGACACGCCCTGGTG	960
Qy	281	GLUALAAsnHisLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla	300
Db	961	GAGCCCAACCCCTGCTGCACGAGACGACACGACAGGATGGCGCTGAGCAAGACG	1020
Qy	301	GLuIleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAsp	320
Db	1021	GAATCTGGGTAAATTGGAACATGTTCTGGGCAGTCAAGCCCAACTATGGCGAGGAC	1080
Qy	321	LeuThrArgHisHisAspGluLeu	328
Db	1081	CTGACCGGCACCATGATGAGCTG	1104
RESULT 10			
AAAX00656			
XX	ID	AAAX00656 standard; DNA; 1507 BP.	
XX	AC	AAAX00656;	
XX	CC		
XX	DT	25-MAR-1999 (first entry)	
XX	DE	Human secreted protein gene 46 clone HSJBQ79.	
XX	KW	Human; secreted protein; fusion protein; gene therapy; protein therapy;	
XX	KW	diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukæmia;	
XX	KW	developmental abnormality; foetal deficiency; blood; allergy; renal; ds	
XX	KW	immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;	
XX	KW	inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;	
XX	KW	cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;	
XX	KW	osteoporosis; arthritis; testis; lung; thyroiditis; thyroïd; digestion;	
XX	KW	endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.	
XX	OS	Homo sapiens.	
XX	PN	WO9842738-A1.	
XX	PD	01-OCT-1998.	
XX	PF		
XX	PE	19-MAR-1998; 98WO-US05311.	
XX	PR	30-MAY-1997; 97US-0050937.	
XX	PR	21-MAR-1997; 97US-0041276.	
XX	PR	21-MAR-1997; 97US-0041277.	
XX	PR	21-MAR-1997; 97US-0041281.	
XX	PR	21-MAR-1997; 97US-0042344.	
XX	PR	30-MAY-1997; 97US-0048069.	
XX	PR	30-MAY-1997; 97US-0048094.	
XX	PR	30-MAY-1997; 97US-0048095.	
XX	PR	30-MAY-1997; 97US-0048096.	
XX	PR	30-MAY-1997; 97US-0048099.	
XX	PR	30-MAY-1997; 97US-0048131.	
XX	PR	30-MAY-1997; 97US-0048135.	
XX	PR	30-MAY-1997; 97US-0048154.	
XX	PR	30-MAY-1997; 97US-0048160.	
XX	PR	30-MAY-1997; 97US-0048186.	
XX	PR	30-MAY-1997; 97US-0048187.	
XX	PR	30-MAY-1997; 97US-0048188.	
XX	PR	30-MAY-1997; 97US-0048350.	
XX	PR	30-MAY-1997; 97US-0048351.	

[illegible]

Db	414	GCCTGGGACACGTACGACACGGACCGCGCGTGTGGTGTGGAGGAGCTGGCGAAC	473
Qy	141	AlaThrTyrGlyHisTyrAlaProGlyGluGluPheHisAspValGluAspAlaGluThr	160
Db	474	GCCACCTATGGCCACTACGCGCCCGGTGAAGAATTTTCATGACGTGGAGATGACAGACC	533
Qy	161	TyrIleSlyMetLeuAlaArgAspGluArgPheArgValAlaAspGlnAspGlyAsp	180
Db	534	TACAAAAAGATGCTGGCTCGGAGGACGGCGTTCGGGTGGCCGACCAAGATGGGGAC	593
Qy	181	SerMetAlaThrArgGluLeuThrAlaPheLeuHisProGluGluPheProHisMet	200
Db	594	TCGATGCCACTCGAGGAGAGCTGACAGCCTTCCTGCACCCGAGGAGTCCCTCACATG	653
Qy	201	ArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgHisAspGlyTyrVal	220
Db	654	CGGACATCGTGTTCCTGAACCCCTGGAGGACCTGGACAGAACAAAGATGGCTATGTC	713
Qy	221	GlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGluProAla	240
Db	714	CAGGTGGAGGAGTACATCGCGGATCTGTACTACGCGAGCCTGGGGAGGAGCGCGG	773
Qy	241	TrpValGlnThrGluArgGlnGlnPheArgAspPheArgAspLeuAsnLysAspGlyHis	260
Db	774	TGGGTGCACAGCGAGAGCGACAGTTCGGGACTTCCGGGATCTGAACAAGGATGGCAC	833
Qy	261	LeuAspGlySerGluValGlyHisTyrPheValLeuProPheAlaGlnAspGlnProLeuVal	280
Db	834	CTGGATGGGAGTGAGTGGCCACTGGGTGCTGCCCTGCCAGGACCCAGCCCTGGTG	893
Qy	281	GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla	300
Db	894	GAAGCCAAACACCTCTGCAGCAGAGCGACACGACAGGATGGGCGGCTGAGCAAGCG	953
Qy	301	Glu-IleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAs	320
Db	954	SA-AATCCTGGGTAAATTGAACATGTTTGTGGCAGTCAGGCCACCACTATGGYGAGGA	1012
Qy	320	pLeuThrArgHisHisAspGluLeu	328
Db	1013	CCTGACCGCGCACCATGAGCTG	1037
RESULT 11			
AA141601			
ID	AA141601	standard; cdNA; 1507 BP.	
AC	AA141601;		
XX			
DT	19-APR-2002	(first entry)	
DE		Human colon cancer related coding sequence SEQ ID NO: 12.	
KW		Human; colon cancer; cytostatic; drug design; adenomatous polyp;	
KW		colorectal carcinoma; high metastatic potential colon tumour;	
KW		metastatic colon cancer; gene; ss.	
XX		Homo sapiens.	
OS			
XX		WO200196523-A2.	
PN		20-DEC-2001.	
XX		15-JUN-2001; 2001WO-US19313.	
PF		15-JUN-2000; 2000US-211835P.	
XX		(CHIR) CHIRON CORP.	
PA		Kennedy GC, Kang S, Reinhard C, Jefferson AB;	
XX		WPI; 2002-164362/21.	
DR		Detecting a cancerous colon cell, useful for diagnosing colon cancer	
PT			

ore: 300.00
Matches: 327

[illegible]

[illegible]

PR	27-SEP-2000;	2000US-0235833.
PR	27-SEP-2000;	2000US-0235836.
PR	29-SEP-2000;	2000US-0236327.
PR	29-SEP-2000;	2000US-0236367.
PR	29-SEP-2000;	2000US-0236368.
PR	29-SEP-2000;	2000US-0236369.
PR	29-SEP-2000;	2000US-0236370.
PR	02-OCT-2000;	2000US-0236802.
PR	02-OCT-2000;	2000US-0237037.
PR	02-OCT-2000;	2000US-0237038.
PR	02-OCT-2000;	2000US-0237039.
PR	13-OCT-2000;	2000US-0237040.
PR	13-OCT-2000;	2000US-0239935.
PR	13-OCT-2000;	2000US-0239937.
PR	20-OCT-2000;	2000US-0240960.
PR	20-OCT-2000;	2000US-0240960.
PR	20-OCT-2000;	2000US-0241121.
PR	20-OCT-2000;	2000US-0241125.
PR	20-OCT-2000;	2000US-0241786.
PR	20-OCT-2000;	2000US-0241787.
PR	20-OCT-2000;	2000US-0241808.
PR	20-OCT-2000;	2000US-0241809.
PR	01-NOV-2000;	2000US-0241826.
PR	01-NOV-2000;	2000US-0244617.
PR	08-NOV-2000;	2000US-0246474.
PR	08-NOV-2000;	2000US-0246475.
PR	08-NOV-2000;	2000US-0246476.
PR	08-NOV-2000;	2000US-0246477.
PR	08-NOV-2000;	2000US-0246478.
PR	08-NOV-2000;	2000US-0246523.
PR	08-NOV-2000;	2000US-0246524.
PR	08-NOV-2000;	2000US-0248525.
PR	08-NOV-2000;	2000US-0248526.
PR	08-NOV-2000;	2000US-0248527.
PR	08-NOV-2000;	2000US-0248528.
PR	08-NOV-2000;	2000US-0248532.
PR	08-NOV-2000;	2000US-0246609.
PR	08-NOV-2000;	2000US-0246610.
PR	08-NOV-2000;	2000US-0246611.
PR	17-NOV-2000;	2000US-0246613.
PR	17-NOV-2000;	2000US-0249207.
PR	17-NOV-2000;	2000US-0249208.
PR	17-NOV-2000;	2000US-0249209.
PR	17-NOV-2000;	2000US-0249210.
PR	17-NOV-2000;	2000US-0249211.
PR	17-NOV-2000;	2000US-0249212.
PR	17-NOV-2000;	2000US-0249213.
PR	17-NOV-2000;	2000US-0249214.
PR	17-NOV-2000;	2000US-0249215.
PR	17-NOV-2000;	2000US-0249216.
PR	17-NOV-2000;	2000US-0249217.
PR	17-NOV-2000;	2000US-0249218.
PR	17-NOV-2000;	2000US-0249244.
PR	17-NOV-2000;	2000US-0249245.
PR	17-NOV-2000;	2000US-0249264.
PR	17-NOV-2000;	2000US-0249265.
PR	17-NOV-2000;	2000US-0249297.
PR	17-NOV-2000;	2000US-0249299.
PR	01-DEC-2000;	2000US-0249300.
PR	01-DEC-2000;	2000US-0250160.
PR	05-DEC-2000;	2000US-0250399.
PR	05-DEC-2000;	2000US-0251030.
PR	05-DEC-2000;	2000US-0251988.
PR	06-DEC-2000;	2000US-0256719.
PR	08-DEC-2000;	2000US-0251479.
PR	08-DEC-2000;	2000US-0251856.
PR	08-DEC-2000;	2000US-0251866.
PR	08-DEC-2000;	2000US-0251869.
PR	08-DEC-2000;	2000US-0251989.
PR	11-DEC-2000;	2000US-0251990.
PR	05-JAN-2001;	2000US-0259678.
XX		(HUMA-) HUMAN GENOME SCING.
PA		

XX
FI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-463568/50.
XX P-PSDB; AAU19946.
XX
XX Isolated nucleic acid molecule encoding a calcium-binding protein is
XX used in preventing, treating or ameliorating a medical condition -
XX
XX Claim 4; SEQ ID No 65; 542pp; English.
XX
XX The present invention relates to the isolation of novel human
XX calcium-binding proteins (AAU19892-AAU19965), and cDNA and genomic
XX sequences encoding for these proteins. The sequences of the invention
XX are useful in the diagnosis, prevention and/or prognosis of diseases
XX associated with aberrant calcium flux. Such disorders include
XX neurological diseases (e.g. amyotrophic lateral sclerosis, ALS),
XX immune dysfunction (e.g. severe combined immunodeficiency, SCID),
XX digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic
XX disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or
XX infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The
XX novel calcium-binding proteins are also useful as screening tools to
XX identify antagonists and/or agonists that may enhance or inhibit
XX activities mediated by calcium-binding proteins. The polynucleotides of
XX the invention are also useful in gene therapy. AAS31577-AAS31654
XX represent cDNA sequences encoding for the novel human calcium-binding
XX proteins.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).
XX
XX Sequence 1480 BP; 329 A; 458 C; 479 G; 214 T; 0 other:..
XX SQ

Alignment Scores:		
Proj. No.:	1.08E-217	
Score:	249.00	Length: 1480
Percent Similarity:	99.39%	Matches: 327
Best Local Similarity:	99.39%	Conservative: 0
Query Match:	97.91%	Mismatches: 1
DB:	22	Indels: 2
		Gaps: 0

US-09-768-840-1 (1-328) x AAS31631 (1-1480)

Qy	1	Met	Met	Tp	Arg	Pro	Ser	Val	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Arg	His	Gly	Ala	Gln	Gly	20	
Db	47	ATG	ATG	TCT	GGC	GAC	CAT	CAG	TTC	TCT	GCT	GTT	GTT	GCT	ACT	GAG	CAC	GGG	CCC	AGG	GG	106	
Qy	21	Lys	Pro	Ser	Pro	Asp	Ala	Gly	Pro	His	Gly	Gln	Gly	Arg	Val	His	Gln	Ala	Ala	Pro	Leu	40	
Db	107	ANG	CCAT	CCCC	CAG	ACG	GAG	CCCT	CAT	GCG	ACG	GGG	AGG	GGT	GC	ACC	AGG	CGG	CCCC	CCG	166		
Qy	41	Ser	Asp	Ala	Pro	His	Asp	Asp	Ala	His	Gly	Asn	Phe	Gln	Tyr	Asp	His	Glu	Ala	Phe	Leu	60	
Db	167	AGC	GAC	GCT	CCC	CAT	GAT	GAC	GCC	ACG	GGG	AAC	TTC	CAG	TAC	GAC	CAT	GAG	GCT	TTC	CTG	226	
Qy	61	Gly	Arg	Glu	Val	Ala	Lys	Glu	Phe	Asp	Gln	Leu	Thr	Pro	Glu	Glu	Ser	Gln	Ala	Arg	Leu	80	
Db	227	GG	ACG	GGA	AGT	TGCC	CA	AGG	AA	TTC	GAC	CAACT	CAC	CCC	CAG	AGG	AA	AGC	CGG	CCG	CTG	286	
Qy	81	Gly	Arg	Ile	Val	Asp	Arg	Met	Asp	Arg	Ala	Gly	Asp	Gly	Asp	Gly	Tyr	Trp	Val	Ser	Leu	100	
Db	287	GGC	GGAT	CTG	TG	AC	CCAT	GAT	GAC	CGC	CGG	GGG	ACG	CGC	AGC	GGC	AGC	GCT	GGT	CTG	CTG	346	
Qy	101	Glu	Leu	Arg	Ala	Thr	Phe	Ala	His	Thr	Gln	Gln	Arg	His	Ile	Arg	Asp	Ser	Val	Ser	Ala	120	
Db	347	GAG	CTT	CGC	CGT	TGG	ATC	CGC	CAC	ACG	CAG	CAG	CGC	GGC	GC	ACAT	CAC	GGG	ACT	CGGT	GAG	CGCG	406
Qy	121	Ala	Thr	Asp	Thr	Tyr	Asp	Thr	Asp	Arg	Asp	Gly	Arg	Val	Gly	Tyr	Glu	Glu	Leu	Arg	Asn	140	
Db	407	GC	CTG	GGG	CAC	GT	AC	GAC	ACG	GGC	CGC	AGC	GGC	GT	TGG	GTT	GGG	AGG	AGC	TGCC	CAAC	466	
Qy	141	Ala	Thr	Tyr	Gly	His	Tyr	Ala	Pro	Gly	Glu	Clu	Pro	Phe	His	Asp	Val	Glu	Asp	Ala	Glu	Thr	160

Db	467	GCACCTATGGCCACTACGCGCGGTGAAGAAATTCATGACCTGGAGGATGCAGAGACC	526	18-APR-2000; 2000US-0198123.
Qy	161	TyTlysMetLeuAlaArgSpGluAArgPheArgValAlaAspGlnAspGlyAsp	180	19-MAY-2000; 2000US-0205515.
Db	527	TACAAAAAGATGCTGGCTCGGACGAGCGCGGTTTCGGGTGGCGGACGAGATGGGAC	586	07-JUN-2000; 2000US-0209467.
Qy	181	SerMetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMet	200	28-JUN-2000; 2000US-0214886.
Db	587	TCGATGCCCACTCAGAGGAGCTGCACAGCTTCCTGCACCCCGAGGATTCCTTCACATG	646	30-JUN-2000; 2000US-0215135.
Qy	201	ArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrVal	220	07-JUL-2000; 2000US-0216647.
Db	647	CGGACATCGTGATGCTGAACCCCTGGAGGACCTGGACAGAAACAAAGATGGCTATGTC	706	07-JUL-2000; 2000US-0216880.
Qy	221	GlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGluProAla	240	11-JUL-2000; 2000US-0217487.
Db	707	CAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCGAGCCTGGGAGGAGGCGCGG	766	11-JUL-2000; 2000US-0217496.
Qy	241	TrpValGlnThrGluAArgGlnPheArg-AspPheArgAspLeuAsnLysAspGlyHis	260	14-JUL-2000; 2000US-0218290.
Db	767	TGGGTGCAGACGGAGAGCCAGCTCTG-GGACTTCGGGATCTGAACAAGATGGGCA	825	26-JUL-2000; 2000US-0220964.
Qy	260	sLeuAspGlySerGluValGlyHisTrpValLeuProProAlaGlnAspGlnProLeuVa	280	26-JUL-2000; 2000US-0224518.
Db	826	CCTGGAGGGAGTGAAGTGGGCCACTGGGTGCTGCCCTGCCCAGGACCCCTGCT	885	14-AUG-2000; 2000US-0224519.
Qy	280	IgluAlaAsnHisLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAl	300	14-AUG-2000; 2000US-0225213.
Db	886	GGAAGCAACACCTGCTGTCAGCAGAGCGACGACGACGACGACGACGACGACGACG	945	14-AUG-2000; 2000US-0225214.
Qy	300	aGluIleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAs	320	14-AUG-2000; 2000US-0225266.
Db	946	GGAATCCTGGTAAATGGAACATGTTTGTGGGAGTCTGGCCACCACTATGTTGAGGA	1005	14-AUG-2000; 2000US-0225267.
Qy	320	pLeuThrArgHisHisAspGluLeu	328	14-AUG-2000; 2000US-0225268.
Db	1006	CCTGACCCGGCACCATGATGAGCTG	1030	14-AUG-2000; 2000US-0225268.
RESULT 15				
ID	ABK43732	standard; cDNA; 1480 BP.		
XX	AC	ABK43732;		
XX	DT	05-JUN-2002 (first entry)		
XX	DE	DNA encoding novel central nervous system protein #312.		
XX	KW	Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;		
XX	KW	hyperproliferative disorder; neoplasm; cardiovascular disorder;		
XX	KW	cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;		
XX	KW	nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;		
XX	KW	acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;		
XX	KW	adenocarcinoma; reproductive system disorder; testicular feminisation;		
XX	KW	endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;		
XX	KW	respiratory disorder; renal disorder; kidney failure; blood disorder;		
XX	KW	myocardial infarction; wound healing; cell proliferation; skin aging;		
XX	OS	food additive; food preservative; gene therapy; gene; ss.		
XX	PN	Homo sapiens.		
XX	PD	WO200155318-A2.		
XX	PP	02-AUG-2001.		
XX	PP	17-JAN-2001; 2001WO-US01332.		
XX	PP	31-JAN-2000; 2000US-0179065.		
XX	PP	04-FEB-2000; 2000US-0180628.		
XX	PP	24-FEB-2000; 2000US-0184654.		
XX	PP	02-MAR-2000; 2000US-0186350.		
XX	PP	16-MAR-2000; 2000US-0189874.		
XX	PP	17-MAR-2000; 2000US-0190076.		

Tue May 20 14:43:23 2003

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|||||
Db 647 CGGACATCGTGATTGCTGAACCTGGAGGACCTGGACAGAAACAAGATGGCTATGTC 706
QY 221 GlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGluProAla 240
Db 707 CAGGTGGAGGAGTACATCGCGGATCTGTACTACGCGAGCCTGGGGAGGAGGAGCGGCG 766
QY 241 TrpValGlnThrGluArgGlnGlnPheArg-AspPheArgAspLeuAsnLysAspGlyHi 260
Db 767 TGGGTGCAGACGGAGAGCAGCAGTCTCTG-GGACTTCGGGATCTGAACAAGGATGGCA 825
QY 260 sLeuAspGlySerGluValGlyHisTrpValLeuProAlaGlnAspGlnProLeuVa 280
Db 826 CCTGGACGGGAGTCAGGTGGGCCACTGGGTGCTGCCCTGCCAGGACGAGCCCTGGT 885
QY 280 lGluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAl 300
Db 886 GGAGGCCAACCAACCTGCTGCACGAGAGCGACCGGACAGGAGCGGGCGGTGAGCAAAGC 945
QY 300 sGluIleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAs 320
Db 946 GGAAATCCTGGGTAAATTGGAACATGTTTGTGGCAGTCAGGCCACCAACTATGGTGAGGA 1005
QY 320 pLeuThrArgHisHisAspGluLeu 328
Db 1006 CCTGACCGCGGACCAACGATGAGCTG 1030

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Search completed: May 20, 2003, 09:06:01
Job time : 326 secs

GenCore version 5.1.4_p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search; using frame_plus_p2n model

Run on: May 19, 2003, 22:09:52 ; Search time 1718 Seconds
(without alignments)
3092.037 Million cell updates/sec

Title: US-09-768-840-1
Perfect score: 328
Sequence: 1 MMWRPSVLLLLLRHGAQG.....FVGSQATNYGDELTRHDEL 328

Scoring table: OLIGO

Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Word size: 1

Total number of hits satisfying chosen parameters: 32308016

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-Q/cgn2.1/USPTO.spool/US09768840/runat_14052003_095833_17373/app_query.fasta_1.519
-DB-EST -QFMT-fastap -SURFIX-olip2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=1 -MATRIX-oligo -TRANS-human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE-quality -THR_MIN=1 -ALIGN=15 -MODE-LOCAL -OUTFMT=ptc
-NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER-US09768840-ECGN_1_1_1906-erunat_14052003_095833_17373 -NCPU=6 -ICPU=3
-NO_XLUPY -NO_WMAP -LARGQUERY -NEG SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-XGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mus:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	300	91.5	1092	9	AL544155	AL544155 AL544155
2	261	79.6	1111	14	BM920379	BM920379 AGENCOURT
3	245	75.0	883	9	AL543374	AL543374 AL543374
4	241	73.5	824	13	BI820206	BI820206 603037040
5	221	67.4	1103	14	BM918836	BM918836 AGENCOURT
6	207	63.1	790	12	BG775172	BG775172 602650360
7	207	63.1	1082	13	BM543703	BM543703 AGENCOURT
8	200	61.0	908	14	BQ712731	BQ712731 AGENCOURT
9	197	60.1	661	14	BM723848	BM723848 UI-P-E01-
10	197	60.1	775	12	BE875623	BE875623 601487063
11	189	57.6	681	13	BM042085	BM042085 603616096
12	176	53.7	1070	14	BM903507	BM903507 AGENCOURT
13	173	52.7	1001	9	AL550009	AL550009 AL550009
14	173	52.7	1175	13	BM543816	BM543816 AGENCOURT
15	153	46.6	909	9	AL520512	AL520512 AL520512
16	149	45.4	852	9	AL543274	AL543274 AL543274
17	140	42.7	931	12	BE880649	BE880649 601491556
18	133	40.5	954	9	AL573989	AL573989 AL573989
19	130	39.6	515	9	AA456267	AA456267 xx99F04.r
20	124	37.8	588	9	AI751749	AI751749 cn11f11.x
21	122	37.2	555	10	AV723508	AV723508 AV723508
22	121	36.9	505	10	AW239200	AW239200 xb37c05.y
23	118	36.0	549	10	BE245256	BE245256 TCBAP1D24
24	114	34.8	610	12	BF055054	BF055054 7183C04.x
25	112	34.1	1009	9	AL570372	AL570372 AL570372
26	104	31.7	376	10	AW068453	AW068453 cn24a12.y
27	98	29.9	624	14	BM716710	BM716710 UI-E-EJ0-
28	90	27.4	1005	9	AL520513	AL520513 AL520513
29	83	25.3	465	10	AW353288	AW353288 34695 MAR
30	83	25.3	917	12	BE874464	BE874464 601489415
31	77	23.5	900	9	AL569912	AL569912 AL569912
32	76	23.2	295	9	AA853047	AA853047 NHTBCre02
33	74	22.6	664	14	BQ574092	BQ574092 UI-H-E20-
34	73	22.3	660	14	BQ182243	BQ182243 UI-H-EU0-
35	73	22.3	660	14	BQ773463	BQ773463 UI-H-FE0-
36	72	22.0	658	14	BQ044993	BQ044993 UI-H-EU0-
37	71	21.6	303	10	BE185284	BE185284 IL5-HT073
38	68	20.7	395	10	BE015071	BE015071 127229 MA
39	68	20.7	559	10	AW631777	AW631777 91062 MAR
40	68	20.7	574	13	BI344949	BI344949 373596 MA
41	68	20.7	596	13	BI337575	BI337575 361049 MA
42	65	19.8	431	9	AA405402	AA405402 z05610.r
43	65	19.8	565	12	BF073720	BF073720 220427 MA
44	65	19.8	565	12	BF075553	BF075553 224687 MA
45	63	19.2	654	12	BE889141	BE889141 601513590

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION AL544155 LTI_NFL006_PL2 Homo sapiens CDNA clone CSOD1020YC22 5
prime, mRNA linear EST 16-FEB-2001
ACCESSION AL544155
VERSION
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1092)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization

**JOURNAL
COMMENT**

Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segreg@genoscope.cns.fr, Web : www.genoscope.cns.fr

FEATURES

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Location/Qualifiers
1. .1092
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DI020YC22"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="Placenta"
/notes=Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dN) primer. Five prime end
was enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ 3 others
212 389 156 t

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http://fulllength.invitrogen.com	3 others
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Pred. No.:	300.00	Matches:	327
Score:	99.99%	Conservative:	0
Percent Similarity:	99.99%	Mismatches:	1
Best Local Similarity:	99.99%	Indels:	2
Query Match:	91.46%	Gaps:	0
DB:			

200 758-840-1 (1-328) X AL544155 (1-1092)

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Db		37	ATGATGTGGCGACCATCAGTTCTGCTGCTTCGTTCCTACTGAGGCACGGGGCCAGGGG	96		
QY		21	LysProSerProAspAlaGlyProHisGlyGlnGlnArgValHisGlnAlaAProLeu	40		
Db		97	AAGCCATCCCACAGCACGAGGCCCTCATGCCAGGGGAGGTCACACGAGCGCCCCCTG	156		
QY		41	SerAspAlaProHisAspAspAlaHisGlyAsnPheGlnTyrrAspHisGluAlaPheLeu	60		
Db		157	AGCAGACGCTCCCCATGATGAGCGCCACCGGAAGCTCCCACTACGACCATTGAGGCTTTCCTG	216		
QY		61	GlyArgGluValAlaLysGluPheAspGlnLeuThrProGluLysSerGlnAlaArgLeu	80		
Db		217	GGACGGGAAGTGCCAAAGGAATTCGACCAACTCACCCACAGAGAAAGCCAGGCCGCTCTG	276		
QY		81	GlyArgILLEalAspArgMetAspArgAlaGlyAspGlyAspGlyTrpValSerLeuAla	100		
Db		277	GGCGGATCGTGGACCGCATGGACCGCGCGGGGACGGCCAGCGCTGGTGTGCTGGTGGCC	336		
QY		101	GluLeuArgAlaTriPileAlaHisThrGlnGlnArgHisIleArgAspSerValSerAla	120		
Db		337	GAGCTTCGGCGCTGGATCGCACACGACGACGACGGCGCATACGGGACTCGGTGAGCGCG	396		
QY		121	AlaTrpAspThrTyrrAspThrAspArgAspGlyArgValGlyTrpGluGluLeuA:gAsn	140		
Db		397	GCCTGGGCACACCTACGACACGACCGCCGACGGGGCGTGTGGTGTGGAGGAGCTGCGCAAC	456		
QY		141	AlaThrTyrrGlyHisThrAlaProGluGluGluPheHisAspValGluAspAlaGluThr	160		
Db		457	GCCACCTATGGCCACCTACGCGCCCGGTGAAGAATTCATGACGTGGAGATGTCAGAGACC	516		
QY		161	TyrLysLysMetLeuAlaAspGluArgArgPheArgValAlaAspGlnAspGlyAsp	180		
Db		517	TACAAAAGATGCTGGCTGGGACAGCGGCGCTTCCGGGGTGGCCGACCAAGATGGGGAC	576		
QY		181	SerMetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMet	200		

Db	577	TCGATGCCCACTCGACAGGAGCTGACAGCGCTTCCTCTGCACCCGAGGAGGTCCCTCACATG	636		
QY	201	ArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrVal	220		
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QY	221	GlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGluProAla	240		
Db	697	CAGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGGAGGAGGCGCGCG	756		
QY	241	TrpValGlnThrGluArgGlnGlnPheArgAspPheArgAspLeuAsnLysAspGlyHis	260		
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QY	281	GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla	300		
Db	877	GAAACCAACCACTGCTGCAGAGAGCAGACGAGAGGATGGCGGCTGAGCAAGC-	935		
QY	301	Glu-IleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAs	320		
Db	936	GAAATCCCTGGGTAAATGGACATGTTTGTGGCAGTCAGGCCACCACTATGCGGAG	995		
QY	320	pLeuThrArgHisHisAspGluLeu	328		
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RESULT 2	BM920379	1111 bp	mRNA	linear	EST 12-MAR-2002
LOCUS	AGENCOURT_6709368	NIH_MGC_122	Homo sapiens	cdna	clone IMAGE:5750333
DEFINITION	5', mRNA sequence.				
ACCESSION	BM920379				
VERSION	BM920379.1	GI:19370758			
KEYWORDS	EST				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	1 (bases 1 to 1111)				
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/				
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)				
	Unpublished (1999)				
	Contact: Robert Strausberg, Ph.D.				
	Email: cgabbs-remail.nih.gov				
	Tissue procurement: Life Technologies, Inc.				
	cdna Library Preparation: Life Technologies, Inc.				
	cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)				
	DNA Sequencing by: Agencourt Bioscience Corporation				
	DNA distribution: MGC clone distribution information can be				
	found through the I.M.A.G.E. Consortium/LLNL at:				
	http://image.llnl.gov				
	Plate: LLAM12781	row: c column: 06			
	High quality sequence spot: 686.				

FEATURES
SOU

Location/Qualities
1. .lllll
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/clone="IMAGE:5750333"
/clone_lib="NIH_MGC_122"
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/notes="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
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anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note

[illegible]

us-09-768-840-1.1.olip2n.rst

Tue May 20 14:43:24 2003

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141 AlathrTyrglyHisTyraAlaProglyGluGluPheHisAspValGluAspAlaGluThr 160
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161 TyrlsLysMetLeuAlaArgAspGluArgPheArgValAlaAspGlnAspGlyAsp 180
521 TACAAAAGATCTGGCTCGGACGAGCGCGTTCGGGTGGCCGACAGGATGGGGAC 580
181 SerMetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMet 200
581 TCGATGGCCACTCGAGAGGAGCTGACAGCTTCCTGACCCCGAGGAGTTCCTCCATG 640
201 ArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrrVal 220
641 CGGGACATCGTATGCTGAACCTGGAGGACCTGGAGACAGAAAGATGGGTATGTC 700
221 GlnValGluGluTyrrIleAlaAspLeuTyrrSerAlaGluPro-GlyGluGluProAl 240
701 CAGGTGGAGAGTACATCGCATCTGTACTCGCCGAGCCTGGGGAGGAGGAGCGGC 760
240 aTrrValGlnThrGluArgGlnPheArgAspPheArgAspLeuAsnLysAspGly 259
761 GTGGGTCCACGACGAGGAGGACGAGTCCGGGACTTCGGGATCTGAACAGGATGG 818

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LOCUS 603037040F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5178104 5',
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ACCESSION B1820206
VERSION B1820206.1 GI:159311756
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 824)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M11443 row: p column: 09
High quality sequence stop: 801.
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male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
180 a 227 c 298 g 119 t

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Alignment Scores: 13e-209 Length: 824
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Score: 99.61% Conservatives: 0
Percent Similarity: 99.61% Mismatches: 1
Best Local Similarity: 73.48% Indels: 1
Query Match: 13 Gaps: 0
DB:

US-09-768-840-1 (1-328) x B1820206 (1-824)
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Db 2 GACGCTCCCATGATGACGCCCGGGAACCTCCAGTACCACTGAGGCTTTCCTGGGA 61
Oy 62 ArgGluValAlaLysGluPheAspGlnLeuThrProGluGluSerGlnAlaArgLeuGly 81
Db 62 CGGGAAGTGGCCAGGAAATTCGACCACTCACCCACAGAGAAAGCCAGCCCTGCTGGG 121
Oy 82 ArgIleValAspArgMetAspArgAlaGlyAspGlyAspGlyTyrrValSerLeuAlaGlu 101
Db 122 CGGATCGTGGACCGATGACCGCGCGGGGACGCGGACGCGCTGGTGTGCTGGCCGAG 181
Oy 102 LeuArgAlaThrIleAlaHisThrGlnGlnArgHisIleArgAspSerValSerAlaAla 121
Db 182 CTTCCGCGCTGGTGCACACGACGAGCGGCACATACGGGACTCGGTGAGCGCGGCC 241
Oy 122 TrpAspThrTyrrAspThrAspArgAspGlyArgValGlyTyrrGluGluLeuArgAsnAla 141
Db 242 TGGGACACGTACGACACGCGGCGCGGCGGTGTGGTGGGAGGAGCTCGCGAACGCC 301
Oy 142 ThrTyrrGlyHisTyrrAlaProglyGluGluPheHisAspValGluAspAlaGluThrTyrr 161
Db 302 ACCTATGGCCACTACGCGCGCGGTGAAGAATTCATGACGTGGAGGATGCGACAGACTAC 361
Oy 162 LysLysMetLeuAlaArgAspGluArgPheArgValAlaAspGlnAspGlyAspSer 181
Db 362 AAAAAGATGTGGCTCGGAGGAGCTGACAGCCTTCGTCACCCCGAGGAGTTCCTCATCGCG 421
Oy 182 MetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMetArg 201
Db 422 ATGGCCACTCGAGAGGAGCTGACAGCCTTCGTCACCCCGAGGAGTTCCTCATCGCG 481
Oy 202 AspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrrValGln 221
Db 482 GACATCGGTGATTGCTGAACCCCTCGAGGACCTGGATGATGAACAAAGATGCTATGTCAG 541
Oy 222 ValGluGluTyrrIleAlaAspLeuTyrrSerAlaGluProglyGluGluGluProAlaTrp 241
Db 542 GTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCTGGGAGGAGGAGCGCGCTGG 601
Oy 242 ValGlnThrGluArgGlnGlnPheArgAspPheArgAspLeuAsnLysAspGlyHisLeu 261
Db 602 GTCGACGAGGAGGAGGAGCAGCTTCGGGACTTCGGGATCTCGAAGAGATGGGACCTG 661
Oy 262 AspGlySerGluValGlyHisTrpValLeuProAlaGlnAspGlnProLeuValGlu 281
Db 662 GATGGAGTGGAGTGGGCGGCTGGGTGCTGCCCGCTGCCAGGAGGAGGAGGAGGAGGAG 721
Oy 282 AlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLys 299
Db 722 GCAAG-CACCTGCTGCACGAGAGCGACGACGAGGATGGCGGCTGAGCAGA 774

RESULT 5
B1820206 1103 bp mRNA linear EST 12-MAR-2002
LOCUS 603037040F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5747916
DEFINITION 5' mRNA sequence.
ACCESSION B1820206
VERSION B1820206.1 GI:19369215
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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BASE COUNT
ORIGIN


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BASE COUNT      167 a    225 c    283 g    115 t
ORIGIN

Alignment Scores:
Pred. NO.:      1-25e-178
Score:          207.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match:    63.11%
Db:             12
Matches:         207
Conservative:    0
Mismatch:        0
Indels:          0
Gaps:            0
Length:         790
Note: this is a NIH_MGC Library."

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[illegible]

nick quality sequence stop: 592:

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1. .1082
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/db_xref="taxon:9606"
/clone="IMAGE:589020"
/clone_lib="NIH_MGC_125"

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/ab_host="DH10B"
/notes="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
Site_1: EcoRV (destroyed); Site_2: NotI; RNA source: pool
of three ovaries, from females ranging in age from 38 to
49 yo. Library is oligo-dr primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 2.1 kb, insert size range 1-3.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
#036"

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218 a	337 c	375 q	152 t
tracking code 030:			

Alignment Scores:	1.7e-178	Length:	1082
Pred. No.:	207.00	Matches:	220
Score:	99.55%	Conservative:	0
Percent Similarity:	99.55%	Mismatches:	0
Best Local Similarity:	63.11%	Indels:	1
Query Match:	13	Gaps:	0

88-768-840-1 (1-328) x BM543703 (1-1082)

US-09-768-840_1 (1-526).
 QY 1 MetMetrrpargproSerVallLeuLeuLeuLeuLeuLeuLeuLeuLeuArqHisGlyAlaGInGly 20
 Db 70 ATGATGTGGCGACCATAGTCTTCCTTGCTTTCTTGTTACTAGGCACGGGGCCAGGGG 12
 QY 21 LysProSerProAspAagLagProHisGlyGInGlyArgValHisGlnAlaAlaProLeu 40
 Db 130 AAGCATTCCCAGACGAGCCCTCATGTCGCCAGGAGGAGGTGCACCAGGCGGCCCCCTTG 18
 QY 41 SerAspAlaProHisAspAspAlaHisGlyAsnPheGlnTyrAspHisGluAlaPheLeu 60
 Db 190 AGCGACGCTCCCCATGATGATGACGCCACAGGAATTCAGTAGCACCATGAGGCTTTCCTG 24
 QY 61 GlyArgGluValAlaLysGluPheAspGlnLeuThrProGluGluSerGlnAlaArgLeu 80
 Db 250 GACCGGHAATGGCCAAGAAATTCGACAACATCACCCCAGAGAAGAACGAGCCCGTCTG 32
 QY 81 GlyArgIleValAspArgMetAspArgAlaGlyAspGlyAspGlyTrpValSerLeuAla 100
 Db 310 GGCGGATCTGTGACCGCATGACCGCCGCGGGGACGGCGACGGCTGGGTGTGCTGCTGGCC 36
 QY 101 GluLeuArgAlaTrpIleAlaHisThrGlnAlaHisIleArgAspSerValSerAla 120
 Db 370 GAGCTTCGCGCTGGATCGCGCACACGACGACGCGGCACATACGGGACTTCGGTGNAGCGG 44
 QY 121 AlaTrpAspThrTyrAspThrAspArgAspGlyArgValGlyTrpGluLeuLeuArgAsn 140
 Db 430 GCCTGGGACACGTACGACACGACGCGCGACGGCGGTGGGTGGGAGAGCTGGCGAAC 48
 QY 141 AlaThrTyrGlyHisTyrAlaProGlyGluGluPheHisaspValGluAspAlaGluThr 160
 Db 490 GCCACCTATGGCCACTACGCGCCCGGTGAAGAAATTCATACGCTGGAGGATTCGACAGACC 56
 QY 161 TyrLysLysMetLeuAlaArgAspGluArgArgPheArgValAlaAspGlnAspGlyAsp 180
 Db 550 TACAAAAAGATGTGCTCGGACACAGCGGGCTTCCGGGTGGCCGACAGGATGGGGAC 64
 QY 181 SerMetAlaThrArgGluLeuLeuThrAlaPheLeuHis-ProGluclupheProHisme 200
 Db 610 TCGATGGCCACTCGAGAGAGCTGACAGCCTTCCTGCAACCCCGGAGGATTCCTCTCACAT 68
 QY 200 targaSpIlleValIlealacIuThreUgluaSpuAspLeuAspArgasnLysaspGlyTyrVa 220
 Db 670 CGGGACATCGTGAATGCTGTAACACCCCTGGAGCACTGGACAGAAACAACAGATGGCTATGT 69

75-00-759-840-1 (1-328) x BG775172 (1-790)

[illegible]

RESULT	7
BM543703	
LOCUS	
DEFINITION	ACBNCOURT_6492387 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5589020 linear EST 20-FEB-2002
	1082 bp mRNA
	BM543703
	5'... sequence

3', mRNA sequence:
ACCESSION BM543703

BM543703.1 GI:18774318

KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens

ORGANISM
HOMO SAPIENS
Eukaryota; Metazoa; Cho

Mammalia; Eutheria; Pri-

1 (bases 1 to 1082)

AUTHORS
TIMOTHY F.
NIH-MGC <http://mgc.nci.nih.gov>
National Institutes of Health

JOURNAL
Unpublished (1999)

COMMENT

Contact: Robert Straus

Email: cgapbs-femail@nrc.ca

cDNA Library preparation

CDNA Library Arrayed by

DNA Sequencing by: Age

clone distribution: M. found through the T. M. A.

Found through the Internet
http://image.llnl.gov

Plate: LLAM12361 row:


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Db 371 GCCTGGACACGTACGACACGCGCGGTGGTGGGAGGAGTGGCGCAC 430
Qy 141 AlatrThrTyGlyHisTyAlaProGlyGluGluPheHisAspValGluAspAlaGluThr 160
Db 431 GCCACCTATGCCCACTACGCGCGCGGTGAAGAATTCATGACGCTGGAGGATCGACAGACC 490
Qy 161 TyrLysLysMetLeuAlaArgAspGluArgGluArgGluArgGluArgGluArgGluArg 180
Db 491 TACAAAAGATGCTGGCTCGGGACGAGCGCGGTTCGCGGTGGCGGACACGAGGATGGGAC 550
Qy 181 SerMetAlatrThrArgGluGluLeuThrAlaPheLeuHisProGluGluPhe 197
Db 551 TCGATGCCCACTCGAGAGGAGTGCACAGCTTCCTGCACCCCGAGGAGTTC 601

RESULT 11
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LOCUS BM042085
DEFINITION 603616096F1 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:5420806 5',
mRNA sequence.
ACCESSION BM042085
VERSION 1
KEYWORDS 603616096F1 GI:16771352
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 681)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DRP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1875 row: p column: 23
High quality sequence stop: 681.
Location/Qualifiers
1. 681
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/db_xref="taxon:9606"
/clone="IMAGE:5420806"
/tissue_type="melanotic melanoma, cell line"
/note="Organ: skin; Vector: pOTB7; Site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT 139 a 199 c 244 g 99 t
ORIGIN

Alignment Scores:
Pred. No.: 2,8e-162 Length: 681
Score: 189.00 Matches: 189
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.62% Indels: 0
DB: 13 Gaps: 0

US-09-768-840-1 (1-328) x BM042085 (1-681)

Qy 21 LysProSerProAspAlaGlyProHisGlyGlnGlyArgValHisGlnAlaProLeu 40
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Db 115 AAGCCATCCCAACGACGCGCCCTCATGCCAGGGAGGGTGCACACGCGCGCCCCCTG 174
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Db 175 AGCGAGCGCTCCCATGATGACGCCACGGGAACTTCCAGTACGACCATGAGGCTTTCCTG 234
Qy 61 GlyArgGluValAlaLysGluPheAspGlnLeuThrProGluGluSerGlnAlaArgLeu 80
|||||
Db 235 GGACGGGAAGTGGCCAGGAATTCGACCACTCACCACAGAGAAACCCAGGCCCTGCTG 294
Qy 81 GlyArgIleValAspArgMetAspArgAlaGlyAspGlyAspGlyTyrValSerLeuAla 100
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Db 295 GGGCGGATCGTGGACCGCATGACCGCGGGGACGCGCGGTGGTGGTGGCTGGCC 354
Qy 101 GluLeuArgAlaTyrPheAlaHisThrGlnGlnArgHisIleArgAspSerValSerAla 120
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Db 355 GAGCTTCGCGGTGGATCGGCACACGACGACGACGACGACGACGACGACGACGACGACG 414
Qy 121 AlaTyrAspThrTyrAspThrAspArgAspGlyArgValGlyTyrPheGluLeuArgAsn 140
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Db 415 GCCTGGGACACGTACGACACGACGCGCGCGGTGGTGGGAGGAGTGGCGAAC 474
Qy 141 AlaThrTyrGlyHisTyrAlaProGlyGluGluPheHisAspValGluAspAlaGluThr 160
|||||
Db 475 GCCACCTATGCCCACTACGCGCGCGGTGAAGAATTCATGACCTGGAGGATCGACAGACC 534
Qy 161 TyrLysLysMetLeuAlaArgAspGluArgGluArgGluArgGluArgGluArgGluArg 180
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Db 535 TACAAAAGATGCTGGCTCGGGACGAGCGCGGTTCGCGGTGGCGGACACGAGGATGGGAC 594
Qy 181 SerMetAlatrThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMet 200
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Db 595 TCGATGCCCACTCGAGAGGAGTGCACGCTTCCTGCACCCCGAGGAGTTCCTCATCATG 654
Qy 201 ArgAspIleValIleAlaGluThrLeu 209
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Db 655 CGGGACATCGTATGCTGCTGAAACCGCTG 681

RESULT 12
BM042085
LOCUS BM042085
DEFINITION 6621943 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5721868
5', mRNA sequence.
ACCESSION BM042085
VERSION 1
KEYWORDS 6621943 GI:19352864
SOURCE EST.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1070)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM12707 row: a column: 05
High quality sequence stop: 595.
Location/Qualifiers
1. 1070
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/db_xref="taxon:9606"
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/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;"

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Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036." 159 t

[illegible]

RESULT 13

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LOCUS	
DEFINITION	AL550009 LTI_NFL006_pl2 Homo sapiens cDNA clone CS9D1053YN17 5
ACCESSION	AL550009
VERSION	AL550009.1 GI:12886549
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 1001)
AUTHORS	Li W.B., Gruber C., Jesse J. and Polayes D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage Bp 191 91006 Evry cedex - France Email : seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr. http://seqref.genoscope.cns.fr, seqref@qualifiers.com

FEATURES

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODI053YN17"
/clone.lib="LTI_NFL006_PU2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com 8 others
151+

	212 a	271 c	359 g	131 l
BASE COUNT				
ORIGIN				

[illegible]

1-328) y AL550009 (1-1001)

[illegible]

us-09-768-840-1.olip2n.rst

Tue May 20 14:43:24 2003

Job time : 1749 secs

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/lab_host="DH10B"
/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
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enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : filiang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT      142 a      278 c      291 g      197 t      1 others
ORIGIN

Alignment Scores:      2,49e-129      Length:      909
Pred. No.:      153.00      Matches:      180
Score:      98.90%      Conservative:      0
Percent Similarity:      98.90%      Mismatches:      1
Best Local Similarity:      46.65%      Indels:      2
Query Match:      9      Gaps:      0
DB:

US-09-768-840-1 (1-328) x AL520512 (1-909)
QY 148 ProGluGluPheHisAspValGluAspAlaGluThrTyrLysLysMetLeuAlaArg 167
Db 904 CCGGGAAGAATTTCATGAGCTGGAGGATGCAGAGACCTACAAAAGATGCTGCTCG 845
QY 168 AspGluArgArgPheArgValAla-AspGlnAspGlyAspSerMetAlaThrArgGlu 187
Db 844 GACGAGCGCGTTTCGGGT-GCCGCCACAGGATGGGACTTCGATGCCACTCGAGAGGA 786
QY 187 uLeuThrAlaPheLeuHisProGluGluPheProHisMetArgAspIleValIleAl 207
Db 785 GCTGACAGCCTTCCTGCACCCGAGAGACTCCCTCACATCGGGACATCGTGTGCTGA 726
QY 207 uThrLeuGluAspLeuAspArgAsnLysAspClyTyrValGlnValGluLutyrIleAl 227
Db 725 AACCTGGAGGACCTGGACAGAAACAAGATGGCTATGTCAGGTGGAGGAGTACATCGC 666
QY 227 AspLeuTyrSerAlaGluProGlyGluGluProAlaTrpValGlnThrGluArgG 247
Db 665 GGATCTGTACTACCCGAGCCTGGGAGGAGGAGCGCGGTGGTGCAGACGGAGAGCA 606
QY 247 nGlnPheArgAspPheArgAspLeuAsnLysAspGlyHisLeuAspGlySerGluVal 267
Db 605 GCAGTTCGGGACTTCGGGACTGTAACAAGAGTGGGACCTGGATGGGAGTGGGTGGG 546
QY 267 yHisTrpValLeuProAlaGlnAspGlnProLeuValGluAlaAsnHisLeuHi 287
Db 545 CCACGTGGGTGTGTCCTCCAGGACACAGCCCTGGTGGAGCCCAACCACTGCTGCA 486
QY 287 sGluSerAspThrAspLysAspGlyArgLeuSerLysAlaGluIleLeuGlyAsnTrpAs 307
Db 485 CCAGAGCGACACGGACAGAGTGGCGGCTGAGCAGAGCGGAATCCTGGGTAATTGGAA 426
QY 307 nMetPheValGlySerGlnAlaThrAsnTyrGlyGluAspLeuThrArgHisAspG 327
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QY 327 uLeu 328
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Search completed: May 20, 2003, 09:00:34

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OW protein - nucleic search, using frame_plus_p2n model

Run on: May 19, 2003, 22:09:52 ; Search time 58 Seconds
(without alignments)
1734.310 Million cell updates/sec

Title: US-09-768-840-1

Perfect score: 328

Sequence: 1 MWRPSVLLLLLLRHGAQG.....FVGSQATNYCEDLTRHDEL 328

Scoring table: OLIGO

Ygapop 60.0 , Xgapext 60.0

Ygapop 60.0 , Xgapext 60.0

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Word size: 1

Total number of hits satisfying chosen parameters: 878598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-LIST=45 -DOCALLIGN=200 -START=1 -END=1 -MATRIX=oligo -TRANS=human4.0.cdi
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_XLPXY -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -DELOP=6 -DELEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA.*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	328	100.0	1055	2	US-08-828-242-2
2	328	100.0	1055	4	US-09-206-498-2
3	328	100.0	1463	2	US-08-910-927B-2
4	328	100.0	1463	4	US-09-270-270-2
5	118	36.0	1490	4	US-09-484-970B-53
6	9	2.7	823	3	US-08-675-885-1
7	9	2.7	2160	4	US-09-588-256-1
8	9	2.7	2658	2	US-08-910-927B-4
9	9	2.7	2658	4	US-09-270-270-4
10	8	2.4	36	1	US-08-455-860-10
11	8	2.4	36	1	US-08-383-749-10
12	8	2.4	57	3	US-08-894-511-3

13	8	2.4	57	3	US-08-894-511-4
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15	8	2.4	58	4	US-08-860-038-15
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38	8	2.4	334	4	US-09-195-106-7
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41	8	2.4	427	4	US-08-905-223-158
42	8	2.4	435	4	US-09-171-209-44
43	8	2.4	443	4	US-08-896-164-10
44	8	2.4	498	4	US-09-134-001C-2491
45	8	2.4	506	1	US-08-469-802B-7

ALIGNMENTS

RESULT 1
US-08-828-242-2
; Sequence 2, Application US/08828242
; Patent No. 5871970
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,242
; FILING DATE: Filed Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0261 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166

[illegible]

321 LeuThrArgHisHisAspGluLeu 328
 Qy |||||
 321 LeuThrArgHisHisAspGluLeu 328
 Qy |||||

RESULT 2
US-09-206-499-2
; Sequence 2, Application US/09206499

Patent No. 6194383
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
INVENTOR: Goli, Surya K.

; TITLE OF INVENTION: NOVEL CALCIUM BINDING
 ;
 ; TITLE OF INVENTION: PROTEIN
 ;
 ; NUMBER OF SEQUENCES: 4
 ;
 ; CORRESPONDENCE ADDRESS:

ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto

```

;
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; COMPATIBLE: FASTFEO for Windows Version 2.0

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SOFTWARE. LICENSE.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/206,499
FILING DATE:

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:
:
: CLASSIFICATION:
:
: PRIOR APPLICATION DATA:
:
: APPLICATION NUMBER: 08/828,242
:
: FILING DATE: 03/31/1997
:
:

```

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0261 US

REFERENCE/ DOCUMENT NO. :
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166

```

; INFORMATION FOR SEQ ID NO. 2:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 1055 base pairs
; TYPE: nucleic acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; COMPILED BY: COMPIL01

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LIBRARY: CON10104
;
CLONE: 2509570
; US-09-206-499-2

Alignment Scores:	6.25e-290	Length:	1055
Pred. No.:	328.00	Matches:	328
Score:	100.00%	Conservative:	0
Percent Similarity:			

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DB:
Query Match: 4
Best Local Similarity: 100.00%
Percent Similarity: 100.00%
Indels: 0
Mismatches: 0
Gaps: 0

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US-09-768-840-1 (1-328) x US-09-206-499-2 (1-1055)

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1055 base pairs
TYPE: nucleic acid
STRAINEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: CONTUT01
CLONE: 2509570
JS-08-828-242-2

Alignment Scores:		
Scaled No.:	6.25e-290	1055
Score:	328.00	328
Percent Similarity:	100.00%	0
Best local Similarity:	100.00%	0
Query Match:	2	0
Mismatches:	0	0
Indels:	0	0
Gaps:	0	0
Matches:	0	0
Conservative:	0	0

US-09-768-840-1 (1-328) x US-08-828-242-2 (1-1055)

[illegible]

21 LysProSerProAspAlaGlyProHisGlyClnGlyArgValHisIsoleu...
 QY |||||
 94 AAGCCATCCCAGACGACGGCCCTCATGCCAGGGGAGGGTGCACAGGGGCCCCCTG 153
 Db |||||

Qy 41 SerAspAlaProHisAspAspAlaHisGlyAsnPheGIntTyAspHisGluArpneu 00
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 Db 154 AGCGAGCTCCCATGATGACGCCACGGGAACCTCCAGTACGACCATGAGGCTTTCCTG 213

61 GlyArgGluValAlaIysGluPheAspGlnLeuThrProGluGluSerGlnAlaArgLeu 80
QY |||||
214 GSACGSGAAGTGGCCAAAGGAATTCGACCAACTCACCCACAGGAGAAAGCCAGGCCGCTGTG 273

D6
214 GRCGGGAGTCTTTT
81 GlyArgIleValAspArgMetAspArgAlaGlyAspGlyAspGlyTrpValSerLeuAla 100
QY
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[illegible][illegible]

Db	GCCTGGGACACGTACGACACGGACCGCGACGGCGGTGGAGGAGGACGCGCGG	160
Qy	AlaThrTyrGlyHisTyrAlaProGlyGluGluPheHisAspValGluAspAlaGluThr	141

Db 454 GCCACCTATGCCCACTACGCGCCGGGTGAAGAATTTCATGACTGCCTGGAGGATGCAGAGACC 513
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Gv 161 TvrLvsLysMetLeuAlaArgAspGluAArgApPheArgValAlaaspGlnAspGlyAsp 180
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514 TACAAAAGATGCTGGCTCGGACGAGCGCGTTTCGGGTGGCCGACAGGATGGGGAC 573

[illegible][illegible]

	QY	221	GlnValGluUglutyrIlealaAspleutySerAlaGluProGlyArgLysPheLeu	753
	Dδ	694	CAGCTGGAGGATACATCGCGGATCTGTACTCAGCCGAGCCTGGGAGGAGGCCGC	760

QY 241 TrpValGlnThrGluArgGlnGlnPheArgAspPheArgAspLeuAsnLysAspGlyHis
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 754 TGGGTGCAGCGGAGAGCGACAGTTCGGGACTTCGGGATCTGACACAGGATGGGCAC 813

TYPE: DNI
ORGANISM
FEATURE:

Query Match: 2.74% Indels: 0
DB: 2 Gaps: 0

US-09-768-840-1 (1-328) x US-08-910-927B-4 (1-2658)

Qy 68 PheAspGlnLeuThrProGluGluSer 76
|||||
Db 286 TTTCATCAGCTGACACCAAGAGAGC 312

RESULT 9

US-09-270-270-4
; Sequence 4, Application US/09270270
; Patent No. 6235477
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/270,270
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/910,927
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0358 US
; TELEPHONE: 650-855-0355
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2658 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BLADN0703
; CLONE: 1601793

US-09-270-270-4

Alignment Scores:
Pred. No.: 45,1 Length: 2658
Score: 9,00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.74% Indels: 0
DB: 4 Gaps: 0

US-09-768-840-1 (1-328) x US-09-270-270-4 (1-2658)

Qy 68 PheAspGlnLeuThrProGluGluSer 76
|||||
Db 286 TTTCATCAGCTGACACCAAGAGAGC 312

RESULT 10

US-08-455-860-10
; Sequence 10, Application US/08455860
; Patent No. 5686281
; GENERAL INFORMATION:
; APPLICANT: ROBERTS, MARGO R
; APPLICANT: ANDERSON, STEPHEN J
; TITLE OF INVENTION: CHIMERIC RECEPTOR MOLECULES FOR DELIVERY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CELL GENESYS, INC.
; STREET: 322 LAKESIDE DRIVE
; CITY: FOSTER CITY
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 94404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,860
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/383,749
; FILING DATE: 03-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MANDEL, SARALYNN
; REGISTRATION NUMBER: 31,853
; REFERENCE/DOCKET NUMBER: CELL 19
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 358-9600 x 345
; TELEFAX: (415) 349-7392
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

US-08-455-860-10

Alignment Scores:
Pred. No.: 6,42 Length: 36
Score: 8,00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2,44% Indels: 0
DB: 1 Gaps: 0

US-09-768-840-1 (1-328) x US-08-455-860-10 (1-36)

Qy 9 LeuLeuLeuLeuLeuArgHis 16
|||||

Db 2 CTGCTCCTCTTACTCTCGGCAC 25

RESULT 11

US-08-383-749-10
; Sequence 10, Application US/08383749
; Patent No. 5712149
; GENERAL INFORMATION:
; APPLICANT: ROBERTS, MARGO R
; APPLICANT: ANDERSON, STEPHEN J
; TITLE OF INVENTION: CHIMERIC RECEPTOR MOLECULES FOR DELIVERY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CELL GENESYS, INC.
; STREET: 322 LAKESIDE DRIVE
; CITY: FOSTER CITY

PRIOR APPLICATION DATA: FR 95/02117


```

; REFERENCE/DOCKET NUMBER: ST95013-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3816
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 57 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotide"
US-08-894-511-4

Alignment Scores:
Pred. No.: 9.89 Length: 57
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.44% Indels: 0
DB: 3 Gaps: 0

US-09-768-840-1 (1-328) x US-08-894-511-4 (1-57)
Qy 7 ValLeuLeuLeuLeuLeuLeu 14
Db 5 GTTCTCTCTCTCTCTCTCTCT 28

RESULT 14
US-08-860-038-9/c
; Sequence 9, Application US/08860038
; Patent No. 6287762
; GENERAL INFORMATION:
; APPLICANT: CROUZET, Joel
; APPLICANT: SCHERMAN, Daniel
; APPLICANT: WILS, Pierre
; TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, Mailstop 3043
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,038
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/15162
; FILING DATE: 16-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO FR95/01468
; FILING DATE: 08-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky Esq., Martin F.
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: ST94090-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3816
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotide"
US-08-860-038-9

Alignment Scores:
Pred. No.: 10.1 Length: 58
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.44% Indels: 0
DB: 4 Gaps: 0

US-09-768-840-1 (1-328) x US-08-860-038-9 (1-58)
Qy 8 LeuLeuLeuLeuLeuLeuLeuArg 15
Db 27 CTTCTCTCTCTCTCTCTCTCTCGG 4

RESULT 15
US-08-860-038-15/c
; Sequence 15, Application US/08860038
; Patent No. 6287762
; GENERAL INFORMATION:
; APPLICANT: CROUZET, Joel
; APPLICANT: SCHERMAN, Daniel
; APPLICANT: WILS, Pierre
; TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, Mailstop 3043
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,038
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/15162
; FILING DATE: 16-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO FR95/01468
; FILING DATE: 08-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky Esq., Martin F.
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: ST94090-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3816
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotide"
US-08-860-038-15

Alignment Scores:
Pred. No.: 10.1 Length: 58
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0

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us-09-768-840-1.olip2n.rni

Tue May 20 14:43:23 2003

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.44% Indels: 0
DB: 4 Gaps: 0

US-09-768-840-1 (1-328) x US-08-860-038-15 (1-58)

Qy 8 LeuLeuLeuLeuLeuLeuArg 15

|||||

Db 27 CTCCTCTCTCTCTCTCTCTCGG 4

Search completed: May 20, 2003, 08:31:14
Job time : 74 secs

GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 19, 2003, 22:09:53 ; Search time 138 Seconds
(without alignments)
3138.490 Million cell updates/sec

Title: US-09-768-840-1
Perfect score: 328
Sequence: 1 MMWRPSVLLLLLRHGAQG.....FVGSQATNYGDELTRHDEL 328

Scoring table: OLIGO

Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 828747 seqs, 660231138 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1655407

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO.spool/US09768840/runat_14052003_095834_17410/app_query.fasta_1.519
-DB=Published.Applications_NA -QFMT=fastap -SURF=olip2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo
-TRANS=human40.cdl -LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
-ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09768840 -CGN_1_130 @runat_14052003_095834_17410
-NCPU=6 -ICPU=3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Published.Applications_NA:

Query	Score	Match	Length	ID	Description
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:					
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:					
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:					
5: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:					
6: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:					
7: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:					
8: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:					
9: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:					
10: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:					
11: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:					
12: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:					
13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:					
14: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:					
15: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:					

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	328	100.0	1055	10	US-09-768-840-2
2	328	100.0	1463	10	US-09-847-809A-2
3	328	100.0	1503	9	US-09-905-291A-220
4	328	100.0	1503	9	US-09-902-853-220

5	328	100.0	1503	9	US-09-907-824-220	Sequence 220, App
6	328	100.0	1503	9	US-09-907-841-220	Sequence 220, App
7	328	100.0	1503	9	US-09-904-011-220	Sequence 363, App
8	328	100.0	1503	9	US-10-028-072-363	Sequence 220, App
9	328	100.0	1503	9	US-09-906-742-220	Sequence 363, App
10	328	100.0	1503	9	US-10-121-049-363	Sequence 363, App
11	328	100.0	1503	9	US-10-123-904-363	Sequence 363, App
12	328	100.0	1503	9	US-10-140-470-363	Sequence 363, App
13	328	100.0	1503	9	US-09-906-838-220	Sequence 220, App
14	328	100.0	1503	9	US-09-907-613-220	Sequence 220, App
15	328	100.0	1503	9	US-08-907-942-220	Sequence 220, App
16	328	100.0	1503	9	US-10-175-746-363	Sequence 363, App
17	328	100.0	1503	9	US-10-176-918-363	Sequence 363, App
18	328	100.0	1503	9	US-10-176-921-363	Sequence 363, App
19	328	100.0	1503	9	US-10-137-865-363	Sequence 363, App
20	328	100.0	1503	9	US-10-140-474-363	Sequence 363, App
21	328	100.0	1503	9	US-09-904-820-220	Sequence 220, App
22	328	100.0	1503	9	US-09-904-859-220	Sequence 220, App
23	328	100.0	1503	9	US-09-909-204-220	Sequence 220, App
24	328	100.0	1503	9	US-10-142-431-363	Sequence 363, App
25	328	100.0	1503	9	US-10-143-114-363	Sequence 363, App
26	328	100.0	1503	9	US-09-904-786-220	Sequence 220, App
27	328	100.0	1503	9	US-09-906-646-220	Sequence 220, App
28	328	100.0	1503	9	US-09-906-700-220	Sequence 220, App
29	328	100.0	1503	9	US-10-140-002-363	Sequence 363, App
30	328	100.0	1503	9	US-09-902-903-220	Sequence 220, App
31	328	100.0	1503	9	US-09-903-749A-220	Sequence 220, App
32	328	100.0	1503	9	US-09-903-786-220	Sequence 220, App
33	328	100.0	1503	9	US-10-142-419-363	Sequence 363, App
34	328	100.0	1503	9	US-09-902-736-220	Sequence 220, App
35	328	100.0	1503	9	US-09-904-119-220	Sequence 220, App
36	328	100.0	1503	9	US-09-904-956-220	Sequence 220, App
37	328	100.0	1503	9	US-09-907-794-220	Sequence 220, App
38	328	100.0	1503	9	US-10-123-262-363	Sequence 363, App
39	328	100.0	1503	9	US-10-142-423-363	Sequence 363, App
40	328	100.0	1503	9	US-09-902-692-220	Sequence 220, App
41	328	100.0	1503	9	US-09-903-520-220	Sequence 220, App
42	328	100.0	1503	9	US-09-903-943-220	Sequence 220, App
43	328	100.0	1503	9	US-09-904-462-220	Sequence 220, App
44	328	100.0	1503	9	US-09-905-056-220	Sequence 220, App
45	328	100.0	1503	9	US-09-907-925-220	Sequence 220, App

ALIGNMENTS

RESULT 1
US-09-768-840-2
; Sequence 2, Application US/09768840
; Patent No. US20010012831A1
; GENERAL INFORMATION:
; APPLICANT: Hüllman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/768,840
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/206,499


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; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 220
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-905-291A-220

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Alignment Scores:					
Pred. No.:	0	Length:	1503		
Score:	328.00	Matches:	328		
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Best Local Similarity:	100.0%	Mismatches:	0		
Query Match:	100.0%	Indels:	0		
DB:	9	Gaps:	0		

US 00-769-940-1 (1-328) x US-09-905-291A-220 (1-1503)

[illegible]

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QY	281	GlulAaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla	300
Db	875	GAAGCAACACACTCTCTGCAGAGAGGCGACACGGACAAGGATGGCGGCTGAGCAAGCG	934
QY	301	GlulLeuLeuGlyAsnThrAspMetPheValGlySerGlnAlaThrAsnTyrGlyGluAsp	320
Db	935	GAATCTCTGGGTAAATGGACATGTTTGTGGCAGTCAGGCGCCACCACTATGGCGAGAC	994
QY	321	LeuThrArgHisHisAspGluLeu	328
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RESULT 4

US-09-902-853-220

; Sequence 220, Application us/09902853

; Publication No. US20020192659A1

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Flivaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and transmembrane Polypeptides and Nucle

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/902,853

; CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: US/09/665,350

; PRIOR FILING DATE: 2000-09-18

; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26

; PRIOR APPLICATION NUMBER: US 60/146,222

; PRIOR FILING DATE: 1999-07-28

; PRIOR APPLICATION NUMBER: PCT/US99/20594

; PRIOR FILING DATE: 1999-09-08

; PRIOR APPLICATION NUMBER: PCT/US99/20944

; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: PCT/US99/21090

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/21547

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/23089

; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: PCT/US99/28214

; PRIOR FILING DATE: 1999-11-29

; PRIOR APPLICATION NUMBER: PCT/US99/28313

; PRIOR FILING DATE: 1999-11-30

; PRIOR APPLICATION NUMBER: PCT/US99/28564

APPLICANT: WOOD, WILLIAM, I.
 APPLICANT: WOOD, WILLIAM, I.
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

[illegible]

455	Db	GCACCTATGGCCACTACGCCCCCGGTGAACAAATTTTCATGACGTGGAGGATGCAGAGACC	514
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515	Db	TACAAAAAGATGCTGCCTCGGGACAGCGGGTTCGGGTGGCCGACAGGATGGGAC	574
181	QY	SerMetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMet	200
575	Db	TCGATGGCCACTCGAGAGGAGCTGCACGCCCTCCTGCACCCGAGGAGTTCCTTCACATG	634
201	QY	ArgspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrrVal	220
635	Db	CGGACATCGTGAATTCCTGAACCCCTGGAGGACCTGGACAAACAAGATGGCTATGTC	694
221	QY	GlnValGluGluIrrIleAlaAspLeuTyrrSerAlaGluProGlyGluGluGluProAla	240
695	Db	CAGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGGAGGAGGAGCCGCGC	754
241	QY	TrpValGlnThrGluAArgGlnGlnPheArgspPheArgAspLeuAsnLysAspGlyHis	260
755	Db	TGGGTGCAGACGGAGAGCGCAGAGTTCGCGGACTTCGCGGATCTGAACAAGATGGGAC	814
261	QY	LeuAspGlySerGluValGlyHisTrpValLeuProProAlaGlnAspGlnProLeuVal	280
815	Db	CTGGATGGAGTGAAGTGGGCCACTGGGTGCTGCCCTGCCAGGACCAGCCCTGGTG	874
281	QY	GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla	300
875	Db	GAAGCCCAACCACTGCTGCACGAGAGCGACACGACAAAGATGGCGGCTGCACCAAGCG	934
301	QY	GluIleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrrGlyGluAsp	320
935	Db	GAATTCCTGGGTAAATGGAAACATGTTGTGGCGAGTCAGGCCCAACTATGGCGAGGAC	994
321	QY	LeuThrArgHisHisAspGluLeu	328
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RESULT 8
US/10-028-072-363
Sequence 363, Application US/10028072
Publication No. US2003004311A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/028.072
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
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us-09-768-840-1.olip2n.rnpb

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4	PRIOR APPLICATION NUMBER: 60/059184
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PRIOR FILING DATE:	1998-06-17
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PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090863
PRIOR FILING DATE:	1998-06-26
PRIOR APPLICATION NUMBER:	60/091360
PRIOR FILING DATE:	1998-07-01
PRIOR APPLICATION NUMBER:	60/091519
PRIOR FILING DATE:	1998-07-02
PRIOR APPLICATION NUMBER:	60/091982
PRIOR FILING DATE:	1998-07-07

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Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
DB:	9	Gaps:	0	

ПС-09-768-840-1 (1-328) x US-10-028-072-363 (1-1503)

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QY	21	Lys	Pro	Ser	Pro	Asp	Ala	Gly	Pro	His	Gly	Gln	Gly	Arg	Val	His	Gln	Ala	Pro	Leu	40		
DB	95	A	A	G	C	A	T	C	C	C	A	G	C	A	G	C	C	C	T	A	T	154	
QY	41	Ser	Asp	Ala	Pro	His	Asp	Asp	Ala	His	Gly	Asn	Phe	Gln	Tyr	Asp	His	Glu	Ala	Phe	Leu	60	
DB	155	A	C	G	A	C	G	C	T	C	C	A	T	G	A	T	G	A	T	G	A	214	
QY	61	Gly	Arg	Glu	Val	Ala	Lys	Glu	Phe	Asp	Gln	Leu	Thr	Pro	Glu	Glu	Ser	Gln	Ala	Arg	Leu	80	
DB	215	G	A	C	G	G	G	A	G	T	G	G	C	A	A	T	C	C	C	C	A	274	
QY	81	Gly	Arg	Ile	Val	Asp	Arg	Met	Asp	Arg	Ala	Gly	Asp	Gly	Asp	Gly	Val	Ser	Leu	Ala	100		
DB	275	G	G	C	G	G	A	T	G	T	G	A	C	C	G	C	G	G	G	A	334		
QY	101	Glu	Leu	Arg	Ala	T	Trp	Ile	Ala	His	Thr	Gln	Gln	Arg	His	Ile	Arg	Asp	Ser	Val	Ser	Ala	120
DB	335	G	A	C	T	T	C	G	C	G	T	G	A	T	C	G	C	A	C	A	394		
QY	121	Ala	Trp	Asp	Thr	Tyr	Asp	Thr	Asp	Arg	Asp	Gly	Arg	Val	Gly	Trp	Glu	Leu	Arg	Asn	140		
DB	395	G	C	T	G	G	A	C	A	G	T	A	C	A	C	A	C	A	C	A	454		
QY	141	Ala	Thr	Tyr	Gly	His	Tyr	Ala	Pro	Gly	Glu	U	Phe	His	Asp	Val	Glu	Asp	Ala	Glu	Thr	160	
DB	455	G	C	A	C	T	T	G	C	C	A	T	A	C	A	C	A	C	A	C	514		
QY	161	Tyr	Lys	Lys	Met	Leu	Ala	Arg	Asp	Glu	Arg	Phe	Arg	Val	Ala	Asp	Gln	Asp	Gly	Asp	180		
DB	515	T	A	C	A	A	A	A	G	A	T	G	T	G	C	T	G	G	G	C	574		
QY	181	Ser	Met	Ala	Thr	Arg	Glu	Glu	Leu	Thr	Ala	Phe	Leu	His	Pro	Glu	Glu	Phe	Pro	His	Met	200	
DB	575	T	C	G	A	T	G	C	C	A	C	T	C	T	G	C	A	C	C	C	634		
QY	201	Arg	Asp	Ile	Val	Ile	Ala	Glu	Thr	Leu	Glu	Asp	Leu	Asp	Arg	Asn	Lys	Asp	Gly	Tyr	Val	220	

635	Db		CGGGACATCGTGATTCTGAAACCCCTGGAGGACCTGGACAGAAAAAAGATGGCTATGTC	594
221	QY		GlnValGluGlnTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGluGluProAla	240
695	Db		CAGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTTGGGAGGAGGAGCGCGC	754
241	QY		TrpValGlnThrGluArgGlnGlnPheArgAspPheArgAspLeuAsnLysAspGlyHis	260
755	Db		TGGGTGCAGACGGAGAGGACAGCAGTCCCGGACTTCGGGATCTGAACAAGGATGGGCAC	814
261	QY		LeuAspGlySerGluValGlyHisTrpValLeuProProAlaGlnAspGlnProLeuVal	280
815	Db		CTGGATGGAGTGGAGTGGGCGCACTGGGTGCTGCCCTGCCCGACGACCCCTGGTG	874
281	QY		GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla	300
875	Db		GAAGCCACACCCCTGCTGCACACAGCGGCACACGACAAAGGATGGCGGCTGAGCAAAAGC	934
301	QY		GluIleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAsp	320
935	Db		GAATCCCTGGGTAAATTGGAACATGTTTGTGGCAGTCAGGCCACCACTATGGCGAGGAC	994
321	QY		LeuThrArgHisHisAspClnLeu	328
995	Db		CTGACCCGCGCACACGATGAGCTG	1018

RESULT 9
HS-09-906-742-220

US-09-906-742-220
; Sequence 220, Application US/09906742
US20030023054A1

; Publication No. US20
: GENERAL INFORMATION:

7 GENERAL INFORMATION: 1
7 APPLICANT: Genentech, Inc. 2
7 APPLICANT: Ashkenazi, Avi. 3
7 APPLICANT: Botstein, David 4
7 APPLICANT: Desnoyers, Luc 5
7 APPLICANT: Eaton, Dan L. 6
7 APPLICANT: Ferrara, Napoleone 7
7 APPLICANT: Flivartoff, Ellen 8
7 APPLICANT: Fong, Sherman 9
7 APPLICANT: Gao, Wei-Qiang 10
7 APPLICANT: Gerber, Hanspeter 11
7 APPLICANT: Gerritsen, Mary E. 12
7 APPLICANT: Goddard, A. 13
7 APPLICANT: Godowski, Paul J. 14
7 APPLICANT: Grimaldi, Christopher J. 15
7 APPLICANT: Gurney, Austin L. 16
7 APPLICANT: Hillan, Kenneth, J. 17
7 APPLICANT: Kljavin, Ivar J. 18
7 APPLICANT: Mather, Jennie P. 19
7 APPLICANT: Pan, James 20
7 APPLICANT: Paoni, Nicholas F. 21
7 APPLICANT: Roy, Margaret Ann 22
7 APPLICANT: Stewart, Timothy A. 23
7 APPLICANT: Tumas, Daniel 24
7 APPLICANT: Williams, P. Mickey 25
7 APPLICANT: Wood, William, I. 26
7 TITLE OF INVENTION: Secreted and Tr 27
7 TITLE OF INVENTION: Acids Encoding 28
7 FILE REFERENCE: 10466-14 29
7 CURRENT APPLICATION NUMBER: US/09/99- 30
7 CURRENT FILING DATE: 2001-07-16 31
7 PRIOR APPLICATION NUMBER: 09/665,35 32
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7 PRIOR APPLICATION NUMBER: PCT/US00/ 34
7 PRIOR FILING DATE: 2000-02-22 35
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7 PRIOR FILING DATE: 1999-07-07 37
7 PRIOR APPLICATION NUMBER: US 60/14 38
7 PRIOR FILING DATE: 1999-07-26 39
7 PRIOR APPLICATION NUMBER: US 60/14 40
7 PRIOR FILING DATE: 1999-07-28 41
7 PRIOR APPLICATION NUMBER: PCT/US99 42

APPLICANT: WILLIAMS, P. MICHAEL
 APPLICANT: WOOD, WILLIAM, I.
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACID SEQUENCES ENCODING THE SAME

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: PRIOR FILING DATE: 1999-09-08
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: PRIOR APPLICATION NUMBER: PCT/US00/00219
: PRIOR FILING DATE: 2000-01-05
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: SEQ ID NO 220
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: TYPE: DNA
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US-09-906742-220

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Alignment Scores:	
Pred. NO.:	0
Score:	328.00
Percent Similarity:	100.00%
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Length:	1503
Matches:	328
Conservative:	0
Mismatches:	0
Indels:	0
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US-09-768-840-1 (1-328) x US-09-906-742-220 (1-1503)

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QY	181	SerMetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMet	200
Db	575	TCGATGGCCACTCGAGAGAGGAGCTGACAGCTTCCTGTCACCCCGAGGAGTTCCCTCACATG	634
QY	201	ArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrVal	220
Db	635	CGGGACATCGTGAATTCGTGAAACCTCGAGGACCTGCACAGAACAAGATGGCTATGTC	694
QY	221	GlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGluProAla	240
Db	695	CAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCAGCTCGGGAGGAGGAGCGCGG	754
QY	241	TrpValGlnThrGluArgGlnGlnPheArgAspPheArgAspLeuAsnLysAspGlyHis	260
Db	755	TGGGTGCAGACGGAGAGCGACGACTTCCGGGACTTCGGGGATCTGAACAAAGATGGGCAC	814
QY	261	LeuAspGlySerGluValGlyHisTrpValLeuProProAlaGlnAspGlnProLeuVal	280
Db	815	CTGATGGGAGTGAGGTGGGCCACTGGGTGCTGCCCTGCCAGACCAAGGAGGAGGAGG	874
QY	281	GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgGluSerLysAla	300
Db	875	GAAGCCAAACCACTGCTGCACGAGAGCGACACGAGTGGGGCTGAGCAAAAGCG	934
QY	301	GluIleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAsp	320
Db	935	GAATCTCGGGTAATTGGAAACATGTTGTGGCAGTCAGGCCCAACCACTATGGCAGGAC	994
QY	321	LeuThrArgHisHisAspGluLeu	328
Db	995	CTGACCCCGCACCAAGATGAGCTG	1018
RESULT 10			
US-10-121-049-363			
; Sequence 363, Application US/10121049			
; Publication No. US20030022239A1			
; GENERAL INFORMATION:			
; APPLICANT: Baker, Kevin P.			
; APPLICANT: Beresini, Maureen			
; APPLICANT: DeForge, Laura			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Filvaroff, Ellen			
; APPLICANT: Gao, Wei-Qiang			
; APPLICANT: Gerritsen, Mary E.			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Sherwood, Steven			
; APPLICANT: Smith, Victoria			
; APPLICANT: Stewart, Timothy A.			
; APPLICANT: Tumas, Daniel			
; APPLICANT: Watanabe, Colin K			
; APPLICANT: Wood, William			
; APPLICANT: Zhang, Zemin			
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
; TITLE OF INVENTION: ACIDS ENCODING THE SAME			
; FILE REFERENCE: P3330R1C17			
; CURRENT APPLICATION NUMBER: US/10/121.049			
; CURRENT FILING DATE: 2002-04-12			
; Prior Application removed - See File Wrapper or Palm			
; NUMBER OF SEQ ID NOS: 550			
; SEQ ID NO 363			
; LENGTH: 1503			
; TYPE: DNA			
; ORGANISM: Homo Sapien			
US-10-121-049-363			
Alignment Scores:			

Alignment Scores:

[illegible]

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QY 121 AlaTrpAspThrTyrAspThrAspArgAspGlyArgValGlyTyrPgluLuuLeuArgAsn 140
Db 395 GCCTGGGACACGTACACACGGACCGCGCGCGTGTGGTGGGAGGAGCTGGCGAAC 454
QY 141 AlaThrTyrGlyHisTyrAlaProGlyGluGluPheHisAspValGluAspAlaGluThr 160
Db 455 GCCACCTATGGCCACTACGCGCGCGTGAAGAAATTCATGACGTGGAGGAGTGCAGAGCC 514
QY 161 TyrLysMetLeuAlaArgAspGluArgArgPheArgValAlaAspGlnAspGlyAsp 180
Db 515 TACAAAAGATGCTGGCTGGGACGAGCGCGGTTCCTGGGAGGAGTGCAGAGCC 574
QY 181 SerMetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMet 200
Db 575 TCGATGGCCACTCGAGAGGAGCTGACAGCCTTCCTGCACCCCGAGGAGTTCCTTCACATG 634
QY 201 ArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrVal 220
Db 635 CGGGACATCGTGATTGCTGAAACCTGGAGGACCTGGACAGAAACAAAGATGGCTATGTC 694
QY 221 GlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGluGluProAla 240
Db 695 CAGGTGGAGGAGTACATCGCGGATCTGACTACGCCGAGCTGGGAGGAGGAGCGCGG 754
QY 241 TrpValGlnThrGluArgGlnGlnPheArgAspPheArgAspLeuAsnLysAspGlyHis 260
Db 755 TGGGTGCAGACGAGACGACAGTTCGGGACTTCGGGATCTGAACAAGATGGGCAC 814
QY 261 LeuAspGlySerGluValGlyHisTyrValLeuProAlaGlnAspGlnProLeuVal 280
Db 815 CTGGATGGGAGTGGAGTGGCCACTGGGTCTGCCCTGCCAGGACCGCCCTGGTG 874
QY 281 GluAlaAsnHisLeuLeuHisGluSerAspThrAspPlyAspGlyArgLeuSerLysAla 300
Db 875 GAAGCCACCACTGCTGCAGAGACGACGACGACGACGACGACGACGACGACGACGACG 934
QY 301 GluIleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyLuuasp 320
Db 935 GAATCTCTGGGTAAATGGAACTGTTGTGGCAGTGCAGCCACCACTATGGGAGGAC 994
QY 321 LeuThrArgHisHisAspGluLeu 328
Db 995 CTGACCCGCGACACCATGATGAGTGT 1018

```

RESULT 12

US-10-140-470-363

Sequence 363, Application US/10140470

Publication No. US2003002231A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Naureen

APPLICANT: DeForge, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Flivaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tamas, Daniel

APPLICANT: Watanabe, Colin K

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P33031C160

CURRENT APPLICATION NUMBER: US/10/140,470

CURRENT FILING DATE: 2002-05-06

Prior Application removed - See Palm or File Wrapper

NUMBER OF SEQ ID NOS: 550

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; SEQ ID NO 363
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-470-363

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Alignment Scores:

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Pred. No.: 0 Length: 1503
Score: 328.00 Matches: 328
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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US-09-768-840-1 (1-328) x US-10-140-470-363 (1-1503)

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QY 1 MetMetTrpArgProSerValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 20
Db 35 ATGATGTGGCGACCATCAGTTCTGCTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTG 94
QY 21 LysProSerProAspAlaGlyProHisGlyGlnGlyArgValHisGlnAlaAlaProLeu 40
Db 95 AAGCCATCCCGACAGCAGCGCCCTCATGGCCAGGGAGGTGCACCCAGCGCCGCCCTG 154
QY 41 SerAspAlaProHisAspAspAlaHisGlyAsnPheGlnTyrAspHisGluAlaPheLeu 60
Db 155 AGGCACGCTCCCATGATGACGCCACGCCACGCCGAACTTCCAGTACGACCATGAGGCTT 214
QY 61 GlyArgGluValAlaLysGluPheAspGlnLeuThrProGluGluSerGlnAlaArgLeu 80
Db 215 GGACGGGAAGTGCCCAAGGAATTCGACCAACTCACCCAGAGAGAAAGCCAGCCGCTG 274
QY 81 GlyArgIleValAspArgMetAspArgAlaGlyAspGlyAspGlyTyrPValSerLeuAla 100
Db 275 GGCGGATCGTGACCGCATGACCGCGCGGGGAGCGGCGCGGCGGCGGCGGCGGCGGCG 334
QY 101 GluLeuArgAlaTrpIleAlaHisThrGlnGlnArgHisIleArgAspSerValSerAla 120
Db 335 GAGCTTCGGCGGTGATCGGCACACGCGCAGCAGCGGCGACATACGGGACTCGGTGAG 394
QY 121 AlaTrpAspThrTyrAspThrAspArgAspGlyArgValGlyTyrPgluLuuLeuArgAsn 140
Db 395 GCCTGGGACACGTACGACACGCGCGCGCGGTGTGGGTTCGGAGGAGCTGGCGAAC 454
QY 141 AlaThrTyrGlyHisTyrAlaProGlyGluGluPheHisAspValGluAspAlaGluThr 160
Db 455 GCCACCTATGGCCACTACGCGCGCGGTGAAGAAATTCATGACGTGGAGGATGCAGAGCC 514
QY 161 TyrLysMetLeuAlaArgAspGluArgArgPheArgValAlaAspGlnAspGlyAsp 180
Db 515 TACAAAAGATGCTGGCTGGGACGACGCGCGGTTCGGGTTCGCCAGCAGGATGGGAC 574
QY 181 SerMetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMet 200
Db 575 TCGATGGCCACTCGAGAGGAGCTGACAGCCTCTCTCACCCCGGAGGAGTTCCTCATATG 634
QY 201 ArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrVal 220
Db 635 CGGGACATCGTGATGCTGAACCTTGGAGGACCTGGAGGAGCTGGAGGAGGAGGAGGAG 694
QY 221 GlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGluGluProAla 240
Db 695 CAGGTGGAGGAGTACATCGCGGATCTGACTCAGCCGAGCCTGGGAGGAGGAGGAGGAG 754
QY 241 TrpValGlnThrGluArgGlnGlnPheArgAspPheArgAspLeuAsnLysAspGlyHis 260
Db 755 TGGGTGCAGACGAGGAGGAGGAGTTCGGGACTTCCGGGATCTCGAACAAGATGGGCAC 814
QY 261 LeuAspGlySerGluValGlyHisTyrValLeuProAlaGlnAspGlnProLeuVal 280
Db 815 CTGGATGGGAGTGGAGTGGCCACTGGGTGCTGCCCTGCCAGGACCGCCCTGGTG 874
QY 281 GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla 300

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[illegible]

QY	241	TTPValGlnThrGluArgGlnGlnPheArgAspPheArgAspLeuAsnLysAspGlyHis	260
Db	755	TGGGTGCACAGCGAGCAGCAGCTCCGGGACTTCGGGATCTGACACAGGATGGGCAC	814
QY	261	LeuAspGlySerGluValGlyHisTrpValLeuProProAlaGlnAspGlnProLeuVal	280
Db	815	CTGGATGGAGTGAAGTGGGCCACTGGGTGCTGCCTGCCAGCAGCACGCCCTGGTG	874
QY	281	GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla	300
Db	875	GAAGCCAAACCACTGCTGCACGAGCGACACGGACAAGATGGCGGCTGACAAAGCG	934
QY	301	GluIleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTrpGlyGluAsp	320
Db	935	GAATCTCGGTATTTGGAAACATGTTTGTGGCCACTCAGCCACCAACTATGCGAGGAC	994
QY	321	LeuThrArgHisHisAspGluLeu	328
Db	995	CTGACCGGGCCACCAGATGAGCTG	1018

RESULT 14

US-09-907-613-220
; Sequence 220, Application US/09907613
; Publication No. US20030027145A1

GENERAL INFORMATION:

1	APPLICANT:	Genentech, Inc.	
2	APPLICANT:	Askenazi, Avi	
3	APPLICANT:	Botstein, David	
4	APPLICANT:	Desnovers, Luc	
5	APPLICANT:	Eaton, Dan L.	
6	APPLICANT:	Ferrara, Napoleone	
7	APPLICANT:	Flivaroff, Ellen	
8	APPLICANT:	Fong, Sherman	
9	APPLICANT:	Gao, Wei-Qiang	
10	APPLICANT:	Gerber, Hanspeter	
11	APPLICANT:	Garritsen, Mary E.	
12	APPLICANT:	Goddard, A.	
13	APPLICANT:	Godowski, Paul J.	
14	APPLICANT:	Grimaldi, Christopher J.	
15	APPLICANT:	Gurney, Austin L.	
16	APPLICANT:	Hillan, Kenneth, J.	
17	APPLICANT:	Klijavin, Ivar J.	
18	APPLICANT:	Mather, Jennie P.	
19	APPLICANT:	Pan, James	
20	APPLICANT:	Raonl, Nicholas F.	
21	APPLICANT:	Roy, Margaret Ann	
22	APPLICANT:	Stewart, Timothy A.	
23	APPLICANT:	Tumas, Daniel	
24	APPLICANT:	Williams, P. Mickey	
25	APPLICANT:	Wood, William, I.	
26	TITLE OF INVENTION:	Secreted and Trans-	
27	TITLE OF INVENTION:	Acids Encoding the	
28	FILE REFERENCE:	10466-14	
29	CURRENT APPLICATION NUMBER:	US/09/907,	
30	CURRENT FILING DATE:	2001-07-17	
31	PRIOR APPLICATION NUMBER:	PCT/US00/0444	
32	PRIOR FILING DATE:	2000-02-22	
33	PRIOR APPLICATION NUMBER:	US 60/143,040	
34	PRIOR FILING DATE:	1999-07-07	
35	PRIOR APPLICATION NUMBER:	US 60/145,69	
36	PRIOR FILING DATE:	1999-07-26	
37	PRIOR APPLICATION NUMBER:	US 60/146,22	
38	PRIOR FILING DATE:	1999-07-28	
39	PRIOR APPLICATION NUMBER:	PCT/US99/205	
40	PRIOR FILING DATE:	1999-09-08	
41	PRIOR APPLICATION NUMBER:	PCT/US99/209	
42	PRIOR FILING DATE:	1999-09-13	
43	PRIOR APPLICATION NUMBER:	PCT/US99/210	
44	PRIOR FILING DATE:	1999-09-15	
45	PRIOR APPLICATION NUMBER:	PCT/US99/215	
46	PRIOR FILING DATE:	1999-09-15	
47	PRIOR APPLICATION NUMBER:	PCT/US99/230	

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: PRIOR FILING DATE: 1999-10-05
: PRIOR APPLICATION NUMBER: PCT/US99/28214
: PRIOR FILING DATE: 1999-11-29
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: 1999-11-30
: PRIOR APPLICATION NUMBER: PCT/US99/28564
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/28565
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: PCT/US99/30911
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: PCT/US99/30999
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: PCT/US00/00219
: PRIOR FILING DATE: 2000-01-05
: NUMBER OF SEQ ID NOS: 423
: SEQ ID NO 220
: LENGTH: 1503
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-907-613-220

Alignment Scores:
Pred. No.: 0
Score: 328.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 9
Length: 1503
Matches: 328
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

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US-09-768-840-1 (1-328) x US-09-907-613-220 (1-1503)

Alignment Scores:

[illegible]

[illegible]

Qy 161 TyrLysLysMetLeuAlaArgAspGluArgArgPheArgValAlaAspGlnAspGlyAsp 180
Db 515 TACAAAAGATGCTGGCTCGGGACGAGCGCGTTCCCGGTGGCCGACAGGATGGGAC 574
Qy 181 SerMetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMet 200
Db 575 TCGATGGCCACTCGAGAGGAGCTGACAGCCTTCCCTGCACCCCGAGAGTTCCCTCACATG 634
Qy 201 ArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrVal 220
Db 635 CGGGACATCGTGATTCTGAAACCCCTGGAGGACCTGGACAGAAACAAGATGGCTATGTC 694
Qy 221 GlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGluProAla 240
Db 695 CAGGTGGAGGAGTACATCGCGATCTGTACTCAGCCGAGCCCTGGGGAGGAGCGCGCG 754
Qy 241 TrpValGlnThrGluArgGlnGlnPheArgAspPheArgAspLeuAsnLysAspGlyHis 260
Db 755 TGGGTGCACAGCGAGAGCGACAGTTCGGGACTTCGGGATCTGAACAAGGATGGGCAC 814
Qy 261 LeuAspGlySerGluValGlyHisTrpValLeuProProAlaGlnAspGlnProLeuVal 280
Db 815 CTGGATGGGACTGAGTGGGCCACTGGGTGCTGCCCTGCCACAGGACCGCCCTGGTG 874
Qy 281 GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla 300
Db 875 GAAGCAACCACTGCTGCACGAGAGCGACACGACAGGATGGCGGCTGAGCAAGCG 934
Qy 301 GluIleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAsp 320
Db 935 GAAATCCCTGGGTAAATTGGAACATGTTTGTGGGCAGTCAGGCCACCACTATGGCGAGGAC 994
Qy 321 LeuThrArgHisHisAspGluLeu 328
Db 995 CTGACCCGGCACCAAGATGACCTG 1018

Search completed: May 20, 2003, 09:50:38
Job time : 170 secs

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Tue May 20 14:43:33 2003

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EMBL; D43952; BAA07896.1; JOINED.
EMBL; D43954; BAA07896.1; JOINED.
EMBL; D43955; BAA07896.1; JOINED.
PIR; A45337; A45337.
MGD; MGI:104559; Rcn.
InterPro; IPR002048; EF-hand.
InterPro; IPR000886; ER_target.
Pfam; PF00036; ehand; 6.
SMART; SM00054; EFh; 3.
PROSITE; PS00014; ER_TARGET; 1.
PROSITE; PS00018; EF_HAND; 4.
Calcium-binding; Endoplasmic reticulum; Signal; Glycoprotein; Repeat;
Repeat.
SIGNAL 1 23 RETICULOCALBIN 1.
CHAIN 24 325 EF-HAND 1.
CA_BIND 86 97 EF-HAND 2 (POSSIBLY ANCESTRAL).
CA_BIND 122 133 EF-HAND 3.
CA_BIND 173 184 EF-HAND 4.
CA_BIND 210 221 EF-HAND 5.
CA_BIND 251 262 EF-HAND 6 (POSSIBLY ANCESTRAL).
CA_BIND 287 298 PREVENT SECRETION FROM ER.
CA_BIND 322 325 N-LINKED (GLCNAC. . .) (PARTIAL).
SITE 47 47 K -> G (IN REF. 3).
CONFLICT 24 24 R -> I (IN REF. 3).
CONFLICT 34 34 SEL -> DEE (IN REF. 3).
CONFLICT 37 39
SEQUENCE 325 AA; 38113 MW; 0470B10B5A8BC76D CRC64;

Query Match 68.6%; Score 48; DB 1; Length 325;
Best Local Similarity 69.2%; Pred. No. 0.69;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLNKGDLGSEV 13
Db 251 DLNKGDLKDEI 263
IIIIIIII I I

RESULT 2
RCN1_HUMAN STANDARD; PRT; 331 AA.
AC Q15293;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Reticulocalbin 1 precursor.
GN RCN1 OR RCN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=96172582; PubMed=8586628;
RA Ozawa M.;
RT "Cloning of a human homologue of mouse reticulocalbin reveals
conservation of structural domains in the novel endoplasmic reticulum
resident Ca(2+)-binding protein with multiple EF-hand motifs.";
RL J. Biochem. 117:1113-1119(1995).
[2]
SEQUENCE FROM N.A.
RA Coville G.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: MAY REGULATE CALCIUM-DEPENDENT ACTIVITIES IN THE
ENDOPLASMIC RETICULUM LUMEN OR POST-ER COMPARTMENT.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
SITES; POTENTIAL SITES II AND VI HAVE LOST AFFINITY FOR CALCIUM
(BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CREC FAMILY.
CC -1- SIMILARITY: CONTAINS 6 EF-HAND CALCIUM-BINDING DOMAINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; D42073; BAA07670.1;
EMBL; AL078612; CAB53067.1;
Genew; HGNC:9934; RCN1.
MIN; 602735;
InterPro; IPR002048; EF-hand.
InterPro; IPR000886; ER_target.
Pfam; PF00036; ehand; 6.
SMART; SM00054; EFh; 3.
PROSITE; PS00014; ER_TARGET; 1.
PROSITE; PS00018; EF_HAND; 4.
Calcium-binding; Endoplasmic reticulum; Signal; Glycoprotein; Repeat;
Polymorphism.
SIGNAL 1 29 RETICULOCALBIN 1.
CHAIN 30 331 EF-HAND 1 (POTENTIAL).
CA_BIND 92 103 EF-HAND 2 (POSSIBLY ANCESTRAL).
CA_BIND 128 139 EF-HAND 3 (POTENTIAL).
CA_BIND 179 190 EF-HAND 4 (POTENTIAL).
CA_BIND 216 227 EF-HAND 5 (POTENTIAL).
CA_BIND 257 268 EF-HAND 6 (POSSIBLY ANCESTRAL).
CA_BIND 293 304 PREVENT SECRETION FROM ER.
CA_BIND 328 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
SITE 53 53 T -> N (IN DBSNP:1061145).
CARBOHYD 71 71 /FTID=VAR_011964.
VARIANT 73 73 D -> Y (IN DBSNP:1804281).
VARIANT 74 74 Q -> E (IN DBSNP:1061143).
VARIANT 188 188 /FTID=VAR_011966.
VARIANT 331 331 R -> P (IN DBSNP:1061080).
SEQUENCE 331 AA; 38890 MW; 608AAD53693F789 CRC64;

Query Match 68.6%; Score 48; DB 1; Length 331;
Best Local Similarity 69.2%; Pred. No. 0.7;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLNKGDLGSEV 13
Db 257 DLNKGDLKDEI 269
IIIIIIII I I

RESULT 3
PPE2_HUMAN STANDARD; PRT; 753 AA.
ID PPE2_HUMAN
AC Q14830; O14831;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serine/threonine protein phosphatase with EF-hands-2 (BC 3.1.3.16)
(PPEF-2).
GN PPE2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A. (ISOFORMS PPEF-2(S) AND PPEF-2(L)).
RP TISSUE=Retina;
RX MEDLINE=97471020; PubMed=9326663;
RA Sherman P.M., Sun H., Macke J.P., Williams J., Smallwood P.M.,
Nathans J.;
RT "Identification and characterization of a conserved family of protein
serine/threonine phosphatases homologous to Drosophila retinal
degeneration C (rdgc).";
RL Proc. Natl. Acad. Sci. U.S.A. 94:11639-11644(1997).
CC -1- FUNCTION: MAY PLAY A ROLE IN PHOTOTRANSDUCTION. MAY
DEPHOSPHORYLATE PHOTOACTIVATED RHODOPSIN. MAY FUNCTION AS A

Tue May 20 14:43:33 2003

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FT METAL 179 179 IRON (BY SIMILARITY).
FT METAL 181 181 IRON (BY SIMILARITY).
FT METAL 208 208 IRON AND MANGANESE (BY SIMILARITY).
FT METAL 240 240 MANGANESE (BY SIMILARITY).
FT ACT_SITE 241 241 GENERAL ACID (BY SIMILARITY).
FT METAL 292 292 MANGANESE (BY SIMILARITY).
FT METAL 492 492 MANGANESE (BY SIMILARITY).
FT METAL 757 757 AA; 86644 MW; 821B3D1061AC00C8 CRC64;
SQ SEQUENCE 757 AA; 86644 MW; 821B3D1061AC00C8 CRC64;

Query Match. 67.1%; Score 47; DB 1; Length 757;
Best Local Similarity 66.7%; Pred. No. 2.4;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DLNKGHLDGSE 12
| | | | | : |
DB 709 DFNKGHDHINE 720

RESULT 5
NAGH_CLOPE STANDARD; PRT; 1628 AA.
ID NAGH_CLOPE AC P26831;
DT 01-AUG-1992 (Rel. 23, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hyaluronoglucosaminidase precursor (EC 3.2.1.35) (Hyaluronidase)
DE (Mu toxin).
GN NAGH OR CPE0191.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CPN50.
RC MEDLINE=94322189; PubMed=8177218;
RA Canard B., Garnier T., Saint-Joanis B., Cole S.T.;
RA "Molecular genetic analysis of the nagH gene encoding a hyaluronidase
of Clostridium perfringens.";
RT Mol. Gen. Genet. 243:215-224(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=13 / Type A;
RA PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RA "Complete genome sequence of Clostridium perfringens, an anaerobic
flesh-eater.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
RL -1- FUNCTION: Putative virulence factor which is likely to act on
connective tissue during gas gangrene.
CC -1- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-linkages between N-
acetyl-beta-D-glucosamine and D-glucuronate residues in
hyaluronate.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- CAUTION: The partially purified protein from strain CPN50 is
approximately 70 kDa smaller than the sequence indicated here.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M61878; AAX23259.1;
CC EMBL: AF003185; BAB79897.1;
CC PIR: S27540; S27540.
CC InterPro: IPR002105; Dockerin_1.
CC InterPro: IPR000421; FA58_C.
CC Pfam: PF00404; Dockerin_1; 2.
CC Pfam: PF00754; F5_F8_type_C; 1.

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DR SMART: SM00231; FA58C; 1.
KW Hydrolase; Glycosidase; Toxin; Repeat; Signal; Complete proteome.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 1628 HYALURONOGUCOSAMINIDASE.
FT DOMAIN 703 1032 3 X APPROXIMATE REPEATS.
FT REPEAT 703 748 1.
FT REPEAT 848 894 2.
FT REPEAT 987 1032 3.
FT VARIANT 147 147 G -> A (IN STRAIN CPN50).
FT VARIANT 172 175 KIQS -> EIKN (IN STRAIN CPN50).
FT VARIANT 250 250 V -> M (IN STRAIN CPN50).
FT VARIANT 548 548 A -> E (IN STRAIN CPN50).
FT VARIANT 558 558 D -> E (IN STRAIN CPN50).
FT VARIANT 614 614 G -> S (IN STRAIN CPN50).
FT VARIANT 944 944 I -> V (IN STRAIN CPN50).
FT VARIANT 950 950 N -> S (IN STRAIN CPN50).
FT VARIANT 979 979 T -> I (IN STRAIN CPN50).
FT VARIANT 982 982 I -> L (IN STRAIN CPN50).
FT VARIANT 1042 1042 I -> F (IN STRAIN CPN50).
FT VARIANT 1043 1043 MISSING (IN STRAIN CPN50).
FT SEQUENCE 1628 AA; 182474 MW; D4252A2512BBED69 CRC64;
SQ SEQUENCE 1628 AA; 182474 MW; D4252A2512BBED69 CRC64;

Query Match. 62.9%; Score 44; DB 1; Length 1628;
Best Local Similarity 61.5%; Pred. No. 17;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLNKGHLDGSEV 13
| | | | | : |
DB 1607 DLNKGDSIDEYEI 1619

RESULT 6
PPEL_HUMAN STANDARD; PRT; 653 AA.
ID PPEL_HUMAN AC 014829; Q15253; Q9UJH0; Q9NU21;
DT 16-OCT-2001 (Rel. 40, Created)
DT 15-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serine/threonine protein phosphatase with EF-hands-1 (EC 3.1.3.16)
DE (PPEF-1) (Protein phosphatase with EF calcium-binding domain) (PPEF)
DE (Serine/threonine protein phosphatase 7) (PF7).
GN PPEF1 OR PPEF OR PPP7C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=97471020; PubMed=9326663;
RA Sherman P.M., Sun H., Macke J.P., Williams J., Smallwood P.M.,
RA Nathans J.;
RA "Identification and characterization of a conserved family of protein
serine/threonine phosphatases homologous to Drosophila retinal
degeneration C.";
RT Proc. Natl. Acad. Sci. U.S.A. 94:11639-11644(1997).
RN [2]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Fetal brain;
RX MEDLINE=97358589; PubMed=9215685;
RA Montini E., Rugari E.I., van de Vosse E., Andolfi G., Mariani M.,
RA Puca A.A., Consales G.G., den Dunnen J.F., Ballabio A., Franco B.;
RA "A novel human serine-threonine phosphatase related to the Drosophila
retinal degeneration C (rdgC) gene is selectively expressed in sensory
neurons of neural crest origin.";
RT Hum. Mol. Genet. 6:1137-1145(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=98104127; PubMed=9430683;
RA Huang X., Honkanen R.E.;
RA "Molecular cloning, expression, and characterization of a novel human
serine/threonine protein phosphatase, PP7, that is homologous to

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RT Drosophila retinal degeneration C gene product (rdgC).";
 RL J. Biol. Chem. 273:1462-1468(1998).
 RN [4]
 RA SEQUENCE OF 1-355 FROM N.A.
 RP Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 356-653 FROM N.A.
 RA Way P.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: MAY HAVE A ROLE IN THE RECOVERY OR ADAPTATION RESPONSE
 CC OF PHOTORECEPTORS. MAY HAVE A ROLE IN DEVELOPMENT. MAXIMAL
 CC ACTIVITY IS OBSERVED AT PH 8.0.
 CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O -> a protein +
 CC phosphate.
 CC -1- COFACTOR: MAGNESIUM.
 CC -1- ENZYME REGULATION: ACTIVATED BY CALCIUM.
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; 1 (SHOWN HERE), 1A, 1B, 2 AND 3;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING. ISOFORM 3 MAY HAVE NO
 CC FUNCTIONAL SIGNIFICANCE.
 CC -1- TISSUE SPECIFICITY: DETECTED IN RETINA AND RETINAL DERIVED Y-79
 CC RETINOBLASTOMA CELLS. ALSO FOUND IN FETAL BRAIN.
 CC -1- SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES.
 CC -1- SIMILARITY: CONTAINS 1 IQ DOMAIN
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 CC -----
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 CC -----
 DR EMBL; AF023455; AAB82795.1;
 DR EMBL; X97867; CAAG6461.1;
 DR EMBL; AF027977; AAC05825.1;
 DR EMBL; 294056; CAB40074.1;
 DR EMBL; AL096700; CAB86407.1;
 DR HSSP; P08129; IFJM.
 DR Genew; HGNC:9243; PPEFT.
 DR MIM; 300109;
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR000048; IQ-region.
 DR InterPro; IPR004843; M-peptase.
 DR InterPro; IPR004844; S/T-phosphatase.
 DR Pfam; PF00036; ehand; 3.
 DR Pfam; PF00149; Metallophos; 1.
 DR PRINTS; PF00612; IQ; 1.
 DR PRODOM; PR00114; STPHPTASE.
 DR PRODOM; PD000012; EF-hand; 1.
 DR PRODOM; PD000252; S/T-phosphatase; 2.
 DR SMART; SM00054; Efh; 2.
 DR SMART; SM00015; IQ; 1.
 DR SMART; SM00156; PF2AC; 1.
 DR PROSITE; PS00018; EF-HAND; 2.
 DR PROSITE; PS00125; SER_THR_PHOSPHATASE; 1.
 DR PROSITE; PS50096; IQ; 1.
 DR KW Hydrolyase; Calcium-binding; Magnesium; Iron; Manganese; Repeat;
 DR Alternative splicing.
 FT DOMAIN 18 43
 FT CATALYTIC. 121 455
 FT ANCESTRAL CALCIUM SITE. 456 507
 FT EF-HAND 1 (POTENTIAL). 579 590
 FT EF-HAND 2 (POTENTIAL). 619 630
 FT IRON (BY SIMILARITY). 172 172
 FT IRON (BY SIMILARITY). 174 174
 FT IRON (BY SIMILARITY). 201 201
 FT IRON AND MANGANESE (BY SIMILARITY). 233 233
 FT MANGANESE (BY SIMILARITY). 234 234
 FT GENERAL ACID (BY SIMILARITY). 285 285
 FT MANGANESE (BY SIMILARITY). 403 403
 FT MANGANESE (BY SIMILARITY). 403 403
 FT MISSING (IN ISOFORM 1A). 79 132
 FT VARSPLIC

FT VARSPLIC 328 355 MISSING (IN ISOFORM 1B).
 FT VARSPLIC 356 376 IIDILSDPRGKNGCFPTNCR -> SGYYGQRHDIKRES
 FT DFTKK (IN ISOFORM 2).
 FT VARSPLIC 377 653 MISSING (IN ISOFORM 2).
 FT VARSPLIC 356 417 MISSING (IN ISOFORM 3).
 FT CONFLICT 367 367 K -> T (IN REF. 2).
 SQ SEQUENCE 653 AA; 75792 MW; DF7B78C44EE6484 CRC64;
 Query Match 61.4%; Score 43; DB 1; Length 653;
 Best Local Similarity 66.7%; Pred. No. 9.7;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DLNKDGHLDGSE 12
 DB 619 DLNKDGSIDFNE 630
 RESULT 7
 YAE8_YEAST
 ID YAE8_YEAST STANDARD; PRT; 662 AA.
 AC P39722;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Hypothetical 75.2 kDa protein in ACS1-GCV3 intergenic region.
 GN YAL048C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes;
 OC NCB1_TaxID=4912;
 RX STRAIN=S288C / AB972;
 RA Bussey H., Kaback D.B., Zhong W., Vo D.T., Clark M.W., Fortin N.,
 RA Hall J., Ouellette B.F.F., Keng T., Barton A.B., Su Y., Davies C.K.,
 RA Storms R.K.;
 RT "The nucleotide sequence of chromosome I from Saccharomyces
 cerevisiae";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:3809-3813(1995).
 CC -----
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 CC -----
 DR EMBL; U12980; AAC04983.1;
 DR SGD; S0000046; YAL048C.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR005225; Small-GTP.
 DR InterPro; IPR003575; Small-GTPase.
 DR Pfam; PF00036; ehand; 2.
 DR SMART; SM00010; small-GTPase; 1.
 DR TIGRFAMs; TIGR00231; small-GTP; 2.
 DR KW Hypothetical protein.
 SQ SEQUENCE 662 AA; 75150 MW; A68CDA15D79E5910 CRC64;
 Query Match 61.4%; Score 43; DB 1; Length 662;
 Best Local Similarity 53.8%; Pred. No. 9.9;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DLNKDGHLDGSEV 13
 DB 214 DLNQDSYLDNDNEI 226
 RESULT 8
 ITN2_MOUSE
 ID ITN2_MOUSE STANDARD; PRT; 1658 AA.
 AC Q9Z0R6; Q9Z0R5;

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DR PROSITE: PS50031; EH: 2.
DR PROSITE: PS50003; PH DOMAIN; 1.
DR PROSITE: PS50002; SH3; 5. Repeat; Coiled coil; Calcium-binding;
KW Endocytosis; SH3 domain;
KW Alternative splicing.
FT DOMAIN 21 109 EH 1.
FT CA_BIND 66 78 EH 2.
FT DOMAIN 244 333 COILED COIL (POTENTIAL).
FT DOMAIN 364 716 SH3 1.
FT DOMAIN 717 778 SH3 2.
FT DOMAIN 851 909 SH3 3.
FT DOMAIN 941 999 SH3 4.
FT DOMAIN 1013 1077 SH3 5.
FT DOMAIN 1087 1146 DH.
FT DOMAIN 1169 1356 PH.
FT DOMAIN 1395 1505 C2 DOMAIN.
FT DOMAIN 1517 1613 DDQLVIEVQ -> GLQLFEQKTL (IN ISOFORM
FT VARSPLIC 1187 1197 2).
FT VARSPLIC 1198 1658 MISSING (IN ISOFORM 2).
FT CONFLICT 451 452 KQ -> NT (IN REF. 1; AAD19748).
FT CONFLICT 1161 1161 D -> G (IN REF. 1; AAD19748).
FT SEQUENCE 1658 AA; 188776 MW; 7050EFC3F7983A5 CRC64;
SQ
Query Match 61.4%; Score 43; DB 1; Length 1658;
Best Local Similarity 66.7%; Pred. No. 25;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 DLNKGHLGDS 12
Db 66 DLNKGKMDQOE 77
RESULT 9
ID ITN2_HUMAN STANDARD; PRT: 1696 AA.
AC Q9NZM3; Q9NVG0; Q9ULG4; Q9NZM2; Q9HAK4; Q9NXX6; Q95062; Q15812;
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Intersectin 2 (SH3 domain-containing protein 1B) (SH3P18) (SH3P18-like
DE WASP associated protein).
DE ITSN2 OR SH3D1B OR SWAP OR KIAA1256.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
RC TISSUE=Fetal brain, and Fetal liver;
RX MEDLINE=20382722; PubMed=10922467;
RA Pucharcos C., Estivill X., de la Luna S.;
RT "Intersectin 2, a new multimodular protein involved in clathrin-
RT mediated endocytosis."
RL FEBS Lett. 478:43-51(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA Seifert M., Engel M., Welter C.;
RT "Intersectin 2 (SH3D1B), human homolog of mouse Eps2 protein."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RX MEDLINE=20039619; PubMed=10574462;
RA Nagase T., Ishikawa K.-I., Kikuno R., Hirose M., Nomura N.,
RA Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XV.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro."
RL DNA Res. 6:337-345(1999).
RN [4]
RP SEQUENCE OF 258-720 FROM N.A. (ISOFORM 2), AND SEQUENCE OF 1261-1696
RP FROM N.A.

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RC TISSUE-Embryo;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y., Oshima A.,
RT "NEDO human cDNA sequencing project.",
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 821-1284 FROM N.A. (ISOFORM 1).
RA Wilson L.A., Fields D., Cruz L., Friesen J., Siminovich K.A.,
RA "SH3P18-like wasp associated protein (SWAP): A multiple SH3 domain
RT containing protein that interacts with WASP.",
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 944-1191 FROM N.A. (ISOFORM 4).
RA TISSUE-Bone marrow;
RC TISSUE-Bone marrow;
RX MEDLINE-98294438; PubMed-9630982;
RA Sparks A.B., Hoffman N.G., McConnell S.J., Fowlkes D.M., Kay B.K.,
RT "Cloning of ligand targets: systematic isolation of SH3 domain-
RL containing proteins.",
RN Nat. Biotechnol. 14:741-744(1996).
RN [7]
RP ALTERNATIVE SPLICING
RC TISSUE-Fetal liver, and Brain;
RX MEDLINE-21548826; PubMed-11690630;
RA Pucharcos C., Casas C., Nadal M., Estivill X., de la Luna S.,
RT "The human intersectin genes and their spliced variants are
RL differentially expressed.",
RN Blochim. Biophys. Acta 1521:1-11(2001).
CC -1- FUNCTION: Adapter protein that may provide indirect link between
CC the endocytic membrane traffic and the actin assembly machinery.
CC May regulate the formation of clathrin-coated vesicles.
CC -1- SUBUNIT: Belongs to a complex that may contain multimers of ITSN1,
CC ITSN2 and Eps15, and different partners according to the step in
CC the endocytic process.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- ALTERNATIVE PRODUCTS: At least 4 isoforms; 1/ITSN2-L (shown here),
CC 2, 3/ITSN2-S1 and 4/ITSN2-S2/SH3P18; are produced by alternative
CC splicing.
CC -1- TISSUE SPECIFICITY: Ubiquitous. Isoform 1 is primarily expressed
CC in adult heart and liver.
CC -1- MISCELLANEOUS: Overexpression results in the inhibition of the
CC transferrin uptake and the blockage of the clathrin-mediated
CC endocytosis.
CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY (DH) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EF-HAND CALCIUM-BINDING DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC -1- SIMILARITY: CONTAINS 5 SH3 DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 EH DOMAINS.
CC -----
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CC -----
DR EMBL; AF182198; AAF59903.1; -;
DR EMBL; AF182199; AAF59904.1; -;
DR EMBL; AF248540; AAF63600.1; ALT_INIT.
DR EMBL; AB033082; BAA66570.1; ALT_INIT.
DR EMBL; AK021545; BAB13841.1; -;
DR EMBL; AK000302; BAA91068.1; -;
DR EMBL; AF001630; AAD00899.1; -;
DR EMBL; U61167; AAC50593.1; -;
DR HSSP; P29155; 1SEM.
DR Genew; HGNC:6184; ITSN2.
DR MIM; 604464; -;
DR InterPro; IPR000008; C2.
DR InterPro; IPR002048; EF-hand.

DR InterPro; IPR000261; EPS15_repeat.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000219; RhoGEF.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00018; SH3; 5.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RhoGEF; 1.
DR PRINTS; PR00499; P67PHOX.
DR PRINTS; PR00452; SH3DOMAIN.
DR SMART; SM00239; C2; 1.
DR SMART; SM00054; Eph; 2.
DR SMART; SM00027; EH; 2.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RhoGEF; 1.
DR SMART; SM00326; SH3; 5.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS50010; DH_2; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS50031; EH; 2.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR PROSITE; PS50002; SH3; 5.
KW Endocytosis; SH3 domain; Repeat; Coiled coil; Calcium-binding;
KW Alternative splicing.
FT DOMAIN 21 109 EH 1.
FT CA_BIND 66 78 EF-HAND (POTENTIAL).
FT DOMAIN 243 332 EH 2.
FT DOMAIN 360 755 COILED COIL (POTENTIAL).
FT DOMAIN 756 817 SH3 1.
FT DOMAIN 897 955 SH3 2.
FT DOMAIN 980 1038 SH3 3.
FT DOMAIN 1052 1116 SH3 4.
FT DOMAIN 1126 1185 SH3 5.
FT DOMAIN 1208 1394 DH.
FT DOMAIN 1433 1543 PH.
FT VARSPLIC 621 647 C2 DOMAIN.
FT VARSPLIC 1234 1248 MISSING (IN ISOFORM 2).
FT VARSPLIC 1249 1696 FORKMAESGFLTEGE -> WRLLASSRGICCLS (IN
FT VARSPLIC 1192 1696 ISOFORM 3).
FT CONFLICT 290 290 MISSING (IN ISOFORM 3).
FT CONFLICT 678 678 V -> I (IN REF. 4).
FT CONFLICT 822 827 R -> G (IN REF. 4).
FT CONFLICT 944 950 KAVSPK -> FFAAST (IN REF. 5).
FT CONFLICT 1278 1284 WFPKSYV -> EFAAAT (IN REF. 6).
FT CONFLICT 1552 1552 GKMPVQ -> VDAANS (IN REF. 5).
FT CONFLICT 1552 1552 K -> Q (IN REF. 2 AND 3).
SQ SEQUENCE 1696 AA; 193329 MW; 17B5C8629B8CFF9B CRC64;
Query Match 61.4%; Score 43; DB 1; Length 1696;
Best Local Similarity 66.7%; Pred. No. 26;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 DLNKGHLGDS 12
Db 66 DLNKGCKMDQGE 77
||||| : |
RESULT 10
HIS4_PASMU
ID HIS4_PASMU STANDARD; PRT; 249 AA.
AC Q9CLM1;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]
DE imidazole-4-carboxamide isomerase (EC 5.3.1.16)
DE (Phosphoribosylformimino-5-aminimidazole carboxamide ribotide
DE isomerase).
GN HIS4 OR PM1203.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Pasteurella.

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CC EMBL; J05227; AAA30129.1;
CC DR PIR; A35535; A35535; EF-hand.
CC DR InterPro; IPR002048; EF-hand.
CC DR Pfam; PF00036; ehand; 4.
CC DR ProDom; PD000012; EF-hand; 2.
CC DR SMART; SM00054; EFh; 4.
CC DR PROSITE; PS00018; EF-hand; 4.
CC DR Calcium-binding; Repeat.
CC FT CHAIN 1 207
CC FT CHAIN 1 103
CC FT MOD_RES 1 1
CC FT CA_BIND 30 41
CC FT CA_BIND 73 84
CC FT CA_BIND 132 143
CC FT CA_BIND 174 185
CC FT CA_BIND 207 AA; 1932840D4632D571 CRC64;
CC SQ SEQUENCE 207 AA; 1932840D4632D571 CRC64;

Query Match 58.6%; Score 41; DB 1; Length 207;
Best Local Similarity 69.2%; Pred. No. 6.6;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLNKGDLGSEV 13
DB 30 DSNKNGTLDPSEV 42

RESULT 12
CMC3_CAEEL STANDARD; PRT; 587 AA.
ID CMC3_CAEEL
AC Q19529;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable calcium-binding mitochondrial carrier F17E5.2.
GN F17E5.2
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Feloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA McMurray A.A.;
RL Submitted (AUG-1995) to the EMBL/Genbank/DDBJ databases.
CC -|- FUNCTION: CALCIUM-DEPENDENT MITOCHONDRIAL SOLUTE CARRIER (BY
CC -|- SIMILARITY). LOCATION: Integral membrane protein. Mitochondrial
CC -|- SUBCELLULAR LOCATION: Inner membrane (By similarity).
CC -|- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY. ARALAR
CC SUBFAMILY.
CC -|- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
-----
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-----
CC EMBL; Z50873; CAA90761.2;
CC WORMPEP; F17E5.2; CE23667.
CC DR InterPro; IPR002048; EF-hand.
CC DR InterPro; IPR002067; Mit_carrier.
CC DR InterPro; IPR001993; Mitoch_carrier.
CC Pfam; PF00036; ehand; 3.
CC Pfam; PF00153; mito_carr; 3.
CC PRINTS; PR00926; MITOCARRIER.
CC ProDom; PD000012; EF-hand; 1.
CC SMART; SM00054; EFh; 2.
CC PROSITE; PS00018; EF_HAND; 2.

QY 1 DLNKGDLGSEV 13
DB 176 DISKDTLGGSNV 188

RESULT 11
CB23_TETH STANDARD; PRT; 207 AA.
ID CB23_TETH
AC P20473;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 23 kDa calcium-binding protein (TCBP-23) [Contains: 12 kDa calcium-
DE binding protein (TCBP-12)].
OS Tetrahymena thermophila.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
OC Tetrahymenina; Tetrahymena.
OX NCBI_TaxID=5911;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-103.
RC STRAIN=B1868;
CC MEDLINE-90153866; PubMed=2303413;
CC Takemasa Y., Takagi T., Kobayashi T., Konishi K., Watanabe Y.;
CC "The third calmodulin family protein in Tetrahymena. Cloning of the
CC cDNA for Tetrahymena calcium-binding protein of 23 kDa (TCBP-23).";
CC J. Biol. Chem. 265:2514-2517(1990).
CC -|- FUNCTION: EXPECTED TO PLAY A CRUCIAL ROLE IN CALCIUM-DEPENDENT
CC REGULATION OF CILIARY MOVEMENT.
CC -|- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, STRONGEST
CC TO TCBP-25.
-----
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-----
CC EMBL; AE006160; AAK03287.1;
CC InterPro; IPR003009; FMN_enzyme.
CC InterPro; IPR000570; His_biosynth.
CC Pfam; PF00977; His_biosynth; 1.
CC TIGRFAMs; TIGR00007; His_biosynth; 1.
CC Isomerase; Histidine biosynthesis; Complete proteome.
CC SQ SEQUENCE 249 AA; 26758 MW; 3D5CFCC688E985E6 CRC64;

Query Match 60.0%; Score 42; DB 1; Length 249;
Best Local Similarity 61.5%; Pred. No. 5.4;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLNKGDLGSEV 13
DB 176 DISKDTLGGSNV 188

```

DR PROSITE; PS00215; MITOCH_CARRIER; FALSE_NEG.
 KW Hypothetical protein; Mitochondrion; Inner membrane; Repeat;
 KW Transmembrane; Transport; Calcium-binding;
 FT TRANSMEM 265
 FT TRANSMEM 282
 FT TRANSMEM 336
 FT TRANSMEM 356
 FT TRANSMEM 382
 FT TRANSMEM 395
 FT TRANSMEM 433
 FT TRANSMEM 452
 FT TRANSMEM 475
 FT TRANSMEM 534
 FT TRANSMEM 551
 FT CA_BIND 49
 FT CA_BIND 60
 FT CA_BIND 83
 FT CA_BIND 94
 FT DOMAIN 119
 FT DOMAIN 129
 FT CA_BIND 149
 FT CA_BIND 160
 FT DOMAIN 185
 FT REPEAT 185
 FT REPEAT 366
 FT REPEAT 459
 FT REPEAT 460
 SQ SEQUENCE 587 AA; 65906 MW; 19E62936D5A17021 CRC64;

Query Match 58.6%; Score 41; DB 1; Length 587;
 Best Local Similarity 53.8%; Pred. No. 19;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLNKGCHLDGSEV 13
 ||| ||| :| :|
 DB 149 DLNKGCHLDGSEV 161

RESULT 13
 ID SL11_RABIT STANDARD; PRT; 102 AA.
 AC P24480;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Calgizarin (S100C protein).
 GN S100A11 OR S100C OR PCALG.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=92095968; PubMed=1836726;
 RA Watanabe M., Ando Y., Todoroki H., Minami H., Hiroyoshi H.;
 RT "Molecular cloning and sequencing of a cDNA clone encoding a new
 RT calcium binding protein, named calgizarin, from rabbit lung.";
 RL Biochem. Biophys. Res. Commun. 181:644-649(1991).
 RN [2]
 RP SEQUENCE OF 35-49 AND 53-62.
 RC TISSUE=Lung;
 RX MEDLINE=92011625; PubMed=1917990;
 RA Todoroki H., Kobayashi R., Watanabe M., Minami H., Hidaka H.;
 RT "Purification, characterization, and partial sequence analysis of a
 RT newly identified EF-hand type 13-kDa Ca(2+)-binding protein from
 RT smooth muscle and non-muscle tissues.";
 RL J. Biol. Chem. 266:18668-18673(1991).
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- MISCELLANEOUS: BINDS TWO CALCIUM IONS PER MOLECULE WITH AN
 CC AFFINITY SIMILAR TO THAT OF THE S-100 PROTEINS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.

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 or send an email to license@isb-sib.ch).

DR EMBL; D10586; BAA01443.1; ..
 DR PIR; B41004; B41004.
 DR PIR; JQ1300; JQ1300.
 DR HSSP; P31950; IOLS.
 DR InterPro; IPR001751; CAPP_S100.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00036; efhand; 1.
 DR Pfam; PF01023; S100; 1.
 DR ProDom; PD000012; EF-hand; 1.
 DR ProDom; PD003407; CAPP_S100; 1.
 DR PROSITE; PS00018; EF_HAND; 1.
 DR PROSITE; PS00303; S100_CAPP; 1.
 KW Calcium-binding.
 FT CA_BIND 22
 FT CA_BIND 35
 FT CA_BIND 65
 FT CA_BIND 76
 FT CONFLICT 59
 FT CONFLICT 59
 SQ SEQUENCE 102 AA; 11429 MW; 66D1FFBBA4F8DF45 CRC64;

Query Match 57.1%; Score 40; DB 1; Length 102;
 Best Local Similarity 66.7%; Pred. No. 4.8;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 DLNKGCHLDGSE 12
 ||| ||| :| :|
 DB 65 DLNKGCHLDGSE 76

RESULT 14
 ID CLM4_MOUSE STANDARD; PRT; 148 AA.
 AC Q9JNB3; Q9CR31; Q9DIE9;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calmodulin 4 (Calcium-binding protein Dd112).
 GN CALM4 OR DD112.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ikegawa S., Nakamura Y.;
 RT "Dd112, a novel mouse gene implicated in the early stage of ectopic
 RT ossification.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boirelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyushaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -1- FUNCTION: IMPLICATED IN THE EARLY STAGE OF ECTOPIC OSSIFICATION.
 CC -1- SIMILARITY: CONTAINS 3 EF-HAND CALCIUM-BINDING DOMAINS.

Tue May 20 14:43:33 2003

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CC -----
CC EMBL; AB036744; BAA95412.1; -
CC EMBL; AK009556; BAA26608.1; -
CC EMBL; AK009664; BAB26425.1; -
CC EMBL; AK003648; BAB22914.1; -
CC HSSP; P02593; 1CDM.
CC MGD; MGI:1931464; Calm4.
CC InterPro: IPR002048; EF-hand.
CC Pfam: PF00036; ehand; 4.
CC ProDom: PD000012; EF-hand; 2.
CC SMART; SM00054; EFh; 3.
CC PROSITE; PS00018; EF_HAND; 3.
CC Calcium-binding; Repeat.
CC CA_BIND 21 32 EF-HAND 1 (POTENTIAL).
CC CA_BIND 57 68 EF-HAND 2 (POTENTIAL).
CC CA_BIND 93 104 EF-HAND 3 (POTENTIAL).
CC CONFLICT 9 9 E -> V (IN REF. 2; BAB22914).
CC CONFLICT 124 124 M -> V (IN REF. 2; BAB22914).
CC CONFLICT 146 148 VEN -> I (IN REF. 1).
CC SEQUENCE 148 AA; 16767 MW; 2AE22BC738AD2F9D CRC64;
CC
CC Query Match 57.1%; Score 40; DB 1; Length 148;
CC Best Local Similarity 53.8%; Pred. No. 7;
CC Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
CC
CC QY 1 DLNKGHLDGSRV 13
CC DB 21 DLNKGHLDGSRV 33

RESULT 15
GCAL CHICK STANDARD; PRT; 198 AA.
AC P79880.
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Guanylyl cyclase activating protein 1 (GCAP 1) (Guanylate cyclase
DE activator 1A).
GN GUCALIA OR GCAP1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=96200167; PubMed=8641465;
RA Semple-Rowland S.L., Gorczyca W.A., Buczylo J., Helekar B.S.,
RA Ruiz C.C., Subbaraya I., Palczewski K., Baehr W.,
RA "Expression of GCAP1 and GCAP2 in the retinal degeneration (rd)
RA mutant chicken retina."
RT FEBS Lett. 385:47-52(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn; TISSUE=Liver;
RX MEDLINE=99357925; PubMed=10427104;
RA Semple-Rowland S.L., Larkin P., Bronson J.D., Nykamp K., Streit W.J.,
RA Baehr W.,
RA "Characterization of the chicken GCAP gene array and analyses of
RA GCAP1, GCAP2, and GC1 gene expression in normal and rd chicken
RA pineal."
RT Mol. Vision 5:14-14(1999).
RL

CC -!- FUNCTION: STIMULATES GUANYLYL CYCLASE 1 (GC1) WHEN FREE CALCIUM
CC IONS CONCENTRATION IS LOW AND INHIBITS GC1 WHEN FREE CALCIUM IONS
CC CONCENTRATION IS ELEVATED. THIS CA(2+)-SENSITIVE REGULATION OF GC
CC IS A KEY EVENT IN RECOVERY OF THE DARK STATE OF ROD PHOTORECEPTORS
CC FOLLOWING LIGHT EXPOSURE (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: RETINA, IN ROD AND CONE OUTER SEGMENTS, AND
CC PINAL GLAND.
CC -!- MISCELLANEOUS: BINDS THREE CALCIUM IONS (BY SIMILARITY).
CC -!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
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CC -----
CC EMBL; S82199; AAB47111.1; -
CC EMBL; AF172707; AAD47879.1; -
CC HSSP; P51177; 1JBA.
CC InterPro: IPR002048; EF-hand.
CC InterPro: IPR001125; Recoverin.
CC Pfam: PF00036; ehand; 3.
CC PRINTS; PR00450; RECOVERIN.
CC ProDom: PD000012; EF-hand; 1.
CC SMART; SM00054; EFh; 3.
CC PROSITE; PS00018; EF_HAND; 3.
CC Calcium-binding; Repeat; Vision; Myristate.
CC INIT_MET 0 0 POTENTIAL.
CC LIPID 1 1 MYRISTATE (POTENTIAL).
CC DOMAIN 25 36 ANCESTRAL CALCIUM SITE 1 (POTENTIAL).
CC CA_BIND 62 73 EF-HAND 2 (POTENTIAL).
CC CA_BIND 98 109 EF-HAND 3 (POTENTIAL).
CC CA_BIND 141 152 EF-HAND 4 (POTENTIAL).
CC SEQUENCE 198 AA; 22677 MW; 97B876BBFD2EF959 CRC64;
CC
CC Query Match 57.1%; Score 40; DB 1; Length 198;
CC Best Local Similarity 58.3%; Pred. No. 9.3;
CC Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
CC
CC QY 1 DLNKGHLDGSE 12
CC DB 62 DENKDGVIDFME 73

Search completed: May 14, 2003, 10:43:35
Job time : 3.10557 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 14, 2003, 10:40:47 ; Search time 2.02053 Seconds
(without alignments)
618.525 Million cell updates/sec

Title: US-09-768-840-1-copy_254_266
Perfect score: 70
Sequence: 1 DLNKGDLGSEV 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	68.6	325	2 A45337	reticulocalbin pre
2	48	68.6	331	2 JC4173	reticulocalbin pre
3	46	65.7	170	2 T24463	hypothetical prote
4	45	64.3	289	2 E81259	hypothetical prote
5	43	61.4	163	2 JW0062	fast skeletal trop
6	43	61.4	163	2 JW0063	fast skeletal trop
7	43	61.4	236	2 T33406	hypothetical prote
8	43	61.4	562	2 S51971	probable membrane
9	43	61.4	1181	2 C86349	probable membrane
10	42	60.0	142	2 T02387	F8K7.4 protein - A
11	42	60.0	186	2 T22685	hypothetical prote
12	42	60.0	574	2 G96572	hypothetical prote
13	42	60.0	1636	2 B82736	protein F12M16.12
14	41	58.6	207	2 A35535	hemolysin-type cal
15	41	58.6	282	2 H81358	23K calcium-bindin
16	41	58.6	322	2 A57516	probable signal pe
17	41	58.6	374	2 A42264	DNA supercoiling f
18	41	58.6	475	2 T50686	membrane-associate
19	41	58.6	531	2 G89667	peroxisomal Ca-dep
20	41	58.6	587	2 T21074	protein F17E5.2 (i
21	41	58.6	3110	2 AC0116	hypothetical prote
22	40	57.1	102	1 JQ1300	probable virulence
23	40	57.1	133	2 H87589	calgizarrin - rabb
24	40	57.1	199	2 S68838	EF hand domain pro
25	40	57.1	201	2 C55331	guanylate cyclase-
26	40	57.1	202	2 B55331	guanylate cyclase-
27	40	57.1	273	2 S07014	guanylate cyclase-
28	40	57.1	273	2 JN0037	hypothetical prote
29	40	57.1	313	2 T33849	hypothetical prote

30	40	57.1	373	2 G59629	germination respon
31	40	57.1	373	2 B26470	spore germination
32	40	57.1	530	2 A84847	probable Ca2+ depe
33	40	57.1	751	2 T34490	hypothetical prote
34	40	57.1	3968	2 A44265	trichorax homolog
35	39	55.7	97	2 F82722	hypothetical prote
36	39	55.7	105	1 I37080	calgizarrin - huma
37	39	55.7	178	2 G96667	hypothetical prote
38	39	55.7	237	2 T26660	unknown protein, 5
39	39	55.7	245	2 AD0188	hypothetical prote
40	39	55.7	251	2 JC7513	1-(5-phosphoribosy
41	39	55.7	334	1 S23498	fibroblast growth
42	39	55.7	342	2 E89876	licheninase (EC 3.
43	39	55.7	403	2 S07825	hypothetical prote
44	39	55.7	436	2 A83909	hypothetical prote
45	39	55.7	473	1 A38874	protein-tyrosine-p

ALIGNMENTS

RESULT 1

A45337
reticulocalbin precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 02-Aug-2002
C:Accession: A45337; I55203
R:Ozawa, M.; Muramatsu, T.
J. Biol. Chem. 268, 699-705, 1993
A:Title: Reticulocalbin, a novel endoplasmic reticulum resident Ca(2+)-binding prote
A:Reference number: A45337; MUID:9107083; PMID:8416973
A:Contents: teratocarcinoma OTT6050
A:Accession: A45337
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-325 <OZA>
A:Cross-references: GB:D13003; NID:9220581; PIDN:BAA02366.1; PID:d1002865; PID:g22058
A:Note: sequence extracted from NCBI backbone (NCBIP:121512)
R:Ozawa, M.
J. Biochem. 118, 154-160, 1995
A:Title: Structure of the gene encoding mouse reticulocalbin, a novel endoplasmic re.
A:Reference number: I55203; MUID:96015163; PMID:8537305
A:Accession: I55203
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-325 <RES>
A:Cross-references: GB:D43956; NID:92190295; PIDN:BAA07896.1; PID:g968894
C:Genetics:
A:Introns: 79/2; 144/1; 203/3; 224/1; 290/3
C:Superfamily: reticulocalbin; calmodulin repeat homology
C:Keywords: EF hand
F:1-23/Domaln: signal sequence #status predicted <SIG>
F:322-325/Region: endoplasmic reticulum retention signal

Query Match 68.6%; Score 48; DB 2; Length 325;
Best Local Similarity 69.2%; Pred. No. 1.9;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 DLNKGDLGSEV 13

DB 251 DLNKGDLKDEI 263

RESULT 2

JC4173
reticulocalbin precursor - human
C:Species: Homo sapiens (man)
C>Date: 27-Aug-1995 #sequence_revision 27-Oct-1995 #text_change 02-Aug-2002
C:Accession: JC4173
R:Ozawa, M.
J. Biochem. 117, 1113-1119, 1995
A:Title: Cloning of a human homologue of mouse reticulocalbin reveals conservation of

us-09-768-840-1_copy_254_266.rpr

Tue May 20 14:43:32 2003

```

A:Reference number: JCA173; MUID:96172582; PMID:8586628
A:Accession: JCA173
A:Molecule type: mRNA
A:Residues: 1-331 <OZA>
A:Cross-references: DDBJ:D42073; NID:g1262328; PIDN:BA07670.1; PID:d1008252; PID:g1262328
C:Comment: This protein is a luminal protein of the endoplasmic reticulum, and is a Ca2+
a signal for its retention in the endoplasmic reticulum of cells.
C:Genetics:
A:Gene: GDB:RCN; Rcal
A:Cross-references: GDB:6383031
A:Map position: lrp3-llp3
C:Superfamily: reticulocalbin; calmodulin repeat homology
C:Keywords: calcium binding; calmodulin binding; EF hand; endoplasmic reticulum
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-331/Product: reticulocalbin homolog #status predicted <MAT>
F:79-111/Domain: calmodulin repeat homology <EF1>
F:113-145/Domain: calmodulin repeat homology <EF2>
F:166-198/Domain: calmodulin repeat homology <EF3>
F:203-235/Domain: calmodulin repeat homology <EF4>
F:244-276/Domain: calmodulin repeat homology <EF5>
F:280-312/Domain: calmodulin repeat homology <EF6>
F:328-331/Region: endoplasmic reticulum retention signal

Query Match 68.6%; Score 48; DB 2; Length 331;
Best Local Similarity 69.2%; Pred. No. 1.9; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 3;

QY 1 DLNKGHLGSEV 13
||||| |||
DB 257 DLNKGKLDKDEI 269

RESULT 3
T24463
hypothetical protein T04F3.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T24463
R:Kershaw, J.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z19894
A:Accession: T24463
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-170 <WIL>
A:Cross-references: EMBL:Z72513; PIDN:CAA96671.1; GSPDB:GN00023; CESP:T04F3.4
A:Experimental source: clone T04F3
C:Genetics:
A:Gene: CESP:T04F3.4
A:Map position: 5
A:Introns: 65/3; 76/2; 129/1

Query Match 65.7%; Score 46; DB 2; Length 170;
Best Local Similarity 61.5%; Pred. No. 2; Indels 3; Gaps 0;
Matches 8; Conservative 2; Mismatches 2;

QY 1 DLNKGHLGSEV 13
||||| |||
DB 105 DLKDNFIDGIEI 117

RESULT 4
E81259
hypothetical protein Cj163lc [imported] - Campylobacter jejuni (strain NCTC 11169)
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C:Accession: E81259
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A:Reference number: A81250; MUID:20150912; PMID:10688204
A:Accession: E81259

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-289 <PAR>
A:Cross-references: GB:AL139079; GB:AL111168; NID:g6968971; PIDN:CAB73619.1; PID:g696
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: Cj163lc

Query Match 64.3%; Score 45; DB 2; Length 289;
Best Local Similarity 61.5%; Pred. No. 5.2; Indels 2; Gaps 0;
Matches 8; Conservative 3; Mismatches 2;

QY 1 DLNKGHLGSEV 13
||||| |||
DB 165 DVNKGKRVDSV 177

RESULT 5
JW0062
fast skeletal troponin C alpha - African clawed frog
N:Alternate names: ftnC
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 20-Jun-2000
C:Accession: JW0062
R:Yuasa, H.J.; Cox, J.A.; Takagi, T.
J. Biochem. 123, 1180-1190, 1998
A:Title: Diversity of the troponin C genes during chordate evolution.
A:Reference number: JW0060; MUID:98269050; PMID:9604009
A:Accession: JW0062
A:Molecule type: mRNA
A:Residues: 1-163 <YUA>
A:Cross-references: DDBJ:AB003078; NID:g1945532; PIDN:BA19734.1; PID:g1945533
C:Comment: This protein belongs to the EF-hand Ca2+ binding protein family and functi-
C:Genetics:
A:Introns: 3/3 108/2
A:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: EF hand
F:18-50/Domain: calmodulin repeat homology <EF1>
F:54-86/Domain: calmodulin repeat homology <EF2>
F:94-126/Domain: calmodulin repeat homology <EF3>
F:130-162/Domain: calmodulin repeat homology <EF4>

Query Match 61.4%; Score 43; DB 2; Length 163;
Best Local Similarity 53.8%; Pred. No. 6.2; Indels 3; Gaps 0;
Matches 7; Conservative 3; Mismatches 3;

QY 1 DLNKGHLGSEV 13
||||| |||
DB 107 DKNADGYIDGEEI 119

RESULT 6
JW0063
fast skeletal troponin C beta - African clawed frog
N:Alternate names: ftnC
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 20-Jun-2000
C:Accession: JW0063
R:Yuasa, H.J.; Cox, J.A.; Takagi, T.
J. Biochem. 123, 1180-1190, 1998
A:Title: Diversity of the troponin C genes during chordate evolution.
A:Reference number: JW0060; MUID:98269050; PMID:9604009
A:Accession: JW0063
A:Molecule type: mRNA
A:Residues: 1-163 <YUA>
A:Cross-references: DDBJ:AB003079; NID:g1945534; PIDN:BA19735.1; PID:g1945535
C:Comment: This protein belongs to the EF-hand Ca2+ binding protein family and functi-
C:Genetics:
A:Introns: 3/3 108/2
A:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: EF hand
F:18-50/Domain: calmodulin repeat homology <EF1>
F:54-86/Domain: calmodulin repeat homology <EF2>

```


F:94-126/Domain: calmodulin repeat homology <EF3>
F:130-162/Domain: calmodulin repeat homology <EF4>

Query Match 61.4%; Score 43; DB 2; Length 163;
Best Local Similarity 53.8%; Pred. No. 6.2;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLNKGCHLDGSEV 13
| | | | | | | | | |
Db 107 DKNADYIDGEE 119

RESULT 7
T33406
hypothetical protein H10E21.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T33406

R:Davidson, S.; Wohldmann, P.; Courtney, L.
submitted to the EMBL Data Library, July 1998
A:Description: The sequence of C. elegans cosmid H10E21.
A:Reference number: 221339

A:Accession: T33406
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-236 <DAV>

A:Cross-references: EMBL:AF078783; PIDN:AC26922.1; GSPDB:GN00021; CESP:H10E21.4
A:Experimental source: strain Bristol N2; clone H10E21
C:Genetics:

A:Gene: CESP:H10E21.4
A:Map position: 3
A:Introns: 21/1; 53/1; 116/2; 190/3

Query Match 61.4%; Score 43; DB 2; Length 236;
Best Local Similarity 66.7%; Pred. No. 9.2;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DLNKGCHLDGSE 12
| | | | | | | | | |
Db 59 DLDNRGHLDI 70

RESULT 8
S51971

Probable membrane protein YAL048c - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Date: 05-May-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002

C:Accession: S51971
R:Bussey, H.; Kaback, D.B.; Zhong, W.; Vo, D.T.; Clark, M.W.; Fortin, N.; Hall, J.; Ouel

submitted to the EMBL Data Library, August 1994
A:Description: The sequence of chromosome 1 of Saccharomyces cerevisiae.

A:Reference number: S51956
A:Accession: S51971

A:Molecule type: DNA
A:Residues: 1-662 <BUS>

A:Cross-references: EMBL:U12980; NID:gl326053; PID:g595536; GSPDB:GN00001; MIPS:YAL048c

C:Genetics:
A:Gene: MIPS:YAL048c

A:Cross-references: SGD:S0000046
A:Map position: 1L

C:Keywords: transmembrane protein
F:635-651/Domain: transmembrane #status predicted <TM1>

Query Match 61.4%; Score 43; DB 2; Length 662;
Best Local Similarity 53.8%; Pred. No. 27;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 DLNKGCHLDGSEV 13
| | | | | | | | | |
Db 214 DLNQSYLDNEI 226

RESULT 9

C86349

FK7.4 protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 27-Nov-2001
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alca

nsen, N.F.; Hughes, B.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar

Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kin,

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Matti, R.; Marza

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: C86349

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-1181 <STO>
A:Cross-references: GB:AE005172; NID:g5263313; PIDN:AAD41415.1; GSPDB:GN00141

C:Genetics:
A:Map position: 1

Query Match 61.4%; Score 43; DB 2; Length 1181;
Best Local Similarity 58.3%; Pred. No. 48;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DLNKGCHLDGSE 12
| | | | | | | | | |
Db 21 DLDGCHISGAE 32

RESULT 10
T02387

hypothetical protein At2g44310 [imported] - Arabidopsis thaliana
A:Alternate names: hypothetical protein F4I1.12

C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 02-Feb-2001

R:Roundley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.;

submitted to the EMBL Data Library, May 1998
A:Description: Arabidopsis thaliana chromosome II BAC F4I1 genomic sequence.

A:Reference number: Z14667
A:Accession: T02387

A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-142 <ROU>
A:Cross-references: EMBL:AC004521; NID:g3128166; PID:g3128177

A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Roundley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter

Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: A84877

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-142 <STO>
A:Cross-references: GB:AE002093; NID:g3128177; PIDN:AAC16081.1; GSPDB:GN00139

C:Genetics:
A:Gene: AT2g44310; F4I1.12

A:Map position: 2

Query Match 60.0%; Score 42; DB 2; Length 142;
Best Local Similarity 69.2%; Pred. No. 8;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLNKGCHLDGSEV 13
| | | | | | | | | |
Db 33 DLNKGVLRSSEL 45

Tue May 20 14:43:32 2003

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: B82736

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1636 <STM>

A:Cross-references: GB:AE003938; GB:AE003849; NID:g9105935; PIDN:AAF83821.1; GSPDB:GN

A:Experimental source: strain 9a5C

R:Simons, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer

as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

Submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; palmieri,

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva

M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF1011

Query Match 60.0%; Score 42; DB 2; Length 1636;

Best Local Similarity 53.8%; Pred. No. 1e+02;

Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLNKGHLGSEV 13

DB 558 DLNKGHLGSEV 570

RESULT 14

A35535

23K calcium-binding protein - Tetrahymena thermophila

C:Species: Tetrahymena thermophila

C:Date: 31-Aug-1990 #sequence_revision 18-Nov-1992 #text_change 07-Dec-1999

C:Accession: A35535

R:Takemasa, T.; Takagi, T.; Kobayashi, T.; Konishi, K.; Watanabe, Y.

J. Biol. Chem. 265, 2514-2517, 1990

A:Title: The third calmodulin family protein in Tetrahymena. Cloning of the cDNA for

A:Reference number: A35535; MUID:90153866; PMID:2303413

A:Accession: A35535

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-207 <TAK>

A:Cross-references: GB:J05227; NID:g161860; PID:g161861

A:Note: the authors translated the codon CAA for residue 104 as Glu

C:Genetics:

A:Genetic code: SGC5

C:Superfamily: unassigned calmodulin-related proteins; calmodulin repeat homology

C:Keywords: calcium binding; EF hand

Query Match 58.6%; Score 41; DB 2; Length 207;

Best Local Similarity 69.2%; Pred. NO. 17;

Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLNKGHLGSEV 13

DB 30 DSNKNGTLDFSEV 42

RESULT 15

H81358

probable signal peptidase I (EC 3.4.21.89) Cj0856 [similarity] - Campylobacter jejuni

C:Species: Campylobacter jejuni

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002

C:Accession: H81358

R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Ch

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; B

RESULT 11

T22685

hypothetical protein F55A11.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T22685

R:Kershaw, J.

Submitted to the EMBL Data Library, May 1996

A:Reference number: Z19600

A:Accession: T22685

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-186 <WIL>

A:Cross-references: EMBL:Z72511; PIDN:CAA96655.1; GSPDB:GN000023; CESP:F55A11.1

A:Experimental source: clone F55A11

C:Genetics:

A:Gene: CESP:F55A11.1

A:Map position: 5

A:Introns: 33/3; 59/2; 146/2

Query Match 60.0%; Score 42; DB 2; Length 186;

Best Local Similarity 61.5%; Pred. No. 11;

Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DLNKGHLGSEV 13

DB 89 DLNKGHLGSEV 101

RESULT 12

G96572

protein F12M16.12 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: G96572

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chen, C.W.; Chung, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.B.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, X.; Lin, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: G96572

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-574 <STO>

A:Cross-references: GB:AE005173; NID:g7769854; PIDN:AAF69532.1; GSPDB:GN00141

C:Genetics:

A:Gene: F12M16.12

A:Map position: 1

Query Match 60.0%; Score 42; DB 2; Length 574;

Best Local Similarity 53.8%; Pred. No. 34;

Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DLNKGHLGSEV 13

DB 301 DANNDGLSAAEL 313

RESULT 13

B82736

hemolysin-type calcium binding protein XF1011 [imported] - Xylella fastidiosa (strain 9a

C:Species: Xylella fastidiosa

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C:Accession: B82736

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A:Reference number: A61250; MUID:20150912; PMID:10688204
A:Accession: H81358
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-282 <PAR>
A:Cross-references: GB:AL139076; GB:AL111168; NID:96968128; PIDN:CAB73121.1; PID:9696830
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: lepp; Cj0856
C:Superfamily: signal peptidase I
C:Keywords: hydrolase; serine protease

Query Match 58.6%; Score 41; DB 2; Length 282;
Best Local Similarity 87.5%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 DLNRDGH 8
Db 73 DENKDGHL 80

Search completed: May 14, 2003, 10:46:31
Job time : 5.02053 secs

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GenCore version 5.1.4.p5.4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on:

May 19, 2003, 12:18:31 ; Search time 194 Seconds
(without alignments)
2180.926 Million cell updates/sec

Title:

Perfect score: 1772

Sequence: 1 MMWRPVLILLILRHGAQ.....FVGSQATWYGEDLRRHDEL 328

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 810007 seqs, 644969091 residues

Total number of hits satisfying chosen parameters: 1620014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Published_applications_NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1772	100.0	1055	10	US-09-768-840-2	Sequence 2, Appl1
2	1772	100.0	1463	10	US-09-847-809A-2	Sequence 2, Appl1
3	1772	100.0	1503	9	US-09-905-291A-220	Sequence 220, App
4	1772	100.0	1503	9	US-09-902-853-220	Sequence 220, App

5	1772	100.0	1503	9	US-09-907-824-220	Sequence 220, App
6	1772	100.0	1503	9	US-09-907-841-220	Sequence 220, App
7	1772	100.0	1503	9	US-09-904-011-220	Sequence 220, App
8	1772	100.0	1503	9	US-10-028-072-363	Sequence 363, App
9	1772	100.0	1503	9	US-09-906-742-220	Sequence 220, App
10	1772	100.0	1503	9	US-10-121-049-363	Sequence 363, App
11	1772	100.0	1503	9	US-10-123-904-363	Sequence 363, App
12	1772	100.0	1503	9	US-10-140-470-363	Sequence 363, App
13	1772	100.0	1503	9	US-09-906-838-220	Sequence 220, App
14	1772	100.0	1503	9	US-09-907-942-220	Sequence 220, App
15	1772	100.0	1503	9	US-10-175-746-363	Sequence 363, App
16	1772	100.0	1503	9	US-10-176-918-363	Sequence 363, App
17	1772	100.0	1503	9	US-10-176-921-363	Sequence 363, App
18	1772	100.0	1503	9	US-10-137-865-363	Sequence 363, App
19	1772	100.0	1503	9	US-10-140-474-363	Sequence 363, App
20	1772	100.0	1503	9	US-09-904-820-220	Sequence 220, App
21	1772	100.0	1503	9	US-09-904-859-220	Sequence 220, App
22	1772	100.0	1503	9	US-10-142-431-363	Sequence 363, App
23	1772	100.0	1503	9	US-09-906-646-220	Sequence 220, App
24	1772	100.0	1503	9	US-09-906-700-220	Sequence 220, App
25	1772	100.0	1503	9	US-10-143-114-363	Sequence 363, App
26	1772	100.0	1503	9	US-09-904-786-220	Sequence 220, App
27	1772	100.0	1503	9	US-09-906-646-220	Sequence 220, App
28	1772	100.0	1503	9	US-09-902-903-220	Sequence 220, App
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31	1772	100.0	1503	9	US-10-142-419-363	Sequence 363, App
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33	1772	100.0	1503	9	US-09-904-119-220	Sequence 220, App
34	1772	100.0	1503	9	US-09-904-956-220	Sequence 220, App
35	1772	100.0	1503	9	US-09-907-794-220	Sequence 220, App
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37	1772	100.0	1503	9	US-10-142-423-363	Sequence 363, App
38	1772	100.0	1503	9	US-09-902-692-220	Sequence 220, App
39	1772	100.0	1503	9	US-09-903-943-220	Sequence 220, App
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41	1772	100.0	1503	9	US-09-905-056-220	Sequence 220, App
42	1772	100.0	1503	9	US-09-907-923-220	Sequence 220, App
43	1772	100.0	1503	9	US-09-907-923-220	Sequence 220, App
44	1772	100.0	1503	9	US-09-907-923-220	Sequence 220, App
45	1772	100.0	1503	9	US-09-907-923-220	Sequence 220, App

ALIGNMENTS

RESULT 1
US-09-768-840-2
; Sequence 2, Application US/09768840
; Patent No. US20010012831A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09768,840
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/206,499

FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0261 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1055 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: CONTUNT01
 CLONE: 2950570
 15-09-768-840-2

Alignment Scores:	6.74e-183	Length:	1055
pred. No.:	1772.00	Matches:	328
Score:	100.00%	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	100.00%	Gaps:	0
	10		

760-840-1 (1-338) x US-09-768-840-2 (1-1055)

	US-09-768-840-1	(1 - 5267) A	
QY	1	MetMetRPaqProSerValLeuLeuLeuLeuLeuLeuArgHisGlyAlaGlnGly	20
DfB	34	ATGATGTGGCGCACCATCACTTCTGCTTCCTTGTTACTAGGCACGGGCCAGGGG	93
QY	21	LysProSerProAspaLaGlyProHisGlyGlnGlyArgValHisGlnAlaAaprotein	40
DfB	94	AAGCCATCCCAGACGAGCCTCATGCCAGGGAGGTCACCAGGCGGCCCCCTG	153
QY	41	SerAspaLaproHisaspAspaLaHisGlyAsnPhelntyrAspHisGluAlaPheLeu	60
DfB	154	AGCCAGCGTCCCCATGATGACGCCACGGGAACCTCCAGTAGCACCATTAGAGGCTTTCCTG	213
QY	61	GlyArgGluVaAlatylsGlupuHeAspGlnLeuthrProGluGluSerGlnAlaArGLeu	80
DfB	214	GGACGGGAAGTGGCCAAGGAATTCGACCAACTCACCCAGAGGAAGCCAGGCCCGCTG	273
QY	81	GlyArgIleValaspArgMetAspAglaGlyAspGlyAspGlyTyrrValSerLeuaLa	100
DfB	274	GGCGCGATCGTGGACCGCATGGACCGCGGGGGACGGCGTGGGTTCGCTGGCC	333
QY	101	GluLeuArgAlatrPilleAlaHisThrGlnGlnArqHisIleArqAspSerValSerAla	120
DfB	334	GAGCTTCGGCGGTGGATCGCGCACACGCACGGCGGCACATACGGGACTCGGTGAGCGCG	393
QY	121	AlatrPasThrTyrrAspThrAspArGaspeLyargValglytyrpglucileuLeuArgasn	140
DfB	394	GCCTGGGACACGTACACACGACCGCGCGCGCGTGTGGTGGGAGGAGTCGGCAAC	453
QY	141	AlatrThyrglyhiTyrralaproclglucipuHephHisaspvalcgluaspaLaGluThr	160
DfB	454	GCCACCTATGGCCACTACGCGCCCGGTGAAGAATTCATGACGTGGAGGATCGACAGACC	513
QY	161	TyrrlysMettLeualaarqAspGluArqargpheargValalaAspGlnasppGlyasp	180
DfB	514	TACAAAAAGATGCTGCTCGGACGACGCGCGTTCCTGGGTGGCCGACAGGATGGGAC	573
QY	181	SerMetAlatrArqGluLeuThrAlaphelLeuhisProGluIpheproHisMett	200
DfB	574	TCGATGGCCACTCGAGAGAGTCAGACGCTTCTGCAACCCCGAGGAGTTCCCTCACATG	633
QY	201	ArgspillevallleaGluThrLeuGluAspLeuAsparGAsnLysAspGlyTyrrVal	220
DfB	634	CGGGACAPCFGTAATGTCTGAAACCTGGAGGACCTGGACAGAAAACAAGATGGCTATGTC	693

Qy	221	GlnValGlnGluThrLeuValGlnGlnPheArgAspPheArgAspLeuAsnLysAspGlyHis	260
Db	694	CAGGTGGAGGAGTACATCGGGATCTGTACTCAGCCGAGCCTGGGAGGAGGAGCGCGG	753
Qy	241	TrpValGlnThrGluArgGlnGlnPheArgAspPheArgAspLeuAsnLysAspGlyHis	260
Db	754	TGGGTGCACAGCGAGAGCGACAGTTCCTGGGACTTCCTGGGACTGAACAAGATGGGCAC	813
Qy	261	LeuAspGlySerGluValGlnGlnPheArgAspPheArgAspLeuAsnLysAspGlyHis	280
Db	814	CTGGATGGGAGTGGGTCCTGGGCTGGTGTCTGCCCTGCCAGACGAGCCCTGGTGGT	873
Qy	281	GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla	300
Db	874	GAAGCCAAACCACTCTCTCCACGAGAGCGACACGGACCAAGGATGGCGGCTGAGCAAGCG	933
Qy	301	GluLeuLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAsp	320
Db	934	GAATCTCGGTAAITGGAACATGTTTCTGGCAGTCAGGCCCAACTATATGGCGAGGAC	993
Qy	321	LeuThrArgHisHisAspGluLeu	328
Db	994	CTGACCCGGCACACGATGAGCTG	1017
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US-09-847-809A-2			
; Sequence 2, Application US/09847809A			
; Patent No. US20020081604A1			
; GENERAL INFORMATION:			
; APPLICANT: Bandman, Olga			
; Hillman, Jennifer L.			
; Lal, Preeti			
; Corley, Neil C.			
; Shah, Purvi			
; TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS			
; NUMBER OF SEQUENCES: 6			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Incyte Pharmaceuticals, Inc.			
; STREET: 3174 Porter Drive			
; CITY: Palo Alto			
; STATE: CA			
; COUNTRY: USA			
; ZIP: 94304			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Diskette			
; COMPUTER: IBM Compatible			
; OPERATING SYSTEM: DOS			
; SOFTWARE: FastSeq for Windows Version 2.0			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/09/847,809A			
; FILING DATE: 01-May-2001			
; CLASSIFICATION: <Unknown>			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: 09/270,270			
; FILING DATE: 1999-03-16			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Billings, Lucy J.			
; REGISTRATION NUMBER: 36,749			
; REFERENCE/DOCKET NUMBER: PF-0358 US			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 650-855-0555			
; TELEFAX: 650-845-4166			
; TELEX: <Unknown>			
; INFORMATION FOR SEQ ID NO: 2:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 1463 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; IMMEDIATE SOURCE:			
; LIBRARY: RATRNOT02			
; CLONE: 922578			
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:			

[illegible]

APPLICANT: WILLIAMS, I. MARY
APPLICANT: WOOD, WILLIAM, I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACID ENCODING THE SAME

- 92/0057/24V

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1  PRIOR FILING DATE: 1999-09-15
2  PRIOR APPLICATION NUMBER: PCT/US99/21547
3  PRIOR FILING DATE: 1999-09-15
4  PRIOR APPLICATION NUMBER: PCT/US99/23089
5  PRIOR FILING DATE: 1999-10-05
6  PRIOR APPLICATION NUMBER: PCT/US99/28214
7  PRIOR FILING DATE: 1999-11-29
8  PRIOR APPLICATION NUMBER: PCT/US99/28313
9  PRIOR FILING DATE: 1999-11-30
10 PRIOR APPLICATION NUMBER: PCT/US99/28564
11 PRIOR FILING DATE: 1999-12-02
12 PRIOR APPLICATION NUMBER: PCT/US99/28565
13 PRIOR FILING DATE: 1999-12-02
14 PRIOR APPLICATION NUMBER: PCT/US99/30095
15 PRIOR FILING DATE: 1999-12-16
16 PRIOR APPLICATION NUMBER: PCT/US99/30911
17 PRIOR FILING DATE: 1999-12-20
18 PRIOR APPLICATION NUMBER: PCT/US99/30999
19 PRIOR FILING DATE: 1999-12-20
20 PRIOR APPLICATION NUMBER: PCT/US00/00219
21 PRIOR FILING DATE: 2000-01-05
22 NUMBER OF SEQ ID NOS: 423
23
24 SEQ ID NO 220
25 LENGTH: 1503
26 TYPE: DNA
27 ORGANISM: Homo Sapien
28
29 rs-09-907-824-220

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Alignment Scores:		
Pred. NO.:	1.05e-182	Length: 1503
Score:	1772.00	Matches: 328
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	9	Gaps: 0

US-09-907-824-220 (1-1503)

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QY	181	SerMetalThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMet	200
DB	575	TCGATGGCCACTCGAGAGAGCTGACAGCCTTCCTGACCCCGAGGAGTTCCTCCACATG	634
QY	201	ArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrVal	220
DB	635	CGGACATCGTGATGCTGAAACCCCTGGAGGACCTGGACAGAAAACAAAGATGGCTATGTC	694
QY	221	GlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGluGluProAla	240
DB	695	CAGGTGGAGGAGTAGTACATCGCGGATCTGTACTACCGCAGCCCTGGGAGGAGGAGCGCGC	754
QY	241	TrpValGlnThrGluAraGlnGlnPheArgAspPheArgAspLeuAsnLysAspGlyHis	260
DB	755	TGGGTGTCAGACGGAGAGGCAGCAGTTCGCGGACTTCGCGGATCTGACCAAGGATGGGCAC	814
QY	261	LeuAspGlySerGluValGlyHisTrpValLeuProProAlaGlnAspGlnProLeuVal	280
DB	815	CTTGATGGAGTAGTGAGTGGGCGCATCTGGTGTCTGCCCTCTGCCAGGACGAGCCCTGGTG	874
QY	281	GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla	300
DB	875	GAAGCCACCACTCTGTCACGAGAGGCACACGAGCAAGGATGGCGGCTGACCAAGCG	934
QY	301	GluIleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAsp	320
DB	935	GAATCTCTGGGTAAATGGAAACATGTTGTGGCAGTCAGGCCCACTATGGCGAGGAC	994
QY	321	LeuThrArgHisHisAspGluLeu	328
DB	995	CTGACCCGGCACCAAGATGAGCTG	1018
RESULT 6			
US-09-907-841-220			
; Sequence 220, Application US/09907841			
; Publication No. US20020198366A1			
; GENERAL INFORMATION:			
; APPLICANT: Genentech, Inc.			
; APPLICANT: Ashkenazi, Avi			
; APPLICANT: Botstein, David			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Eaton, Dan L.			
; APPLICANT: Ferrara, Napoleone			
; APPLICANT: Filvaroff, Ellen			
; APPLICANT: Fong, Sherman			
; APPLICANT: Gao, Wei-Qiang			
; APPLICANT: Gerber, Hanspeter			
; APPLICANT: Gerritsen, Mary E.			
; APPLICANT: Goddard, A.			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Grimaldi, Christopher J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Hillan, Kenneth, J.			
; APPLICANT: Kljavin, Ivar J.			
; APPLICANT: Mather, Jennie P.			
; APPLICANT: Pan, James			
; APPLICANT: Paoni, Nicholas F.			
; APPLICANT: Roy, Margaret Ann			
; APPLICANT: Stewart, Timothy A.			
; APPLICANT: Tumas, Daniel			
; APPLICANT: Williams, P. Mickey			
; APPLICANT: Wood, William, I.			
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucle			
; TITLE OF INVENTION: Acids Encoding the Same			
; FILE REFERENCE: 10466-14			
; CURRENT APPLICATION NUMBER: US/09/907,841			
; CURRENT FILING DATE: 2001-11-20			
; PRIOR APPLICATION NUMBER: PCT/US00/04414			
; PRIOR FILING DATE: 2000-02-22			
; PRIOR APPLICATION NUMBER: US 60/143,048			
; PRIOR FILING DATE: 1999-07-07			
; PRIOR APPLICATION NUMBER: US 60/145,698			

RESULT 6

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US-09-307-841-220
; Sequence 220, Application US/0907841
; Publication No. US20020198366A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
;
; TITLE OF INVENTION: Secreted and Tri-
; TITLE OF INVENTION: Acids Encoding
;
; FILE REFERENCE: 10466-14
;
; CURRENT APPLICATION NUMBER: US/09/99-07-07
;
; CURRENT FILING DATE: 2001-11-20
;
; PRIOR APPLICATION NUMBER: PCT/US00/
;
; PRIOR FILING DATE: 2000-02-22
;
; PRIOR APPLICATION NUMBER: US 60/14
;
; PRIOR FILING DATE: 1999-07-07
;
; PRIOR APPLICATION NUMBER: US 60/14

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: PRIOR FILING DATE: 1999-07-26
: PRIOR APPLICATION NUMBER: US 60/146,222
: PRIOR FILING DATE: 1999-07-28
: PRIOR APPLICATION NUMBER: PCT/US99/20594
: PRIOR FILING DATE: 1999-09-08
: PRIOR APPLICATION NUMBER: PCT/US99/20944
: PRIOR FILING DATE: 1999-09-13
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/21547
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/23089
: PRIOR FILING DATE: 1999-10-05
: PRIOR APPLICATION NUMBER: PCT/US99/28214
: PRIOR FILING DATE: 1999-11-29
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ IDS: 423

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; SEQ ID NO 220
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-841-220

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Alignment Scores:	
Pred. No.:	1.05e-182
Score:	1772.00
Length:	1503
Percent Similarity:	Matches: 328
Best Local Similarity:	Conservative: 0
Query Match:	Mismatches: 0
DB:	Indels: 0
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US-09-768-840-1 (1-328) x US-09-907-841-220 (1-1503)

[illegible]

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1  PRIOR APPLICATION NUMBER: PCT/US99/20594
2  PRIOR FILING DATE: 1999-09-08
3  PRIOR APPLICATION NUMBER: PCT/US99/20944
4  PRIOR FILING DATE: 1999-09-13
5  PRIOR APPLICATION NUMBER: PCT/US99/21090
6  PRIOR FILING DATE: 1999-09-15
7  PRIOR APPLICATION NUMBER: PCT/US99/21547
8  PRIOR FILING DATE: 1999-09-15
9  PRIOR APPLICATION NUMBER: PCT/US99/23089
10 PRIOR FILING DATE: 1999-10-05
11 PRIOR APPLICATION NUMBER: PCT/US99/28214
12 PRIOR FILING DATE: 1999-11-29
13 PRIOR APPLICATION NUMBER: PCT/US99/28313
14 PRIOR FILING DATE: 1999-11-30
15 PRIOR APPLICATION NUMBER: PCT/US99/28564
16 PRIOR FILING DATE: 1999-12-02
17 PRIOR APPLICATION NUMBER: PCT/US99/28565
18 PRIOR FILING DATE: 1999-12-02
19 PRIOR APPLICATION NUMBER: PCT/US99/30095
20 PRIOR FILING DATE: 1999-12-16
21 PRIOR APPLICATION NUMBER: PCT/US99/30911
22 PRIOR FILING DATE: 1999-12-20
23 PRIOR APPLICATION NUMBER: PCT/US99/30999
24 PRIOR FILING DATE: 1999-12-20
25 PRIOR APPLICATION NUMBER: PCT/US00/00219
26 PRIOR FILING DATE: 2000-01-05
27 NUMBER OF SEQ ID NOS: 423
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29 SEQ ID NO 220
30 LENGTH: 1503
31 TYPE: DNA
32 ORGANISM: Homo Sapien
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Alignment Scores:	1.05e-182	Length:	1503
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Score:	100.00%	Conservative:	0
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DB:	9		

US-09-768-840-1 (1-328) x US-09-904-011-220 (1-1503)

[illegible]

Db	455	CCACACCTATGGCCACTACGCCGCCGGTGAAGAAATTCATGCTGGAGGATGACAGACC	514
Qy	161	TyrlsLysMetLeuAlaargaspGluArgqPheAqValaAlaaspGlnAspGlyasp	180
Db	515	TACAAAAGATGCTGGCTGGGACGAGCGCGTTTCGGGTGGCCGACAGGATGGGAC	574
Qy	181	SerMetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMet	200
Db	575	TCGATGGCCACTCGAGAGGAGCTGACAGCGCTTCCTGCACCCCGAGGAGTTCCCTCACATG	634
Qy	201	ArgaspIleValIleAlaGluThrLeuGluAaspLeuAspArgasnLysAspGlyTyrVal	220
Db	635	CGGACATCGTGATGTGTGAACCTCTGGAGCCTCGACAGAACAAAGATGGCTATGTC	694
Qy	221	GlnValGluGluTyrIleAlaAaspLeuTyrSerAlaGluProGlyGluGluProAla	240
Db	695	CAGGTGGAGGAGTACATCGCGGATCTGTACTACGCCGAGCCTGGGAGGAGGAGCGCGC	754
Qy	241	TrpValGlnThrGluArgGlnGlnPheArgaspPheArgaspLeuasnLysaspGlyHis	260
Db	755	TGGGTGCAGACGAGAGCGACAGCAGCTTCCTGGGACTTCGGGATCTGAACAAGGATGGGCAC	814
Qy	261	LeuaspGlySerGluValGlyHisTrpValLeuProProAlaGlnAspGlnProLeuVal	280
Db	815	CTGGATGGGAGTGGAGTGGCGCACTGGGTGCTGCCCTCCACGAGCAGCCCTGGTG	874
Qy	281	GluAlaasnHisLeuLeuHisGluSerAspThrAspLysaspGlyArgLeuSerLysAla	300
Db	875	GAAGCCACACCACTGCTCCAGAGAGCGACACGAGCAAGGATGGCGGCTGAGCAAGCG	934
Qy	301	GluIleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAasp	320
Db	935	GAATCTCGGTGAATTGGAAACATGTTGTGGCAGTCAGGCCCACTATGGCGAGGAC	994
Qy	321	LeuThrArgHisAspGluLeu	328
Db	995	CTGACCCGGCACCACTGAGCTG	1018
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; Sequence 363, Application US/10028072			
; Publication No. US20030004311A1			
; GENERAL INFORMATION:			
; APPLICANT: Baker, Kevin P.			
; APPLICANT: Beresini, Maureen			
; APPLICANT: DeForge, Laura			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Flivaroff, Ellen			
; APPLICANT: Gao, Wei-Qiang			
; APPLICANT: Gerritsen, Mary E.			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Sherwood, Steven			
; APPLICANT: Smith, Victoria			
; APPLICANT: Stewart, Timothy A.			
; APPLICANT: Tumas, Daniel			
; APPLICANT: Watanabe, Colin K			
; APPLICANT: Wood, William			
; APPLICANT: Zhang			
; TITLE OF INVENTION:			
; FILE REFERENCE:			
; CURRENT APPLICATION NUMBER: US/10/028,072			
; CURRENT FILING DATE: 2001-12-19			
; PRIOR APPLICATION NUMBER: 60/049911			
; PRIOR FILING DATE: 1997-06-18			
; PRIOR APPLICATION NUMBER: 60/056974			
; PRIOR FILING DATE: 1997-08-26			
; PRIOR APPLICATION NUMBER: 60/059113			
; PRIOR FILING DATE: 1997-09-17			
; PRIOR APPLICATION NUMBER: 60/059115			
; PRIOR FILING DATE: 1997-09-17			
; PRIOR APPLICATION NUMBER: 60/059117			

[illegible]

Prior Filing Date:	1998-06-17
Prior Application Number:	60/089907
Prior Filing Date:	1998-06-18
Prior Application Number:	60/089947
Prior Filing Date:	1998-06-19
Prior Application Number:	60/090349
Prior Filing Date:	1998-06-23
Prior Application Number:	60/090429
Prior Filing Date:	1998-06-24
Prior Application Number:	60/090445
Prior Filing Date:	1998-06-24
Prior Application Number:	60/090538
Prior Filing Date:	1998-06-24
Prior Application Number:	60/090863
Prior Filing Date:	1998-06-26
Prior Application Number:	60/091360
Prior Filing Date:	1998-07-01
Prior Application Number:	60/091519
Prior Filing Date:	1998-07-02
Prior Application Number:	60/091982
Prior Filing Date:	1998-07-07

Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:

	1-05e-182	Length:	1503
	1772.00	Matches:	328
	100.00%	Conservative:	0
	100.00%	Mismatches:	0
	100.00%	Indels:	0
	9	Gaps:	0

US-09-768-840-1 (1-328) x US-10-028-072-363 (1-1503)

QY	1	MetMetTPrAqProSerValLeuLeuLeuLeuLeuArHisGlyAlaGlncly	20
Db	35	ATGATGTGGCGACCATCATAGTTCTCTCCTTCTACTTGAGGCAGGCCAGGG	94
QY	21	LysProSerProAspAlaglyProHisiGlycInglyArgvVaiHisGlnAlaLaProLeu	40
Db	95	AAGCCATCCCCAGACGCAAGGCCCTCATGGCCAGGGAGGGTGCACCAGGGGCCCCCCTG	154
QY	41	SerAspAlaProHiSaspAlahisiclyAsnPhelNtyrAspHisGluAlaPheLeu	60
Db	155	AGCGAGCGTCCTCCATGATGACCCCGCCGGAACTTCCAGTAGCACCATGAGGCTTTCCTG	214
QY	61	GlyArgGluValAlaLysGluPheaSpGlnLeuThrProGluGluSerGlnAlaArgLeu	80
Db	215	GGACGGGAAGTGGCCAAGGAATTGCACCAACTCACCOCAGAGGAACCCAGGCCCTCTG	274
QY	81	GlyArgilevalaspargmetaspargalagilyaspGlyaspGlyTrpValSerLeuAla	100
Db	275	GGCGGGATPGTGGACCCGATGACCGCGGGGGGACGCGCGGTGTGGCTGGCC	334
QY	101	GluLeuArgAlatrPlleAlaHisThrGlnArqHisIleArqAspSerValSerAla	120
Db	335	GAGCTTCGCGCGTGGATTCGCGCACACGACGACGCGGCACATACAGGACTCGGTGAGCGCG	394
QY	121	AlatTPAspThrTyRspThrAspArgaspGlyArgValgIyrrpGluLeuArqasn	140
Db	395	GCGTGGGACAGTCACGACACGGACCGCGCGGTGTGGGTGGGAGGAGCTGGCAGC	454
QY	141	AlathrTyrglyHisTyralaProglyGluclupheHisaspValcluasPaladlUthr	160
Db	455	GCACCTATFGCCACATAGCGCCCGGTGAAGAATTCATGACGTGAGGATGCAGAGACC	514
QY	161	TyrLysLyseMetLeualaaArgaspluararqphearqValaalaspcInaspGlyasp	180
Db	515	TACAAAAGATGCTGGCTCGGAGAGCGCGGTTCGGGTGGGCCGCCAGCATGGGAC	574
QY	181	SerMetAlathrArgGlucluLeuThrAlaPheLeuHisProGluGluPheProhisMet	200
Db	575	TCGATGGCCACTCGAGAGAGCTGACACCTTCCTGTCACCCCGAGGAGTTCCCTCACATG	634

D6	5/5	TGATGGCCACAGCGCCTTAAAGTTGTTCATTGCCTCAATTAATCATGA
QY	201	ArgAspIleValIleAlaGluThrLeuGluAspLeuGlnLysAspGlyTyrVal

US-09-768-840-1 (1-328) x US-09-906-742-220 (1-1503)

QY 161 TyrLysLysMetLeuAlaArqAspGluArqAqPheAtgValAlaAspGlnAspGlyAsp 180
Db 515 TACAAAAGATGCTGGCTCGGAGAGAGCGCGCTTTCCGGGTGGCCGACCAGGATGGGGAC 574
QY 181 SerMetalanThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMet 200
Db 575 TCGATGCCACTCGAGAGAGCTGACAGCCTTCTGCACCCCGAGGAGTTCCCTCATG 634
QY 201 ArgAspileValIleAlaGluThrLeuGluAspLeuAspArgAsnLysaspGlyTyrrVal 220
Db 635 CGGACATCTGATTCTCAACCCCTGGAGNACTTGACAGAACAAGATGGCTATGTC 694
QY 221 GlnValGluLuTyrrIleAlaaspLeuTyrrSerAlaGluProGlyGluGluPuOAla 240
Db 695 CAGTGGAGAGTACATCGCGGATGTGTACTCACCCGAGCTGGGAGGAGGAGCGGCG 754
QY 241 TrpValGlnThrGluArgGlnGlnPheArgAspPheArgaspLeuasnLysaspGlyHis 260
Db 755 TGGGTGCAGACGAGAGGACGACAGTTCGGGACTTCGGGGATCTGAACAAGATGGCGAC 814
QY 261 LeuAspGlySerGluValGlyHisTrpValLeuProProAlaGlnAspGlnProLeuVal 280
Db 815 CTGGATGGGAGTAGAGTGGGCCACTGGGTGCTGCCCTGCCACGACCAGCCCCCTGGTG 874
QY 281 GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla 300
Db 875 GAAGCCAACCACTGCTGCACGAGCGACGACCGAACAGGATGGCGGCTGAGCAAAAGCG 934
QY 301 GluIleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrrGlyLysasp 320
Db 935 GAAATCCCTGGGTAAATGGAACATGTTGTGGCAGTCAGSCCCACCACTATGGCAGGAC 994
QY 321 LeuThrArgHisHisAspGluLeu 328
Db 995 CTGACCCGGCACCGATGAGCTG 1018

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US-10-121-049-363
; Sequence 363, Application US/10121049
; Publication No. US2003002239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gudney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Collin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C17
; CURRENT APPLICATION NUMBER: US/10/121,049
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 363
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-121-049-363

Alignment Scores:

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QY	121	AlaTrpAspThrTyrAspThrAspArgAspGlyArgValGlyTrpGluGluLeuArgAsn	140
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QY	141	AlaThrTyrGlyHisTyrAlaProGlyCiuPheHisAspValGluAspAlaGluThr	160
Db	455	GCACCTATGGCCACTACGCCGCCGGTGAAGATTTTCATCACGTGGAGGATSCAGAGACC	514
QY	161	TyrLysLysMetLeuAlaArgAspGluArgPheArgValAlaAspGlnAspGlyAsp	180
Db	515	TACAAAAGATGCTGGCTCGGAGCAGCGCGTTCCGGGTGCCGCCAGGATGGGGAC	574
QY	181	SerMetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluCiuPheProHisMet	200
Db	575	TGATGGGCCACTCGAGAGGAGCTCACAGCCTTCCTGCACCCGAGGAGTTCCCTCACATG	634
QY	201	ArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrVal	220
Db	635	CGGCACATCGTATTGCTGAACCCCTGGAGGACCTGCACAGAACAAAGATGGCTATGTC	694
QY	221	GlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGlyCiuCiuLupProAla	240
Db	695	CAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCGGAGCCTGGGGAGGAGGCGGCG	754
QY	241	TrpValGlnThrGluArgGlnGlnPheArgAspPheArgAspLeuAsnLysAspGlyHis	260
Db	755	TGGGTGCAGACGAGAGGACGACGATTCGCGGACTTCGCGGATCTCAACAGGATGGCCAC	814
QY	261	LeuAspGlySerCiuValGlyHisTrpValLeuProProAlaGlnAspGlnProLeuVal	280
Db	815	CTGATGGGAGTAGGTGGGCCACTTGGTGTGTCCTGCCACGACACGCCCTGGTG	874
QY	281	GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla	300
Db	875	GAAGCCAACCACTGCTGCACGACGACACAGGACAAAGATGGGGCTGACCAAGCG	934
QY	301	GluIleLeuGluValAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAsp	320
Db	935	GAATCCTGGGTAAATGGAACTGTTGTGGGCAGTCAGGCCACCAACTATGGCAGGAC	994
QY	321	LeuThrArgHisHisAspGluLeu	328
Db	995	CTGACCCGGCACACCATGATGAGCTG	1018

RESULT 12
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; Sequence 363, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: ACIDS ENCODING THE SAME
; CURRENT APPLICATION NUMBER: P3330R1C160
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See PaIm or File Wrapper
NUMBER OF SEQ ID NOS: 550

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[illegible]

us-09-768-840-1.p2n.rnpb

Qy	161	TyrLysLysMetLeuAlaLeuArgAspGluArgPheArgValAlaAspGlnAspGlyAsp	180
Db	515	TACAAAAGATGCTGGCTCGGACGACGCGCTTCCGGGTGGCCACACGAGATGGGGAC	574
Qy	181	SerMetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMet	200
Db	575	TCGATGGCCACTCCAGAGGAGCTGACAGCCTTCTGCACCCCGAGGATTCCTCTCACATG	634
Qy	201	ArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrVal	220
Db	635	CGGACACATCGTGATGCTGAAACCCCTGGAGAGCTCTGCAGAACAAAGATGCGTATGTC	694
Qy	221	GlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGluGluProAla	240
Db	695	CAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGGAGGAGGCGCGCG	754
Qy	241	TrpValGlnThrGluArgGlnGlnPheArgAspPheArgAspLeuAsnLysAspGlyHis	260
Db	755	TGGGTGCAGACGGAGAGGACGACGAGTCCCGGACTTCCCGGATCTGAACAAGGATGGGCAC	814
Qy	261	LeuAspGlySerGluValGlyHisTrpValLeuProProAlaGlnAspGlnProLeuVal	280
Db	815	CTGGATGGGAGTGAGGTGGGCCACTCGGTGCTGCCCCCTGCCAGGACCAGGCCCTGTGGTG	874
Qy	281	GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla	300
Db	875	GAGCCCAACCCTGCTGCACGAGACGACACGGACAGGATGGGCGGCTGAGCAAAAGCG	934
Qy	301	GluIleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAsp	320
Db	935	GAATCTCGGTAATTGGAACATGTTTGTGGCAGTTCAGGCCACCACTATGGCGAGGAC	994
Qy	321	LeuThrArgHisHisAspGluLeu	328
Db	995	CTACCCCGGCACCAAGATGAGCTG	1018

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Job time : 222 secs

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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 19, 2003, 12:17:36 ; Search time 57 Seconds
(without alignments)
1764.736 Million cell updates/sec

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Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.*

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- 5: /cgn2_6/ptodata/1/ina/6C_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1772	100.0	1055	4	US-09-206-499-2
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4	1772	100.0	1463	4	US-09-270-270-2
5	1683	95.0	1490	4	US-09-484-970B-53
6	842.5	47.5	2658	2	US-08-910-927B-4
7	842.5	47.5	2658	4	US-09-270-270-4
8	456.5	25.8	954	2	US-08-555-722-1
9	456.5	25.8	954	4	US-09-384-301-1
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US-08-459-444-20
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US-09-399-913-29

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14 128 7.2 1400 1 US-08-338-057-1
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16 124.5 7.0 853 3 US-08-963-409-2
17 122.5 6.9 2456 3 US-08-813-150-5
18 118 6.7 1929 2 US-08-818-253-1
19 118 6.7 1929 2 US-08-818-252-1
20 118 6.7 1929 2 US-08-818-253-3
21 118 6.7 1929 2 US-08-818-252-3
22 115 6.5 1929 2 US-08-818-253-5
23 115 6.5 1929 2 US-08-818-252-5
24 115 6.5 1929 2 US-08-818-253-7
25 115 6.5 1929 2 US-08-818-252-7
26 113.5 6.4 1859 4 US-09-399-913-23
27 113.5 6.4 1859 4 US-09-399-913-23
28 111 6.3 1247 4 US-09-399-913-15
29 111 6.3 1247 4 US-09-298-731-15
30 111 6.3 1247 4 US-09-298-731-15
31 110.5 6.2 2191 4 US-09-239-905-1
32 110.5 6.2 2191 4 US-09-399-913-25
33 109.5 6.2 1349 1 US-09-298-731-25
34 109.5 6.2 1349 2 US-07-951-715A-20
35 109.5 6.2 1349 3 US-08-459-448A-20
36 109.5 6.2 1349 3 US-08-459-595A-20
37 109.5 6.2 1349 3 US-08-459-504B-20
38 109.5 6.2 1349 4 US-08-459-444-20
39 108.5 6.1 50937 4 US-09-547-422-20
40 108 6.1 2343 4 US-09-428-517-1
41 108 6.1 2343 4 US-09-399-913-17
42 107.5 6.1 2009 4 US-09-298-731-17
43 107.5 6.1 2009 4 US-09-399-913-13
44 107 6.0 906 1 US-09-298-731-13
45 106.5 6.0 1904 4 US-08-100-874-1
45 106.5 6.0 1904 4 US-09-399-913-29

ALIGNMENTS

RESULT 1
US-08-828-242-2
; Sequence 2, Application US/08828242
; Patent No. 5871970
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goll, Surya K.
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc..
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,242
; FILING DATE: Filed Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0261 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166

[illegible]

	Qy	128	AspArgAspGlyArgValGlyTrpGluGluLeuArgAsnAlaThrTyrGlyHisTyrAla	147
		:::	:::: :: :: :: :: :: ::	
	Db	460	AATGAGCAGCGCTCGTTCCCTGGGAGAGGTATAAAATGCCACCTACGGCTACGTTTTA	519
		:	:: :: :: :: :: :: :: :: :: :: ::	
	Qy	148	ProGlyGluGluPheHisAspValGlnAspAlaGluThrTyrLysLysMetLeuAlaArg	167
		:::	:: :: :: :: :: :: :: :: :: :: ::	
	Db	520	-----GATGATCCAGATCCTGATGATTAACTATATAACAGATGATGGTTAGA	570
		:	:: :: :: :: :: :: :: :: :: :: ::	
	Qy	168	AspGluArgArgPheArgValAlaAspGlnAspGlyAspSerMetAlaThrArgGluGlu	187
		:::	:: :: :: :: :: :: :: :: :: :: ::	
	Db	571	GATGAGCGAGGTTTAAATGGCAGACAAGGATGGAGACTCATTCGCCACCAAGGAGGAG	630
		:	:: :: :: :: :: :: :: :: :: :: ::	
	Qy	188	LeuThrAlaPheLeuHisProGluGluPheProHisMetArgAspIleValIleAlaGlu	207
		:::	:: :: :: :: :: :: :: :: :: :: ::	
	Db	631	TTCACAGCTTTTCCTGCACCTGAGGAGTAGTGACTACATCAAAGATATAGTAGTACAGGAA	690
		:	:: :: :: :: :: :: :: :: :: :: ::	
	Qy	208	ThrLeuGluAspLeuAspArgAsnLysAspGlyTyrValGlnValGluGluTyrIleAla	227
		:::	:: :: :: :: :: :: :: :: :: :: ::	
	Db	691	ACAATGGGAAGATATAGATAAGAAATCGTGATGGTTTCATTGATCTAGAGAGATATTGGT	750
		:	:: :: :: :: :: :: :: :: :: :: ::	
	Qy	228	AspLeuTyrSerAlaGluProGlyGluGluGluProAlaTrpValGlnThrGluArgGln	247
		:::	:: :: :: :: :: :: :: :: :: :: ::	
	Db	751	GACATGTACGCCATGATGGCACTGATGATGATGCCAGAAATGGTAAAACAGACGCGAGAG	810
		:	:: :: :: :: :: :: :: :: :: :: ::	
	Qy	248	GlnPheArgAspPheArgAspLeuAsnLysAspGlyHisLeuAspGlySerGluValGly	267
		:::	:: :: :: :: :: :: :: :: :: :: ::	
	Db	811	CAGTTTGTTCGAGTTTCGGGATTAAGAACCGTGATGGGAAGATGGACAAGGAAGACGACAA	870
		:	:: :: :: :: :: :: :: :: :: :: ::	
	Qy	268	HisTrpValLeuProProAlaGlnAspGlnProLeuValGluAlaAsnHisLeuLeuHis	287
		:::	:: :: :: :: :: :: :: :: :: :: ::	
	Db	871	GACTGGATCTCTCCCTCAGACTATGATCATCGAGCGCAGAACGCCAGCACCTGGTCTAT	930
		:	:: :: :: :: :: :: :: :: :: :: ::	
	Qy	288	GluSerAspThrAspLysAspGlyArgLeuSerLysAlaGluIleLeuGlyAsnTrpAsn	307
		:::	:: :: :: :: :: :: :: :: :: :: ::	
	Db	931	GAATCAGACCACAAAAACAAAGGATGGCAAGCTTACCAAGGAGGAGATCGCTTCACAAGTATGAC	991
		:	:: :: :: :: :: :: :: :: :: :: ::	
	Qy	308	MetPheValGlySerGlnAlaThrAsnTyrGlyGluAspLeuThrArgHisHisasp	326
		:::	:: :: :: :: :: :: :: :: :: :: ::	
	Db	991	TTATTTCTTGGCAGCCAGCCACACATTTTGGGAGGCCCTTACTACGGCATGATGAG	1047
		:	:: :: :: :: :: :: :: :: :: :: ::	

RESULT 7
US-09-270-270-4
; Sequence 4, Application US/09270270
; Patent No. 6235477
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN RETICULOCALBIN ISOFORMS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/270,270
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/910,927
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

16 AGGACCGCGCGCTTGGGGCTGCTGCTGTGC----- 48

[illegible]

Qy 142 ThrTyrGlyHisTyrAlaProGlyGluLeuPheHisAspValGluAspAla-----Glu 159
Db 376 ATGTATGATCGTGTGATGTTGATGAGAACACACGCTCTGGATGATGACGAAGAGGAG 435
Qy 160 ThrTyrLysLysMetLeuAlaArgAspGluArgPheArgValAlaAspGlnAspGly 179
Db 436 TCCTTTAGGAAGCTTCACTTAAAGGACAAAGCGATTTCMAAAGCTAACCAAGATTCA 495
Qy 180 AspSerMetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHis 199
Db 496 GTGCCCGTGTGAGTCTTGAAGAAATTTATGCTTTTGAGCATCTCGAAGAACTGATTAT 555
Qy 200 MetArgAspLeuValLeuAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyr 219
Db 556 ATGACGGAATTTGCTATCAAGAGCTTTAGAGAACATGACAAAATGGTGATGATTT 615
Qy 220 ValGluValGluGluTyrLeuAlaAspLeuTyrSerAlaGluPro---GlyGluGluGlu 238
Db 616 GTTAGTTTGAAGAAATTTCTTGCTGAT---TACAGGTGGATCCCAACTGCAAAATGAAGAT 672
Qy 239 ProAlaTyrValGlnThrGluArgGlnGlnPheArgAspPheArgAspLeuAsnLysAsp 258
Db 673 CCAGATGATGATCTGTTGAGAAACACAGATTCGTGAATGATTATGACAAAGATAACGAT 732
Qy 259 GlyHisLeuAspGlySerGluValGlyHisTyrValLeuProProAlaGlnAspGlnPro 278
Db 733 GGCAGCGCTGTATCCCAAGAGCTGTACCTTGGGTAGTAGTACCTAATAATCAGCGGATTCGA 792
Qy 279 LeuValGluAlaAsnHisLeuHisGluSerAspThrAspLysAspGlyArgLeuSer 298
Db 793 CAAGAGGAGCGCTCATCTCAATGATGAATGATTTGAATGTTGACAAAAGCTCTCT 852
Qy 299 LysAlaGluLeuLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGly 318
Db 853 GAAGAAGAGATTCGAAACCCGAGCTGTTCTCACCAGTGAAGCCACAGATTATGCG 912
Qy 319 GluAspLeuThrArg-----HisHisAspGluLeu 328
Db 913 AGACAGCTCCATGATGACTATTCTCATCATGATGAGCTT 951

RESULT 10
US-08-840-683-1
; Sequence 1, Application US/08840683
; Patent No. 5821051
; GENERAL INFORMATION:
; APPLICANT: Androphy, Elliot J.
; APPLICANT: Chen, Jason J.
; TITLE OF INVENTION: E5-BINDING PROTEINS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/840,683
; FILING DATE: 29-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,059
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: NEP-003

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1192 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-840-683-1
Alignment Scores:
Pred. No.: 9,18e-33 Length: 1192
Score: 391.00 Matches: 96
Percent Similarity: 55.27% Conservative: 56
Best Local Similarity: 34.91% Mismatches: 110
Query Match: 22.07% Indels: 14
DB: 1 Gaps: 6
US-09-768-840-1 (1-328) x US-08-840-683-1 (1-1192)
Qy 64 ValAlaLysGluPheAspGlnLeuThrProGluGluSerGlnAlaArgLeuGlyArgile 83
Db 15 ATCACCAGAAATTTCTCCAA-----ACTAACAATATCAGGTTCGACGGTGGCGGACGG 68
Qy 84 ValAspArgMetAspArgAlaGly-----AspGlyAspGlyTrpValSerLeu 99
Db 69 CTGCGCGCGTGTGATTCGCGGAATTCGCGACTTGGACTCAGATGGTGTGCTACTGA- 127
Qy 100 AlaGluLeuArgAlaTyrPheAlaHisThrGlnGlnArgHisIleArgAspSerValser 119
Db 128 AAGAACTCAGTTCATGGATTCAGATGCTCTTTTAAGCATTTATGCTATCCAGAAGCAAAA 187
Qy 120 AlaAlaTyrAspThrTyrAspThrAspArgAspGlyArgValGlyTrpGluGluLeuArg 139
Db 188 CAACAGTTTGTGATATGATAAACAACAGTGTGATGATGATGCTGCTGCTGGATGAATATAAC 247
Qy 140 AsnAlaThrTyrGlyHisTyrAlaProGlyGluGluPheHisAspValGluAspAla--- 158
Db 248 ATTCAGATGATGATCGTGTGATTCGCTTGTGATGAGAACACCTGCTGGATGATGCAGAA 307
Qy 159 ---GluThrTyrLysLysMetLeuAlaArgAspGluArgArgPheArgValAlaAspGln 177
Db 308 GAGGAGTCTTTAGGAAGCTTCACTTAAAGGACAAAGAGCGATTGAAAAAGCTTAACAG 367
Qy 178 AspGlyAspSerMetAlaThrArgGluGluLeuThrAlaPheHisAspProGluGluPhe 197
Db 368 GATTCAGGTCCCGGTTTGAGCTTTGAAGAAATTTATTCTTTTGAGCATCTCTGAAGAAAGT 427
Qy 198 ProHisMetArgAspPheValAlaGluThrLeuGluAspLeuAspArgAsnLysAsp 217
Db 428 GATTATATGACGGAATTTGTCATTTCAAGAAGCTTTAGAAGAACATGACAAAAATGGTAT 487
Qy 218 GlyTyrValGlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluPro---GlyGlu 236
Db 488 GGATTTGTTAGTTTGAAGAAATTTCTTGGTGTAT---TACAGGTGGATGATCACTCAAAAT 544
Qy 237 GluGluProAlaTyrPheValGlnThrGluArgGlnGlnPheArgAspPheArgAspLeuAsn 256
Db 545 GAAGATCCAGATGGATCTTGTGTGAGAAAGACAGATTCCTGATGATGATGATGATGATGAT 604
Qy 257 LysAspGlyHisLeuAspGlySerGluValGlyHisTyrPheValLeuProProAlaGlnAsp 276
Db 605 AACGATGGCAGGCTTGTATCCCAAGAGCTGTTTACCTTGGTGTGATGATGATGATGATGAT 664
Qy 277 GlnProLeuValGluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArg 296
Db 665 ATTGCACAAGAGGAGCGCTTCATCTAATGATGATGATGATGATGATGATGATGATGATGAT 724
Qy 297 LeuSerLysAlaGluLeuLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsn 316
Db 725 CTCTCTGAAGAGAGATTCTTGAAACCCGCGGACTTTGTTCTCACCAGTGTGAGCCACAGAT 784

QY	317	TyTGlyGluAspLeuThrArg-----HisHisAspGluLeu	328
Db	785	TATGCACAGACGCTCCATGATGACTATTTCTATCATGATGAGCTT	829
RESULT 11			
US-09-484-970B-150			
; Sequence 150, Application US/09484970B			
; Patent No. 6426186			
; GENERAL INFORMATION:			
; APPLICANT: Jones, Karen A.			
; APPLICANT: Volkmoth, Wayne			
; APPLICANT: Walker, Michael G.			
; TITLE OF INVENTION: BONE REMODELING GENES			
; FILE REFERENCE: PB-0014 US			
; CURRENT APPLICATION NUMBER: US/09/484,970B			
; CURRENT FILING DATE: 2000-01-18			
; NUMBER OF SEQ ID NOS: 172			
; SOFTWARE: PERL Program			
; SEQ ID NO 150			
; LENGTH: 1992			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: misc_feature			
; OTHER INFORMATION: Incyte ID No. 6426186 232513.3			
; NAME/KEY: unsure			
; LOCATION: 1421			
; OTHER INFORMATION: a, t, c, g, or other			
US-09-484-970B-150			
Alignment Scores:			
Pred. No.:		7,33e-18	Length: 1992
Score:		255.00	Matches: 87
Percent Similarity:		41.96%	Conservative: 67
Best Local Similarity:		23.71%	Mismatches: 158
Query Match:		14.39%	Indels: 55
DB:		4	Gaps: 12
US-09-768-840-1 (1-328) x US-09-484-970B-150 (1-1992)			
QY	3	TrpArgProSer-----ValLeuLeuLeuLeu	11
Db	319	TGGCGTCCAGGTGGGGTCCCTCCATCTGGCTCGCTCGCTCGCTCGCTCGGG	378
QY	12	LeuLeuLeuArgHisGlyAlaGlnGlyProSerProAspAlaGlyProHisGlyGln	31
Db	379	CGAGTCTTCTGATGGACGGCTGTGCACGGCCTGCCAACCACTCGTCCACT-----CGA	432
QY	32	GlyArgValHisGlnAlaAlaProLeuSerAspAlaProHisAsp-----	46
Db	433	CAGAGAGTAGCCAAACAGGGAGGAGAATGAGATCTGCCCCACGACCACTTGACGGGTG	492
QY	47	-----AspAlaHisGlyAsnPheGlnTyTrpAspHisGluAlaPheLeuGlyArg	62
Db	493	AGCTGGAGATGGACGGGCACCTCAATCGCGGCTTCCACCAGGAGGTCTTCTTAGGCAAG	552
QY	63	GluValAlaLysGluPheAspGlnLeuThrPro-----GluGluSerGlnAlaArg	79
Db	553	GACCTGGGTGGCTTTGATGAGGACGCGGAGCGCGGGCGGAGCAAGCTGATGGTCAT	612
QY	80	Leu-GlyArgIleValAspArgMetAspArgAlaGlyAspGlyAspGlyTrpValSerLe	99
Db	613	CTTTCCAAAGGTGGATGTCAACACTGACCGGAAG-----ATCAGTGC	654
QY	99	uAlaGluLeuArgAlaTrpIleAlaHisThrGlnGlnArgHisIleArgAspSerValse	119
Db	655	CAAGGAGATGCACGCGTGGATCATGGGAAGACCGCGCGAGCACTTCGAGGAGCCATGGA	714
QY	119	rAlaAla-----TrpAspThrTyTrpAspArgAspGlyArgValGlyTrpGln	136
Db	715	GGAGACAGACAGACACTTCGCGCGCGTGGACCTTGACGGGGACGCTCACCGTCTTTGGGA	774

PRIOR APPLICATION DATA:
APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:
NAME: Certone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0493 US.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-835-0555.
TELEFAX: 650-845-4166
TELEX:

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 196 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: ISL1N0701
CLONE: 2379155
-09-048-889-9

Alignment Scores:		
pred ₁₀₀ No.:	2.48e-05	Length:
Score:	136.50	Matches:
Percent Similarity:	33.98%	Conservative:
Best Local Similarity:	21.27%	Mismatches:
Query Match:	7.70%	Indels:
DB:	3	Gaps:
		17
		1496

US-09-768-840-1 (1-328) x US-09-048-889-9 (1-1496)

Qy	29	HISGLYGLNGLYArgValHISGLNAlaAlaProLeuSerAspAlaProHisAspAla	48
Db	17	CACGCCCAAGCAGCG-----TCGCGTCTCTCC-----	43
Qy	49	HISGLYAsnPhelGlnTyrAspHisGLuAlaPheLeuGLYArgGLuValAlaLysGLuPhe	68
Db	44	-----CACCACAGTTACTCAAAAGCTAATCATAGTAGCAAGAAGCA	85
Qy	69	AspGlnLeuThrProGLuGLuSerGlnAlaArgLeuGLYArgIleVal-----	84
Db	86	GGAGAGCAAGTCAAGAAATACGGTGAAGGAGCTCTTCCCAAGTTGTCTAGGTCTCTCCG	145
Qy	85	-----	Asp 85
Db	146	CGCGGTGCCTGGTCTTCGTGCTCAACACCATGGACAGCTCCCGGAAACCGACTCTGGG	205
Qy	86	ArgMetAspArgAlaGLY-----	AspGLYAspGLY 95
Db	206	CGCTTGGACCGCTGGCTCTTGGCAGGCTGGCAGCGCTTTCATCGGAGATGAAAAGT	265
Qy	96	TrpValSerLeuAlaGLuLeuArgAlaTrpIleAlaHISThrGlnGlnArg---HisIle	114
Db	266	TACATAGAACAGAGGAACTCGATGCTTCTTCTCCACATGTGATGAAACTGGGTACT	325
Qy	115	ArgAspSerValSerAlaAla-----	TrpAspThrTrp 125
Db	326	GATGACACGGTCTATGAAGCAAAATTTGCACAGGTGAAACACAGCTTTATGACTACCCAA	385
Qy	126	AspThrAspArgAspGLYArgValGLYTrpGLuGLuLeuArgAsnAlaThrTyrGLYHis	145
Db	386	GATGCGCTCAAGATGCTCGCATTCGGATGAAGAGCTTGCT-----GGTATG	433
Qy	146	TyrAlaProGLYGLuGLuPheHisAspValGLuAspAlaGLuThrTyrLysLysMetLeu	165
Db	434	TTCTTC-----TTATCTGAGGATGAAACATCTTCTCTGCTCTTT	469
Qy	166	AlaArgAspGLu-----	ArgArgPheArgValAlaAsp 176
Db	470	CGCCGGGAAACCCCATCTGGACAGCAGCGTGGAGTTTATGCAGATTTCGCGCAATATGAC	529
Qy	177	GlnAspGLYAspSerMetalathrArgGLuGLuLeuThrAlaPheLeuHisProGLuGLu	196

us-09-768-840-1.p2n.rni

Tue May 20 14:43:25 2003

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Organon Teknika Corporation
STREET: 1330 Piccard Drive
CITY: Rockville
STATE: Maryland
COUNTRY: U.S.A.
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,057
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93.309078.9
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Gormley, Mary E.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1400 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
ORGANISM: Eimeria maxima
STRAIN: Houghton
DEVELOPMENTAL STAGE: sporozoite
IMMEDIATE SOURCE:
LIBRARY: sporozoite cDNA cloned in Lambda ZAPII
CLONE: Em70-1
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1368
US-08-338-057-1

Alignment Scores:
Pred. No.: 0.000184 Length: 1400
Score: 128.00 Matches: 42
Percent Similarity: 40.12% Conservative: 25
Best Local Similarity: 25.15% Mismatches: 70
Query Match: 7.22% Indels: 30
DB: 1 Gaps: 5

US-09-768-840-1 (1-328) x US-08-464-164-1 (1-1400)
QY 70 GlnLeuThrProGluGluSerGlnAlaArgLeuGlyArgIleValAspArgMetAspArg 89
Db 883 AAATTAACAACAATGAGGAGACACGACGAATTAATAAAATCTCCAGAGATGGATAAG 942
QY 90 AlaGlyAspGly-----AspGlyTyrValSerLeuAlaGlu 101
Db 943 AACGGAGACGCAACTCGATAAACAAGAAATTAATGAGGGTATGTTCAATTAATGAAG 1002
QY 102 LeuArgAlaTyr---IleAlaHisThrGlnGlnArgHisIleArgAspSerValSerAla 120
Db 1003 CTAAGAAGGAGAGATGTTCTCTATTAGACAAGAGTGAATTCAGACAGAGTTGAACAA 1062
QY 121 AlaTyrAspThrTyrAspThrAspArgAspGlyArgValGlyTyrGluGluLeuArgAsn 140
Db 1063 GTTCTTGAGGCTGACACTTCGATAGAATGATTTATTAATATTCAGAAATC----- 1116
QY 141 AlaThrTyrGlyHisTyrAlaProGlyGluGluPheHisAspValGluAspAlaGluThr 160
Db 1117 -----GTGACGGTGGCAATGGAT 1134
QY 161 TyrLysLysMetLeuAlaArgAsp-----GluArgArgPheArgValAlaAspGlnAsp 178
Db 1135 AGAAGAAGCTCTGTATCAACAAGACACTTGAAGAGCAGCATTCAGATGTTGACTCGGAT 1194
QY 179 GlyAspSerMetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPhePro 198
Db 1195 GGATCAGGAAATCTCTCTCTGATATAGTACTATATTTGGTGTAAAGCGAG----- 1248
QY 199 HisMetArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGly 218
Db 1249 --TTAGACTCGGAGGATGGCGTCGGTATTAGCAGAAAGTTCAGAAATATATGACGGA 1305
QY 219 TyrValGlnValGluGluTyr 225
Db 1306 GAAGTTGACTTTGAGGAATTT 1326

RESULT 14
US-08-338-057-1
; Sequence 1, Application US/08338057
; Patent No. 5795741
; GENERAL INFORMATION:
; APPLICANT: Tomley, Fiona M.
; APPLICANT: Dunn, Paul P. J.
; APPLICANT: Bumstead, Janene M.
; APPLICANT: Vermeulen, Arno N.
; TITLE OF INVENTION: Coccidiosis poultry vaccine
; NUMBER OF SEQUENCES: 10

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Db 1117 -----GTGACGGTGGCAATGGAT 1134
 Qy 161 TyrLysLysMetLeuAlaArgAsp-----GluArgArgPheArgValAlaAspGlnAsp 178
 Db 1135 AGAAGAACTCTGTTATCAAGACAAAGACTTGAAGAGAGCATTCGAGATGTTCCGACTCGGAT 1194
 Qy 179 GlyAspSerMetAlaThrArgGluGluThrAlaPheLeuHisProGluGluPhePro 198
 Db 1195 GGATCAGAGAAATCTCTCTCTGAAATAGCTACTATATTGGTGTAAAGCGAG-----1248
 Qy 199 HisMetArgAspIleValIleAlaGluThrLeuGluAspArgAsnLysAspGly 218
 Db 1249 ---TTAGACTCGGAGCATGCGCGGTATTAGCACAAGTTGATCGAATATATGACCGA 1305
 Qy 219 TyrValGlnValGluGluTyr 225
 Db 1306 GAAGTTGACTTTGAGGAATTT 1326

RESULT 15
 US-08-668-416-1
 ; Sequence 1, Application US/08668416
 ; Patent No. 5843722
 ; GENERAL INFORMATION:
 ; APPLICANT: Tomley, Fiona M.
 ; APPLICANT: Dunn, Paul P. J.
 ; APPLICANT: Bumstead, Janene M.
 ; APPLICANT: Vermeulen, Arno N.
 ; TITLE OF INVENTION: Coccidiosis poultry vaccine
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS: 10
 ; ADDRESSEE: Akzo No. 5843722el Patent Department
 ; STREET: 1300 Piccard Drive, Suite 206
 ; CITY: Rockville
 ; STATE: Maryland
 ; COUNTRY: U.S.A.
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/668,416
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/464,164
 ; FILING DATE: June 2, 1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Gormley, Mary E.
 ; REGISTRATION NUMBER: 34,409
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 258-5200
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1400 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to mRNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: C-terminal
 ; ORIGINAL SOURCE:
 ; ORGANISM: Eimeria maxima
 ; STRAIN: Houghton
 ; DEVELOPMENTAL STAGE: sporozoite
 ; IMMEDIATE SOURCE:
 ; LIBRARY: sporozoite cDNA cloned in Lambda ZAPII
 ; CLONE: Em70-1
 ; FEATURE:
 ; NAME/KEY: CDS

US-08-668-416-1
 LOCATION: 1..1368
 Alignment Scores:
 Pred. No.: 0.000184 Length: 1400
 Score: 128.00 Matches: 42
 Percent Similarity: 40.12% Conservative: 25
 Best Local Similarity: 25.15% Mismatches: 70
 Query Match: 7.22% Indels: 30
 DB: 2 Gaps: 5
 US-09-768-840-1 (1-328) x US-08-668-416-1 (1-1400)
 Qy 70 GlnLeuThrProGluGluSerGlnAlaArgLeuGlyArgIleValAspArgMetAspArg 89
 Db 883 AAATTAACAACAATGAGGAGACAGACGAAATTAATAAATCTTCAGAAAGATGGATAG 942
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 Db 943 AACGGAGACGGACAACATCGATAACAAGAATTAATGGAGGTTATGTTGAATTAATGAAG 1002
 Qy 102 LeuArgAlaTrp---IleAlaHisThrGlnGlnArgHisIleArgAspSerValSerAla 120
 Db 1003 CTAAAGAGAGAAGATGTTCTCTATTAGACAAGAGTGCATTTGACACAGAAGTTCAACAA 1062
 Qy 121 AlaTrpAspThrTyrAspThrArgAspGlyArgValGlyTrpGluGluLeuArgAsn 140
 Db 1063 GTTCTTGAGGCTGTAGACTTCGATAAGAATGGATTTATTGAATATTCAGAAATTC-----1116
 Qy 141 AlaThrTyrGlyHisTyrAlaProGlyGluGluPheHisAspValGluAspAlaGluThr 160
 Db 1117 -----GTGACGGTGGCAATGGAT 1134
 Qy 161 TyrLysLysMetLeuAlaArgAsp-----GluArgArgPheArgValAlaAspGlnAsp 178
 Db 1135 AGAAGAACTCTGTTATCAAGACAAAGACTTGAAGAGAGCATTCGAGATGTTCCGACTCGGAT 1194
 Qy 179 GlyAspSerMetAlaThrArgGluGluThrAlaPheLeuHisProGluGluPhePro 198
 Db 1195 GGATCAGAGAAATCTCTCTCTCTGAAATAGCTACTATATTGGTGTAAAGCGAG-----1248
 Qy 199 HisMetArgAspIleValIleAlaGluThrLeuGluAspArgAsnLysAspGly 218
 Db 1249 ---TTAGACTCGGAGCATGCGCGGTATTAGCACAAGTTGATCGAATATATGACCGA 1305
 Qy 219 TyrValGlnValGluGluTyr 225
 Db 1306 GAAGTTGACTTTGAGGAATTT 1326

Search completed: May 19, 2003, 13:50:41
 Job time : 75 secs

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GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 19, 2003, 12:17:01 ; Search time 1715 Seconds
(without alignments)
3097.446 Million cell updates/sec

Title: US-09-768-840-1
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Sequence: 1 MMWRPSVLLLLLLLHGAQG.....FVGSQATNYCEDTRRHDEL 328

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-O=/cgn2_1/USPTO_spool/US09768840/runat_14052003_095557_16057/app_query.fasta_1.519
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
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-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: em_esthum.*
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5: em_estov.*
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7: em_estro.*
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19: em_gss_inv.*
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21: em_gss_vit.*
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23: em_gss_mam.*
24: em_gss_mus.*
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26: em_gss_pro.*
27: em_gss_rtd.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1768	99.8	1092	9	AL544155	AL544155 AL544155
2	1654	93.3	1111	14	BM920379	BM920379 AGENCOURT
3	1479	83.5	1005	9	AL520513	AL520513 AL520513
4	1468	82.8	1001	9	AL550009	AL550009 AL550009
5	1467	82.8	1070	14	BM903507	BM903507 AGENCOURT
6	1418	80.0	824	13	B1820206	B1820206 603037040
7	1409.5	79.5	883	9	AL543374	AL543374 AL543374
8	1350.5	76.2	852	9	AL543274	AL543274 AL543274
9	1328.5	75.0	1103	14	BM918836	BM918836 AGENCOURT
10	1321	74.5	1112	11	AK003918	AK003918 Mus muscu
11	1304.5	73.6	1007	13	B1411932	B1411932 602966319
12	1294	73.0	867	13	B1903868	B1903868 603166092
13	1247.5	70.4	914	14	BO885637	BO885637 AGENCOURT
14	1222.5	69.0	908	14	BQ712731	BQ712731 AGENCOURT
15	1214.5	68.5	1082	13	BM543703	BM543703 AGENCOURT
16	1213	68.5	790	12	BG775172	BG775172 602650360
17	1173	66.2	987	14	BQ897322	BQ897322 AGENCOURT
18	1167	65.9	929	14	BQ943986	BQ943986 AGENCOURT
19	1145	64.6	696	14	BM934252	BM934252 UI-M-CG0P
20	1138	64.2	775	12	BE875623	BE875623 601487063
21	1124	63.4	1009	9	AL570372	AL570372 AL570372
22	1115	62.9	681	13	BM042085	BM042085 603616096
23	1106	62.4	661	14	BM723848	BM723848 UI-E-EO1-
24	1074	60.6	752	14	BM946056	BM946056 UI-M-EMO-
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26	1046.5	59.1	1175	13	BQ265449	BQ265449 AGENCOURT
27	1035.5	58.4	917	12	BE874464	BE874464 601489415
28	1028	58.0	688	13	B1433506	B1433506 603170905
29	1027.5	58.0	1028	10	BE569774	BE569774 60132380
30	992	56.0	578	14	BQ564168	BQ564168 g111h05.y
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35	973.5	54.9	653	12	BF582417	BF582417 602094364
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38	950	53.6	861	10	BE285366	BE285366 601091415
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40	945	53.3	571	13	B1338456	B1338456 302241 MA
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43	922	52.0	572	12	BG088768	BG088768 H3157C12-
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45	912	51.5	900	9	AL569912	AL569912 AL569912

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
AL544155 LTI_NFL006_PL2 Homo sapiens CDNA clone CSODI020YC22 5
prime, mRNA sequence.
ACCESSION
AL544155
VERSION
AL544155.1
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1092)
AUTHORS
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE
Full-length cDNA libraries and normalization

1 MethetirpargProSerValLeuLeuLeuLeuLeuLeuAurHISGLIYALAGLINSly 20
| | | | |
26 ATGATGTGGGCACCATCAGTTCCTGCTCTCTGTTACTAGCACCGGCCCCAGGG 85
| | | | |
21 LysProserProaspAlaGlyProHisGlyGlnGlyArgValHisGlnAlaLaProLeu 40
| | | | |
86 AAGCCATCCCCAGCAGCCGCCCTCATGTGCCAGGGGAGGGTGCAcCAGGCGCCCCTG 145
| | | | |
41 SerAspAlaProHisasaspAlaHisGlyAasnPheGIntTyrrAspHisGluUlaPhoLeu 60
| | | | |
146 AGCGAMGCTCCCCCATGATGAMGCCAACCGGAATTCCASTACGAMCATGAGGCTTCCGT 205
| | | | |


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Db      959 AACAAAGGGGAAATCCCGGGGAACCTTGGGAACATGTTTGGGG 1004

RESULT 6
B1820206
LOCUS   824 bp mRNA linear EST 04-OCT-2001
DEFINITION 603037040F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5178104 5',
mRNA sequence.
ACCESSION B1820206
VERSION   B1820206.1 GI:159311756
KEYWORDS EST.
SOURCE    human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 824)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL NIH-MGC http://mgc.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: craps-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: L1AM11443 row: p column: 09
High quality sequence stop: 801.
Location/Qualifiers
1..824
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/db_xref="taxon:9606"
/clone="IMAGE:5178104"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector:
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source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
BASE COUNT 180 a 227 c 298 g 119 t
ORIGIN

Alignment Scores:
Pred. No.: 5,59e-146 Length: 824
Score: 1418.00 Matches: 270
Percent Similarity: 98.55% Conservative: 1
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Query Match: 80.02% Indels: 2
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US-09-768-840-1 (1-328) x B1820206 (1-824)

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Qy      62 ArgGluValAlaLysGluPheAspGlnLeuThrProGluGluSerGlnAlaArgLeuGly 81
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182 CTTCCGCGGTGATCGCGCACAGCAGCAGCGGCACATACGAGACTCGGTGAGCGCGGCC 241

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Db 242 TGGGACACGTAGCAGACACGCGCGACGGCGGTGTGGGTGGAGGAGCTCGGCACACGCC 301

Qy 142 ThrTyRgLyHisTyRAlaProGlyGluGluPheHisAspValGluAspAlaGluThrTyR 161

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Qy 162 LysLysMetLeuAlaArgAspGluArgPheArgValAlaAspGlnAspGlyAspSer 181

Db 362 AAAAGATGCTGGCTCGGACGAGCGCGTTTCCGGGTGGCGGACGACAGATGGGACTCG 421

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Qy 202 AspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyRValGln 221

Db 482 GACATCGTGATTGCTCAAAACCTCGGAGGACCTGGATAGAAACAAAGATGGCTATGTCCAG 541

Qy 222 ValGluGluTyRtleAlaAspLeuTyRSerAlaGluProGlyGluGluGluProAlaTrp 241

Db 542 GTGGAGGAGTACATCGCGGATCTGTACTCAGCGAGCCTGGGAGGAGGAGCGCGCTGG 601

Qy 242 ValGlnThrGluArgGlnGlnPheArgAspPheArgAspLeuAsnLysAspGlyHisLeu 261

Db 602 GTCAGAGGAGGAGGAGGAGGAGTTCGGGACTTCGGGACTTCGAAAGGATGGGACCTTG 661

Qy 262 AspGlySerGluValGlyHisTrpValLeuProProAlaGlnAspGlnProLeuValGlu 281

Db 662 GATGGAGTGTAGGTGGGCGCACTGGGTGCTGCCCGCTGCCCGAGGAGGAGGAGGAGG 721

Qy 282 AlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSer-LysAlaG 301

Db 722 GCAAG-CACCTGCTGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780

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Db 781 AATCTGGGTACTTGGAAACATGTGAGTGGGCGAGCAAGGATGGCGGTGAGCAAAAGCGGA 780

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AL543374

LOCUS AL543374 LTI_NFL006_PL2 883 bp mRNA linear EST 16-FEB-2001

DEFINITION AL543374 prime, mRNA sequence.

ACCESSION AL543374

VERSION AL543374.1 GI:12875852

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 883)

AUTHORS Li, W.B., Gruber, C., Jesse, J., and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

Location/Qualifiers

1..883

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/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-stranded cDNA was digested with Not I and

cloned into the Not I and Eco RV sites of the pCMVSPORT 6

Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
Toyooka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
and Hayashizaki,Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
11217851
5 (bases 1 to 1112)
Adachi,Y., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C.,
Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T.,
Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hirooka,T., Hori,F.,
Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T.,
Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S.,
Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,
Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J.,
Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
Schimi,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I.,
Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
Hayashizaki,Y.
Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>, Tel:81-45-503-9222,
Fax:81-45-503-9216)
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for
further details.
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues. First strand cDNA was primed with a primer
[5' GAGAGAGAGCGCGCGAATCGAGTCTTTTCTTTTCTT 3'], cDNA was
prepared by using trehalose thermo-activated reverse transcriptase
and subsequently enriched for full-length by cap-trapper. cDNA went
through one round of normalization to Rot = 5.0. Second strand cDNA
was prepared with the primer adapter of sequence [5'
GAGAGAGAGATGTCACAGCTCAATTAATTAATTAACCCCCCCCCC 3']. cDNA was
cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end:
XhoI. Host: SOLR.
FEATURES
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1..1112
Location/Qualifiers
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1094..1099
polyA_signal

VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
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2				
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100				

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Query Match:	74.55%	Gaps:	0
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US-09-768-840-1 (1-328) X AK003918 (1-1112)

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QY	90	AlaGlyAspGlyAspGlyTrpValSerLeuAlaGluLeuArgAlaTrpIleAlaHisThr	109
DB	62	GCTGGGACAGCGCGGTGGTGTCTTAGCTAGCTCCGCGGTGGATCGCGGCACACA	121
QY	110	GlnGlnArgHisIleArgAspSerValSerAlaIleTrpAspThrTyrAspThrAspArg	129
DB	122	CAGCAGCGGCACATCCGTGACTCGGTGTAGCGGACCGCTGGCACACTACGACACGGACCG	181
QY	130	AspGlyArgValGlyTrpGluGluLeuArgAsnAlaThrTyrGlyHisTyrAlaProGly	149
DB	182	GACGCGCGGTGGTGGGAGGATGGCAATGCCACTATGGCCANTATGAGCCCGGA	241
QY	150	GluGluPheHisAspValGluAspAlaGluThrTyrLysLysMetLeuAlaArgAspGlu	169
DB	242	GAGGAGTTTCATGATGGAGGATCCGAGACCTACAAGAAGATGCTGGCTCGGGATGAG	301
QY	170	ArgArgPheArgValAlaAspGlnAspGlyAspSerMetAlaThrArgGluGluLeuThr	189
DB	302	CGCGGATTCGGGTAGCCGACCAAGATGCGACTCCATGGCTACTCGGGAAGAGCTGACG	361
QY	190	AlaPheLeuHisProGluGluPheProHisMetArgAspIleValIleAlaGluThrLeu	209
DB	362	GCCTTTCTGCATCCGAGGAGTTCCTCATCGCGGACATCGTGGTAGCAGAGACCCCTG	421
QY	210	GluAspLeuAspArgAsnLysAspGlyTyrValGlnValGluGluTyrIleAlaAspLeu	229
DB	422	GAGGACCTTGACAAAGACAAAGATGGCTACGTGCAGTGGAAAGATATATCGCGACCTG	481
QY	230	TyrSerAlaGluProGlyGluGluProAlaTrpValGlnThrGluArgGlnPhe	249
DB	482	TACTCCGAGGAGCCTGGGGAGGAGGAACCTCGCTGGGTGCAGACAGCGCGCAGAGTTC	541
QY	250	ArgAspPheArgAspLeuAsnLysAspGlyHisLeuAspGlySerGluValGlyHisTrp	269
DB	542	CGAGAGTTCGCGGATCTGAACAGGACGGCGGACTGGATGGCAGTGAACCTCGTTACTGG	601
QY	270	ValLeuProProAlaGlnAspGlnProLeuValGluAlaAsnHisLeuHisGluSer	289
DB	602	GTGTGTCCTCCATCCCGAGGACCGCCCTGCTGGTGAGGCCAACCCACTGCTGCATGAGAC	661
QY	290	AspThrAspLysAspGlyArgLeuSerLysAlaGluIleLeuGlyAsnTrpAsnMetPhe	309
DB	662	GACACGGACAAGGATGCCCGCTGAGCAAGACTGAGATCTTGAGCAACTGGAAACATGTT	721
QY	310	ValGlySerGlnAlaThrAsnTyrGlyGluAspLeuThrArgHisHisAspGluLeu	328
QY	322	CTCCCTCCACCGCTACCACTACGGTGAGGACCTGACAAAGGACCATGATGAGCTC	778

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RESULT 11
BI411932 linear mRNA 1007 bp EST 14-AUG-2001
LOCUS 602966319F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:512172 5',
DEFINITION mRNA sequence.
ACCESSION BI411932

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BI411932.1 GI:15172855
 EST.
 house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 1007)
 1 NHH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabds-remail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 plate: LLAM11297 row: e column: 05
 High quality sequence start: 21
 High quality sequence stop: 805.

FEATURES
SOURCE

1. .1007

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/organism="Mus musculus"
/strain="Czech II"
/db_xref="taxon:10090"
/clone="IMAGE:5121772"
/clone_lib="NCL_CGAP_Lu33"
/tissue_type="pooled lung tumors"
/lab_host="Dh10B (phage-resistant)"
/notes="Organ: lung; Vector: p7713D-pac (Pharmacia) with a modified polylinker; Site.1: NotI; Site.2: EcoRI; 1st strand cDNA was prepared from mRNA obtained from pooled lung tumors with a Not I - oligo(dT) primer [5', TGTTACCAATCTCAAGTGGGAGCGCGCTGCTGTTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7713 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
235 a 267 C 333 G 172 t

```

BASE COUNT	235 a	267 c	333 g	172 t
------------	-------	-------	-------	-------

ORIGIN

Alignment Scores: *	2 55e-133	Length:	1007
Pred. No.:	1304 50	Matches:	269
Score:	86.85%	Conservative:	15
Percent Similarity:	82.26%	Mismatches:	35
Best Local Similarity:	73.62%	Indels:	12
Query Match:	13	Gaps:	3
Ds:			

75-00-768-840-1 (1-328) x BI411932 (1-1007)

[illegible]

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Db 283 GGGCGGATGATAGACCGCATGATCTTGTGGGACAGCGAGCGGTGGTCTCTTAGCT 342
QY 101 GluLeuArgAlaTrpIleAlaHisThrGlnGlnArgHisIleArgAspSerValSerAla 120
Db 343 GAGCTCCGCGCGTGTATGCGGCACACAGCAGCGGCACATCCGTGACTCGGTGAGCGCA 402
QY 121 AlaTrpAspThrTyArgAspThrArgAspGlyArgValGlyTrpGluGluLeuArgAsn 140
Db 403 GCCTGGCACACCTAGCACAGCGCGGCGCGCGTGGTGGGAGGAGTTGCCCAAT 462
QY 141 AlaThrTyGlyHisTyAlaProGlyGluGluPheHisAspVal-GluAspAlaGluTh 160
Db 463 GCCACCTATGCCATATATGACCCCGGAGAGGAGTTTCATGATGTCGAGGATGCCGAGAC 522
QY 160 rTyLysLysMetLeuAlaArgAspGluArgAspGlyArgValAlaAspGlnAspGlyAs 180
Db 523 CTACAAGAAGATGCTGCTCGGATGAGCGCGGCGGATTCGCGGTAGCCGACCAAGATGGCA 582
QY 180 pSerMetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMe 200
Db 583 CTCATGGCTACTCGGGAAGAGCTGACGGCTTTCTGCTATCCGAGGAGTTCCCTCACAT 642
QY 200 tArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyVa 220
Db 643 CGGGACATCGTGTAGCAGACACCTGGAGGACCTTGACAAAGATGCTAGCT 702
QY 220 lGlnValGluGluTyIleAlaAspLeuTySerAlaGluProGlyGlu-GluGluProA 240
Db 703 GCAGGTGGGAAGATATATCGGAGCTGTACTCCGAGGAGCTCGGAGGAGGAACCTG 762
QY 240 laTrpValGlnThrGluArgGlnPheArgAspPheArgAspLeuAsnLysAspGlyH 260
Db 763 CTGGGTGCAGACAGCGCGCAGCAGTC-CGAGAGTTCCGGGATCTGAACAG-CACGGC 820
QY 260 lAsuAspGlySerGluValGlyHisTrpValLeuProAlaGlnAspGlnProLeuV 280
Db 821 GACTGGATGGCAGTGAAGTCGTTACTGAGTGTGCTGCTCCATCCAGGACACCCCTGG 880
QY 280 aIGluAlaAsnHisLeuHisGluSerAspThrAspLysAsp---GlyArgLeuSerL 299
Db 881 TGGAGGGCAACCACTGTG-ATGAGCG---ACCGAAGGATTCGGGTGACCAAGTC 936
QY 299 yAlaGluLeuLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyGlyG 319
Db 937 AAATGAGCAATCAACTGTGTG-----GCCAG-CAGGCCACAATAGGAAGA 983
QY 319 luAspLeuThrArgHis 324
Db 984 CTGACAGCACAGATAT 1000

RESULT 12
LOCUS BI903868
DEFINITION 603166092F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5254318 5',
mRNA sequence.
ACCESSION BI903868
VERSION BI903868.1 GI:16165963
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 867)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

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Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LUAM1642 row: g column: 23
 High quality sequence start: 27
 High quality sequence stop: 837.
 Location/Qualifiers
 1. 867

FEATURES

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 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:5254318"
 /clone_lib="NCI_CGAP_Lu33"
 /tissue_type="pooled lung tumors"
 /lab_host="DH10B (phage-resistant)"
 /notes="Organ: lung; Vector: pRT3D-Pac (Pharmacia) with a modified Polylinker; Site_1: NotI; Site_2: EcoRI; 1st strand cDNA was prepared from mRNA obtained from pooled lung tumors with a Not I - oligo(dT) primer [5', TGTACCAATCTGAATGGAGCGCGCTCTGTTTCTTTTCTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3D vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
 BASE COUNT 200 a 232 c 292 g 143 t
 ORIGIN

Alignment Scores:

Pred. No.: 2.92e-132 Length: 867
 Score: 1294.00 Matches: 244
 Percent Similarity: 95.06% Conservative: 6
 Best Local Similarity: 92.78% Mismatches: 13
 Query Match: 73.02% Indels: 1
 DB: 13 Gaps: 0

US-09-768-840-1 (1-328) x BI903868 (1-867)

```

QY 66 LysGluPheAspGlnLeuThrProGluLysSerGlnAlaArgLeuGlyArgIleValAsp 85
Db 5 CAAGAATTGACACGTCAGTTCCAGAGGAAGCGCGGACTTGGCGGATCGTAGAG 64
QY 86 ArgMetAspArgAlaGlyAspGlyAspGlyTrpValSerLeuAlaGluLeuArgAlaTrp 105
Db 65 CGCATGATCTTCTGGGGACAGCGCGGTGCTCTAGCTGAGTCCGCGGTG 124
QY 106 IleAlaHisThrGlnGlnArgHisIleArgAspSerValSerAlaAlaTrpAspThrTy 125
Db 125 ATCGGCACACAGCAGCGGCACATCCGTGACTCGGTGAGCGCAGCTTGGCACACCTAC 184
QY 126 AspThrAspArgAspGlyArgValGlyTrpGluGluLeuArgAsnAlaThrTyGlyHis 145
Db 185 GACACGAGCGCGCAGCGCGGTGGTGGAGGAGTTGCGCAATGCCACTATGGCCAT 244
QY 146 TyrAlaProGlyGluGluPheHisAspValGluAspAlaGluThrTyLysMetLeu 165
Db 245 TATGAGCCCGAGAGAGGTTTCATGATGGAGGATCCGAGACCTACAAGAAGATGCTG 304
QY 166 AlaArgAspGluArgPheArgValAlaAspGlnAspGlyAspSerMetAlaThrArg 185
Db 305 GCTCGGATGAGCGCGGATTCGGGTAGCCACCAAGATGGGACTCATGGCTACTCGG 364
QY 186 GluGluLeuThrAlaPheLeuHisProGluPheProHisMetArgAspIleValIle 205
Db 365 GAAGAGCTGACGGCTTTCTGCATCCGAGGAGTTCTCTCATCATGCGGACATCGTGGTA 424
QY 206 AlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyValGlnValGluGluTy 225
Db 425 GCAGAGACCTGGAGGACCTTGACAAGAACAAAGATGGCTAGCTGACAGGTGGAAGATAT 484
QY 226 IleAlaAspLeuTySerAlaGluProGlyGluGluProAlaTrpValGlnThrGlu 245
Db 485 ATCGGGACCTGTACTCCGAGGAGCCTGGGAGGAGGAGAACCTGCTTGGGTGCAGACAGAG 544

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Tue May 20 14:43:26 2003

218 a	337 c	375 q	152 t
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BASE CO
ORIGIN

Alignment Scores:	2.44e-123	Length:	1082
Pred. No.:	1214.50	Matches:	238
Score:	86.83%	Conservative:	6
Percent Similarity:	86.83%	Mismatches:	15
Best Local Similarity:	84.70%	Indels:	22
Query Match:	68.54%	Gaps:	2
DG:	13		

ПС-09-768-840-1 (1-328) х BM543703 (1-1082)

	QY	1	MetMetTrrAtqProSerValLeuLeuLeuLeuLeuLeuArgHisGlyAlaGlnGly	20
	Db	70	ATGATGTGGCGACCATCAGTTCTGCTTCTGTGTCTACTGAGGCACGGGGCCCAAGGG	129
	QY	21	LysProSerProAspAlaGlyProHisGlyGlnGlyArgValHisGlnAlaAlaProLeu	40
	Db	130	AAGCCATCCCAGACGACGCCCTCATGCCAGGGAGGGTGACCAGGCGGCCCCCTG	189
	QY	41	SerAspAlaProHisAspAlaHisGlyAsnPheGlnTyraSPHisGluAlaPheLeu	60
	Db	190	AGCGAGCGTCCTCCATGATGACCCACCGGGRACITCCAGTAGCACCATGAGGCTTTCCTG	249
	QY	61	GlyArgGluValAlaLysGluPheAspGlnLeuThrProGluGluSerGlnAlaArgLeu	80
	Db	250	GGACGGGAAGTGCCCAAGAAATCGACCAACTCACCCAGAGAAAGCCAGGCCCGTCTG	309
	QY	81	GlyArgIleValAspArgMetAspArgAlaGlyAspGlyAspGlyTrpValSerIeuAla	100
	Db	310	GGCGGATCGTGGACCGCATGACCGCGCGGGGACGGCGAGCGGTGCTCGCTGCGCC	369
	QY	101	GluLeuArgAlaTrpIleAlaHisThrGlnGlnArgHisIleArgAspSerValSerAla	120
	Db	370	GAGCTTCGCGGTGGATCGCGCACCGCAGCAGCGGCACATACGGGACTCGGTGAGCGCG	429
	QY	121	AlaTrpaspThrTyraSPThrAspArgAspGlyArgValGlyTrpGluGluLeuArgasn	140
	Db	430	GCCTTGGGACACGTACGACACGGACCGCGCGCGCTGTGGTTGGGAGGAGCTGCGCAAC	489
	QY	141	AlaThrTyrglyHisTyralaProglyGluGluPheHisAspValgluAspAlaGluThr	160
	Db	490	GCACCTATGCCCCACTACGCGCCGGTGAAGAATTCATGACGTGGAGATCAGAGACC	549
	QY	161	TyrIySlysMetLeuAlaArgAspGluArgPheArgValAlaAspGlnAspGlyAsp	180
	Db	550	TACAAAAAGATCTGGTTCGGGACGACGCGCTTCGGGTGGCCACACGATGGGAC	609
	QY	181	SerMetAlaThrArgGluGluLeuThrAlaPheLeuHis-ProgluGluPheProHISMe	200
	Db	610	TCGATGGCCACTCGAGAGAGCTGACAGCTTCTCCACCCCGAGGAGTTCCTCTCACAT	669
	QY	200	targAspileValIleAlaGluThrLeuGluAspLeuAspArgAsnLysasgIyTyra	220
	Db	670	GCGGACATCGATTGCTGAAACCTGGAGGACCTCGACAGAAAACAAGATGGCTATGCT	729
	QY	220	I-GlnValGluGluTyrlle-AlaAspleutyrsSerAlaGluPro---GlyGluGluGlu	238
	Db	730	CCCGGTGGAGAGTACCTCCCGGGATCTGGACCTCGCCGAGCCCGGGGAAGAAGGACC	789
	QY	239	ProAlatrpValGlnThrGluArgGlnGlnPheArgAspPheArgAspLeuAsnLysAsp	258
	Db	790	CCCCCTGGGTGCCCAACAAAAAAGGCC-----	819
	QY	259	GlyHisLeuAspGlySerGluValGlyHisTrpValLeuProProAlaGlnAspGln	277
	Db	820	-----AATTCTGGGACHTCCCGGGCCCGGGGAACAA	852

Search completed: May 19, 2003, 13:49:26
Job time : 1729 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 19, 2003, 12:14:45 ; Search time 294 Seconds
(without alignments)
2512.433 Million cell updates/sec

Title: US-09-768-840-1
Perfect score: 1772
Sequence: 1 MMWRPSVLLLLLRHGAQG.....FVGSQATNYGDELTRHDEL 328

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=N_Geneseq_101002 -Qfmt=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_101002:*

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- 2: /SID22/gcgdata/geneseq/geneseq-embl/NA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1772	100.0	1055	19	AAV57600	Human calcium-bind
2	1772	100.0	1055	22	AAH48279	Human calcium bind
3	1772	100.0	1463	20	AAV27229	Human reticulocalb
4	1772	100.0	1503	20	AAV52253	Protein PRO272 cDN
5	1772	100.0	1503	21	AAV58589	Human PRO272 prote
6	1772	100.0	1503	22	AAV521425	Human cDNA sequenc
7	1772	100.0	1503	22	AAV72411	Human PRO272 cDNA
8	1772	100.0	1503	22	AAV74455	Human angiotensins
9	1772	100.0	1542	21	AAV236246	CDNA encoding a bo
10	1766	99.7	1507	20	AAV00656	Human secreted pro
11	1766	99.7	1507	24	AAV41601	Human colon cancer
12	1766	99.7	1507	24	AAV41603	Human colon cancer
13	1764	99.5	1480	22	AAV63890	Human polynucleoti
14	1764	99.5	1480	22	AAV63890	CDNA encoding nove
15	1764	99.5	1480	22	AAV63890	DNA encoding nove
16	1551.5	87.6	1487	22	ABK43732	Human colon cancer
17	972	54.9	586	20	AAV00710	Human secreted pro
18	956	54.0	2055	24	ABQ55036	Human ovarian anti
19	944	53.3	2104	24	ABK64404	Human benign prost
20	944	53.3	2104	24	ABK64404	Colon adenocarcino
21	944	53.3	2358	22	AAV72801	Human cervical can
22	857.5	48.4	948	24	ABK35607	Gene encoding nove
23	857.5	48.4	948	24	ABK35607	Human cDNA sequenc
24	842.5	47.5	2438	22	AAH15818	Open reading frame
25	842.5	47.5	945	19	AAV29034	Human reticulocalb
26	842.5	47.5	1120	20	AAV27230	Human secreted pro
27	842.5	47.5	2478	20	AAV00690	CDNA encoding colo
28	842.5	47.5	3311	19	ABK46189	Human protein comp
29	839.5	47.4	3166	24	ABK63413	Rat sequence diffe
30	838.5	47.3	4300	22	AAV72827	Human cervical can
31	833.5	47.0	2459	22	AAK94764	Human full-length
32	703.5	39.7	1579	23	ABL01941	Drosophila melanog
33	672	37.9	3697	23	ABL01940	Drosophila melanog
34	613.5	34.6	686	24	ABK44106	CDNA #46 encoding
35	570.5	32.2	760	22	AAV05350	Human cDNA clone (
36	537	30.3	300	20	AAV214539	Human gene express
37	530.5	29.9	644	21	AAV35519	Mouse secreted exp
38	523.5	29.5	595	22	AAV35410	CDNA encoding SRT
39	516.5	29.1	701	23	AAV24771	Human prostate exp
40	489	27.6	352	20	AAV40251	Human secreted pro
41	465	26.2	1365	23	ABL14859	Drosophila melanog
42	456.5	25.8	954	18	AAV73913	E6-binding protein
43	456.5	25.8	1818	24	ABQ54937	Human ovarian anti
44	407.5	23.0	572	20	AAV88942	EST clone IB28. H
45	394.5	22.3	4585	23	ABL28758	Drosophila melanog

ALIGNMENTS

RESULT 1
ID AAV57600

XX AAV57600 standard; cDNA; 1055 BP.

AC AAV57600;

XX 15-DEC-1998 (first entry)

DE Human calcium-binding protein encoding cDNA.

KW Human; calcium-binding protein; reticulocalbin; sickle cell anaemia;
KW HCBP; beta thalassemia; cell proliferation; cancer; adenocarcinoma;
KW leukemia; lymphoma; melanoma; sarcoma; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 34..1020

3

101	QY	GluLeuArgAlaTrpIleAlaHisThrGlnGlnArgHisIleArgAspSerValSerAla	120
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103	QY		
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141	QY	AlaThrTyrGlyHisTyrAlaProGlyGluGluPheHisAspValGluAspAlaGluThr	160
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162	QY		
163	QY		
164	QY		
165	QY		
166	QY		
167	QY		
168	QY		
169	QY		
170	QY		
171	QY		
172	QY		
173	QY		
174	QY		
175	QY		
176	QY		
177	QY		
178	QY		
179	QY		
180	QY		
181	QY	SerMetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMet	200
182	QY		
183	QY		
184	QY		
185	QY		
186	QY		
187	QY		
188	QY		
189	QY		
190	QY		
191	QY		
192	QY		
193	QY		
194	QY		
195	QY		
196	QY		
197	QY		
198	QY		
199	QY		
200	QY		
201	QY	ArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrVal	220
202	QY		
203	QY		
204	QY		
205	QY		
206	QY		
207	QY		
208	QY		
209	QY		
210	QY		
211	QY		
212	QY		
213	QY		
214	QY		
215	QY		
216	QY		
217	QY		
218	QY		
219	QY		
220	QY		
221	QY	GlnValGluGluTyrIleAlaAspLeuTyrSerAla	

XX
CO
sequence 1463 BP. 310 A. 459 C: 478 G: 215 T: 1 other;

RESULT 4

US-09-768-840-1 (1-328) x AAX27229 (1-1463)

XX	25-JUN-1999	(first entry)	
DT	Protein PRO272	cDNA clone DNM40620-1183.	
XX			
DE			
XX			
XX			
KW	Secreted protein;	transmembrane protein; human; enterocolitis;	
KW	Zollinger-Ellison syndrome;	gastrointestinal ulceration;	
KW	congenital microvillus atrophy;	skin disease; cell growth;	
KW	abnormal keratinocyte differentiation;	psoriasis; epithelial cancer;	
KW	Parkinson's disease;	Alzheimer's disease; ALS; neuropathy;	
KW	fibromodulin;	dermal scarring; Usher Syndrome; Atrophila areata;	
KW	anti-thrombotic;	wound healing; tissue repair; ss.	
XX			
OS	Homo sapiens.		
XX			
PN	WO9914328-A2.		
XX			
PD	25-MAR-1999.		
XX			
PF	16-SEP-1998;	98WO-US19330.	
XX			
PR	25-NOV-1997;	97US-0066840.	
PR	17-SEP-1997;	97US-0059113.	
PR	17-SEP-1997;	97US-0059115.	
PR	17-SEP-1997;	97US-0059117.	
PR	17-SEP-1997;	97US-0059119.	
PR	17-SEP-1997;	97US-0059121.	
PR	17-SEP-1997;	97US-0059122.	
PR	17-SEP-1997;	97US-0059184.	
PR	18-SEP-1997;	97US-0059263.	
PR	18-SEP-1997;	97US-0059266.	
PR	15-OCT-1997;	97US-0062125.	
PR	17-OCT-1997;	97US-0062285.	
PR	17-OCT-1997;	97US-0062287.	
PR	21-OCT-1997;	97US-0063486.	
PR	24-OCT-1997;	97US-0062814.	
PR	24-OCT-1997;	97US-0062816.	
PR	24-OCT-1997;	97US-0063045.	
PR	24-OCT-1997;	97US-0063120.	
PR	24-OCT-1997;	97US-0063121.	
PR	24-OCT-1997;	97US-0063127.	
PR	24-OCT-1997;	97US-0063128.	
PR	27-OCT-1997;	97US-0063329.	
PR	27-OCT-1997;	97US-0063327.	
PR	28-OCT-1997;	97US-0063541.	
PR	28-OCT-1997;	97US-0063542.	
PR	28-OCT-1997;	97US-0063544.	

DR P-PSDB; AAB33424.
XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of
XX immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
XX arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
XX claim 23. Fig 21: 309pp: English.

Human PRO272 protein UNQ239 encoding cDNA SEQ ID NO:50.

Human; immune related disease; diagnosis; antiinflammatory; cardiant; dermatological; antiarthritis; antirheumatic; immunosuppressive; haemostatic; antihypertensive; antidiabetic; nootropic; neuroprotective; antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic; antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; synglycolarthropathy; systemic sclerosis; sarcoidosis; idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis; systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; autoimmune thrombocytopenia; immune-mediated renal disease; demyelinating disease; hepatobiliary disease; Whipple's disease; inflammatory bowel disease; gluten-sensitive enteropathy; autoimmune disease; immune-mediated skin disease; allergic disease; immunological disease; transplantation associated disease; graft rejection; graft-versus-host-disease; ss.

XX Homo sapiens.

XX WO2000053758-A2.

XX 14-SEP-2000.

XX 02-MAR-2000; 2000WO-US05841.

XX 08-MAR-1999; 99WO-US050328.

XX 10-MAR-1999; 99US-0123618.

XX 12-MAR-1999; 99US-0123957.

XX 23-MAR-1999; 99US-0125775.

XX 12-APR-1999; 99US-0128849.

XX 20-APR-1999; 99WO-US08615.

XX 28-APR-1999; 99US-0131445.

XX 04-MAY-1999; 99US-0132371.

XX 14-MAY-1999; 99US-0134287.

XX 02-JUN-1999; 99WO-US12252.

XX 23-JUN-1999; 99US-0141037.

XX 20-JUL-1999; 99US-0144758.

XX 26-JUL-1999; 99US-0145698.

XX 28-JUL-1999; 99US-0146222.

XX 01-SEP-1999; 99WO-US20111.

XX 08-SEP-1999; 99WO-US20594.

XX 13-SEP-1999; 99WO-US20944.

XX 15-SEP-1999; 99WO-US21090.

XX 15-SEP-1999; 99WO-US21547.

XX 05-OCT-1999; 99WO-US23089.

XX 29-OCT-1999; 99US-0162506.

XX 29-NOV-1999; 99WO-US28214.

XX 30-NOV-1999; 99WO-US28313.

XX 30-NOV-1999; 99WO-US28409.

XX 01-DEC-1999; 99WO-US28301.

XX 01-DEC-1999; 99WO-US28634.

XX 02-DEC-1999; 99WO-US28551.

XX 02-DEC-1999; 99WO-US28564.

XX 16-DEC-1999; 99WO-US30095.

XX 20-DEC-1999; 99WO-US31274.

XX 30-DEC-1999; 99WO-US00219.

XX 05-JAN-2000; 2000WO-US00219.

XX 06-JAN-2000; 2000WO-US00277.

XX 06-JAN-2000; 2000WO-US00376.

XX 11-FEB-2000; 2000WO-US03565.

XX 18-FEB-2000; 2000WO-US04341.

XX 18-FEB-2000; 2000WO-US04342.

XX 22-FEB-2000; 2000WO-US04414.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;

PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;

PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;

XX WPI: 2000-572271/53.

[illegible]

[illegible]

Db 95 AAGCCATCCCGACGACGAGCGCTCATGGCCAGGGAGGGTGCACACGAGCGGCCCCCTGTG 154
 Qy 41 SerAspAlaProHisAspAspAlaHisGlyAsnPhelIntyAspHisGluAlaPheLeu 60
 Db 155 AGCGACGCTCCCATATGATGACGCCCGACCGGAATTCACAGTAGCAGCATGAGCTTTCCTG 214
 Qy 61 GlyArgGluValAlaLysGluPheAspGlnLeuThrProGluGluSerGlnAlaArgLeu 80
 Db 215 GGACGGGAAGTGGCCAAAGAAATTCGACCAACTCACCACAGAGGAAGCAGCGCGTCTG 274
 Qy 81 GlyArgGluValAspArgMetAspArgAlaGlyAspGlyAspGlyTyrPValSerLeuAla 100
 Db 275 GGCGCGATCGTGACCGCATGACCGCGCGGGGAGCGGCGCTGGGTGTCTGCTGCGC 334
 Qy 101 GluLeuArgAlaTrpIleAlaHisThrGlnGlnArgHisIleArgAspSerValSerAla 120
 Db 335 GAGCTTCGCGCGTGGATCGGCACACGACGACGCGGCACATACGGGCTCGGTGAGCGCG 394
 Qy 121 AlaTrpAspThrTyrAspThrAspArgAspGlyArgValGlyTyrPValGluLeuArgAsn 140
 Db 395 GCGTGGACACGTACGACGCGCGCGCGCGCGGTGTGGGTGGAGGAGCTGCGCAAC 454
 Qy 141 AlaThrTyrGlyHisTyrAlaProGlyGluGluPheHisAspValGluAspAlaGluThr 160
 Db 455 GCGACCTATGGCCACTACGCGCGCGCGGTGAAGAAATTCATGCGTGGAGATGCAGAGACC 514
 Qy 161 TyrLysLysMetLeuAlaArgAspGluArgArgPheArgValAlaAlaAspGlnAspGlyAsp 180
 Db 515 TACAAAAGATGCTGGCTCGGAGCGCGCGGTTCGCGGTGGCCGACGAGGATGGGAC 574
 Qy 181 SerMetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMet 200
 Db 575 TCGATGGCCACTCGAGAGGAGCTCACAGCGCTCTCGACCCCGGAGGATTCCTCATG 634
 Qy 201 ArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrVal 220
 Db 635 CGGACATCGTGTGATGCTGAACCCCTGGAGGAGCTGCACAGAAACAAAGATGCTATGTC 694
 Qy 221 GlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGluProAla 240
 Db 695 CAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGCGCGCTGGGAGGAGCGCGG 754
 Qy 241 TrpValGlnThrGluArgGlnGlnPheArgAspPheArgAspLeuAsnLysAspGlyHis 260
 Db 755 TGGTGCAGACGAGAGGAGCAGCAGTTCGCGGACTTCGCGGATCTGAACAAGATGGGCAC 814
 Qy 261 LeuAspGlySerGluValGlyHisTyrPValLeuProProAlaGlnAspGlnProLeuVal 280
 Db 815 CTGGATGGGAGTCACTGGCGGCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 874
 Qy 281 GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla 300
 Db 875 GAAGCCCAACCACTGTGTGCAGGAGCGGACGAGGATGGCGGCTGAGCAAGAGCG 934
 Qy 301 GluIleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAsp 320
 Db 935 GAAATCTCGGTAAATGGACATGTTTGGGCACTGAGGCGGACCACTATGCGGAGGAC 994
 Qy 321 LeuThrArgHisHisAspGluLeu 328
 Db 995 CTGACCGCGCACCGATGAGCTG 1018
 RESULT 8
 AAC97455
 ID AAC97455 standard; cDNA; 1503 BP.
 XX
 AC AAC97455;
 XX
 DT 28-FEB-2001 (first entry)
 XX
 DE Human angiogenesis-associated protein PRO272 cDNA, SEQ ID NO:112.
 XX
 KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;

KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
 KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
 KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
 KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;
 KW Alzheimer's disease; Huntington's disease; stroke; drug screening;
 KW gene therapy; transgenic animal; ss.
 XX Homo sapiens.
 XX
 PN WO200053753-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 05-JAN-2000; 2000WO-US00219.
 XX
 PR 08-MAR-1999; 99WO-US05028.
 PR 12-MAR-1999; 99US-0123957.
 PR 14-MAY-1999; 99US-0134287.
 PR 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 30-NOV-1999; 99WO-US28313.
 PR 30-NOV-1999; 99WO-US28409.
 PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 XX
 (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;
 PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;
 XX
 DR WPI: 2001-090793/10.
 XX P-PSDB; AAB53085.
 PT
 PS New isolated nucleic acid for producing a PRO polypeptide, analyzing
 XX genetic disorders and treating cardiovascular, endothelial or
 XX angiogenic disorders, such as atherosclerosis, wounds or cancer -
 XX
 CC Claim 58; Fig 43; 293pp; English.
 CC
 CC The invention relates to novel human angiogenesis-associated proteins
 CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding
 CC PRO proteins. The invention also relates to vectors and host cells
 CC comprising a PRO nucleic acid, the recombinant production of a PRO
 CC protein, PRO antibodies specific for a PRO protein, fusion proteins
 CC comprising a PRO protein, agonists or antagonists of a PRO protein, and
 CC compounds which inhibit the expression of a PRO gene. The invention
 CC additionally encompasses methods of identifying modulators of PRO
 CC expression or activity; diagnosing a cardiovascular, endothelial or
 CC angiogenic disorder, or a susceptibility to such a disorder by detecting
 CC mutations in a PRO gene, or the expression level of a PRO gene within a
 CC particular tissue; treating a cardiovascular, endothelial or angiogenic
 CC disorder via the administration of a PRO protein, PRO nucleic acid, or
 CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a
 CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the
 CC administration of a PRO protein, or an agonist or antagonist thereof.
 CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO
 CC agonists and PRO antagonists may be used as therapeutic agents to treat
 CC cardiovascular, endothelial or angiogenic disorders, such as
 CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,
 CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,
 CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's
 CC disease, or stroke. PRO nucleic acids are additionally useful in the
 CC recombinant production of PRO proteins, as hybridisation probes to
 CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,

proliferation of erythroid progenitor cells, and to treat various anemias. They can have colony stimulating factor (CSF) activity and can be used to support the growth and proliferation of myeloid cells such as granulocytes, monocytes or macrophages, to prevent or treat myelo-suppression, to support the growth and proliferation of megakaryocytes and platelets, thereby allowing prevention or treatment of platelet disorders such as thrombocytopenia, to support the growth and proliferation of hematopoietic stem cells, either in place of or in conjunction with platelet transfusions, to treat stem cell disorders, such as aplastic anemia and paroxysmal nocturnal hemoglobinuria, or to repopulate the stem cell compartment after irradiation or chemotherapy. They can be used for growth or differentiation of bone, cartilage, tendon, ligament, or nerve tissue, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers, to induce cartilage and/or bone growth in circumstances where bone is not normally formed and thus have an application in healing bone fractures and cartilage damage or defects, prophylactic use in fracture reduction and also in the improved fixation of artificial joints.

SQ Sequence 1542 BP; 321 A; 506 C; 475 G; 240 T; 0 other;

Alignment Scores:		
Pred. No.:	1.39e-152	
Score:	1772.00	Length:
Percent Similarity:	100.0%	Matches:
Best Local Similarity:	100.0%	Conservative:
Query Match:	100.0%	Mismatches:
DB:	21	Indels:
		Gaps:

US-09-768-840-1 (1-328) x AAZ36246 (1-1542)

[illegible]

Db	414	GCCTGGGACACGTACGACACCGGAGCCGGCGGTGTGGGTGTGGGAGGAGCTGCGCAAC	473
Qy	141	AlaThrTyrGlyHisTyrAlaProGlyGluGluPheHisAspValGluAspAlaGluThr	160
Db	474	GCACCTATGGCCACTACGCGCCGGTGAAGAATTTTCATGACGTGGAGGATCGAGAGACC	533
Qy	161	TyrLysLysMetLeuAlaArgAspGluArgPheArgValAlaAspGlnAspGlyAsp	180
Db	534	TACAAAAGATGCTGGCTCGGGACGAGCGGGTTTCGGGTGGCCGACCAAGATGGCATG	593
Qy	181	SerMetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMet	200
Db	594	TCGATGGCCACTCGAGGAGGAGCTGCACACCTTCTGCACCCCGAGGAGTTCCTCCATG	653
Qy	201	ArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrVal	220
Db	654	CGGGACATCGTGATTCTGAAACCCCTGGAGGACCTGGACAGAAACAAGATGGCTATGTC	713
Qy	221	GlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGluProAla	240
Db	714	CAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGAGGAGGAGCGCG	773
Qy	241	TrpValGlnThrGluArgGlnGlnPheArgAspPheArgAspLeuAsnLysAspGlyHis	260
Db	774	TGGGTGCAGAGCGAGGAGCAGCAGTTCCGGGACTTCCGGGATCTGAACAAGGATGGCGAC	833
Qy	261	LeuAspGlySerGluValGlyHisTrpValLeuProAlaGlnAspGlnProLeuVal	280
Db	834	CTGGATGGGAGTGAGGTGGGCCACTGGGTGCTGCCCTGCCAGGACCAGCCCTGGTG	893
Qy	281	GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla	300
Db	894	GAAGCCACCACTGCTGTCACGACGACGACGACGACGACGACGACGACGACGACGACG	953
Qy	301	GluIleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyLysAsp	320
Db	954	SAATTCCTGGGTAATTGGAACATGTTTGGGCGTCTAGCCACCACTATGTYGAGGAC	1013
Qy	321	LeuThrArgHisHisAspGluLeu	328
Db	1014	CTGACCGCGCACCGATGAGCTG	1037
RESULT 11			
AAL41601			
ID AAL41601 standard; cDNA; 1507 BP.			
XX AAL41601;			
XX 19-APR-2002 (first entry)			
XX Human colon cancer related coding sequence SEQ ID NO: 12.			
XX Human; colon cancer; cytostatic; drug design; adenomatous polyp;			
XX colorectal carcinoma; high metastatic potential colon tumour;			
XX metastatic colon cancer; gene; ss.			
XX Homo sapiens.			
XX WO2001196523-A2.			
XX 20-DEC-2001.			
XX 15-JUN-2001; 2001WO-US19313.			
XX 15-JUN-2000; 2000US-211835P.			
XX (CHIR) CHIRON CORP.			
XX Kennedy GC, Kang S, Reinhard C, Jefferson AB;			
XX WPI; 2002-164362/21.			
XX Detecting a cancerous colon cell, useful for diagnosing colon cancer			

[illegible]

Tue May 20 14:43:25 2003

us-09-768-840-1.p2n.rng

```

QY      61 GlyArgGluValAlaIysGluPheAspGlnLeuThrProGluGluSerGlnAlaArgLeu 80
DB      227 GGACGGGAAGTGGCCCAAGAAATTCGACCAACTTCACCCAGAGGAAGCCAGGCCGCTGTG 286
QY      81 GlyArgIleValAspArgMetAspArgAlaGlyAspGlyAspGlyTrpValSerLeuAla 100
DB      287 GGGCGGATCGTGACCGCATGACCGCGCGGGGAGCGGCGACGGCTGTGCTGCTGCC 346
QY     101 GluLeuArgAlaTrpIleAlaHisThrGlnGlnArgHisIleAraAspSerValSerAla 120
DB      347 GAGCTTCGCGCTGGATCGCGACACGCGACGCGGACATACGGGACCTCGGTGAGCGCG 406
QY     121 AlaTrpAspThrTrpAspThrAspArgAspGlyArgValGlyTrpGluGluLeuArgAsn 140
DB      407 GCCTGGGACACGTACGACACGCGCGCGCGCGGCTGGGTGGGAGGAGCTGGCGCAAC 466
QY     141 AlaThrTrpGlyHisThrAlaProGlyGluGluPheHisAspValGluAspAlaGluThr 160
DB      467 GCCACCTATGCCCACTACGCGCGCGGTGAAGAATTTTCATGACGTGGAGGATGCAGACCC 526
QY     161 TyrLysLysMetLeuAlaArgAspGluArgPheArgValAlaAlaAspGlnAspGlyAsp 180
DB      527 TACAAAAGATGCTGGCTCGGGACGACGCGCTTCGCGGTGCGCGACCAAGGATGGGAC 586
QY     181 SerMetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPheProHisMet 200
DB      587 TCGATGGCCACTCGAGAGGAGCTGACAGCCTTCCTGCACCCCGAGGAGTTCCTCTCACATG 646
QY     201 ArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAspGlyTyrVal 220
DB      647 CGGGACATCGTGATTCGTGAACCTTGAGGACCTGGAGGACCTGGACAGAACAAAGATGCTATGTC 706
QY     221 GlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGluGluProAla 240
DB      707 CAGGTGGAGGAGTACATCGCGATCTGTACTCAGCGAGCCTGGGGAGGAGGAGCGCGG 766
QY     241 TrpValGlnThrGluArgGlnPheArgAspPheArgAspLeuAsnLysAspGlyHis 260
DB      767 TGGGTGCGACGAGGAGGAGGAGGAGTTCGGGACCTTCGGGATCTGACACAGGATGGGCAC 826
QY     261 LeuAspGlySerGluValGlyHisTrpValLeuProProAlaGlnAspGlnProLeuVal 280
DB      827 CTGGACGGGAGTGGTGGGCCACTGGTGTGCTGCCCTGCCAGGACCAAGCCCTGGTG 886
QY     281 GluAlaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla 300
DB      887 GAAGCCACCACTGCTGCACGAGAGCGACACGGACACAGGAGGCGCGCTGAGCAAGCG 946
QY     301 GluIleLeuGlyAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAsp 320
DB      947 GAATCTGGGTAAATGGAAACATGTTGTGGGCACTGAGGCCACCACTATGTTGGAGGAC 1006
QY     321 LeuThrArgHisHisAspGluLeu 328
DB      1007 CTCACCGGCAACCACTGAGCTG 1030

RESULT 14
AAS31631
ID      AAS31631 standard; cDNA; 1480 BP.
XX
AC      AAS31631;
XX
DT      04-DEC-2001 (first entry)
DE      cDNA encoding novel human calcium-binding protein #55.
XX
KW      Human; calcium-binding protein; calcium flux; neurological disease;
KW      immune dysfunction; digestive disease; neoplastic disease;
KW      blood disorder; infectious disease; gene therapy; immunosuppressive;
KW      antiarthritic; cytostatic; vasotropic; antibacterial; nootropic;
KW      virucide; ss.
XX
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PR	27-SEP-2000;	2000US-02358334
PR	27-SEP-2000;	2000US-02358336
PR	29-SEP-2000;	2000US-02363227
PR	29-SEP-2000;	2000US-02363667
PR	29-SEP-2000;	2000US-02363668
PR	29-SEP-2000;	2000US-02363669
PR	29-SEP-2000;	2000US-02363670
PR	02-OCT-2000;	2000US-02368002
PR	02-OCT-2000;	2000US-02370737
PR	02-OCT-2000;	2000US-02370738
PR	02-OCT-2000;	2000US-02370739
PR	13-OCT-2000;	2000US-02370440
PR	13-OCT-2000;	2000US-02399935
PR	20-OCT-2000;	2000US-02399937
PR	20-OCT-2000;	2000US-02409602
PR	20-OCT-2000;	2000US-02411221
PR	20-OCT-2000;	2000US-02411785
PR	20-OCT-2000;	2000US-0241786
PR	20-OCT-2000;	2000US-0241787
PR	20-OCT-2000;	2000US-0241808
PR	01-NOV-2000;	2000US-0241809
PR	01-NOV-2000;	2000US-0241826
PR	08-NOV-2000;	2000US-0244617
PR	08-NOV-2000;	2000US-0246474
PR	08-NOV-2000;	2000US-0246475
PR	08-NOV-2000;	2000US-0246476
PR	08-NOV-2000;	2000US-0246477
PR	08-NOV-2000;	2000US-0246478
PR	08-NOV-2000;	2000US-0246523
PR	08-NOV-2000;	2000US-0246524
PR	08-NOV-2000;	2000US-0246526
PR	08-NOV-2000;	2000US-0246527
PR	08-NOV-2000;	2000US-0246528
PR	08-NOV-2000;	2000US-0246532
PR	08-NOV-2000;	2000US-0246609
PR	08-NOV-2000;	2000US-0246610
PR	08-NOV-2000;	2000US-0246611
PR	17-NOV-2000;	2000US-0246613
PR	17-NOV-2000;	2000US-0249207
PR	17-NOV-2000;	2000US-0249208
PR	17-NOV-2000;	2000US-0249209
PR	17-NOV-2000;	2000US-0249210
PR	17-NOV-2000;	2000US-0249211
PR	17-NOV-2000;	2000US-0249212
PR	17-NOV-2000;	2000US-0249213
PR	17-NOV-2000;	2000US-0249214
PR	17-NOV-2000;	2000US-0249215
PR	17-NOV-2000;	2000US-0249216
PR	17-NOV-2000;	2000US-0249217
PR	17-NOV-2000;	2000US-0249218
PR	17-NOV-2000;	2000US-0249224
PR	17-NOV-2000;	2000US-0249245
PR	17-NOV-2000;	2000US-0249246
PR	17-NOV-2000;	2000US-0249247
PR	17-NOV-2000;	2000US-0249259
PR	17-NOV-2000;	2000US-0249259
PR	01-DEC-2000;	2000US-0249300
PR	01-DEC-2000;	2000US-02501160
PR	03-DEC-2000;	2000US-0250130
PR	03-DEC-2000;	2000US-0250130
PR	05-DEC-2000;	2000US-0251988
PR	05-DEC-2000;	2000US-0256719
PR	06-DEC-2000;	2000US-0251479
PR	08-DEC-2000;	2000US-0251856
PR	08-DEC-2000;	2000US-0251868
PR	08-DEC-2000;	2000US-0251989
PR	08-DEC-2000;	2000US-0251989
PR	11-DEC-2000;	2000US-0251990
PR	05-JAN-2001;	2001US-0254967
XX		
PA	(HUMA-)	HUMAN GENOME SCI INC.

[illegible]

Rosen CA, Barash SC, Ruben SM;
WPI; 2001-465568/50.
P-PSDB; AAU19946.

Isolated nucleic acid molecule encoding a calcium-binding protein is used in preventing, treating or ameliorating a medical condition.

Claim 4; SEQ ID No 65; 542pp; English.

Claim 4; SEQ ID No 65; 542pp; English.

The present invention relates to the isolation of novel human calcium-binding proteins (AAU19892-AAU19969), and cDNA and genomic sequences encoding for these proteins. The sequences of the invention are useful in the diagnosis, prevention and/or prognosis of diseases associated with aberrant calcium flux. Such disorders include neurological diseases (e.g. ankytrophic lateral sclerosis, ALS), immune dysfunction (e.g. severe combined immunodeficiency, SCID), digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The novel calcium-binding proteins are also useful as screening tools to identify antagonists and/or agonists that may enhance or inhibit activities mediated by calcium-binding proteins. The polynucleotides of the invention are also useful in gene therapy. AAS31577-AAS31634 represent cDNA sequences encoding for the novel human calcium-binding proteins.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 1480 BP; 329 A; 458 C; 479 G; 214 T; 0 other;

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US-09-768-840-1 (1-328) x AAS31631 (1-1480)

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us-09-768-840-1.1.p2n.rng

Tue May 20 14:43:25 2003

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ID ABK43732
XX ABK43732 standard; cDNA: 1480 BP.
AC ABK43732;
XX
DT 05-JUN-2002 (first entry)
XX
DE DNA encoding novel central nervous system protein #312.
KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
KW adenocarcinoma; reproductive system disorder; testicular feminisation;
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
KW respiratory disorder; renal disorder; kidney failure; blood disorder;
KW myocardial infarction; wound healing; cell proliferation; skin aging;
KW food additive; food preservative; gene therapy; gene; ss.
OS Homo sapiens.
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XX WO200155318-A2.
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PR

Tue May 20 14:43:25 2003

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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

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Run on: May 19, 2003, 12:16:11 ; Search time 3395 Seconds
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Title: US-09-768-840-1

Perfect score: 1772

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Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	1772	100.0	1463	6	AR152960 Sequence
5	1772	100.0	1470	9	BC011346 Sequence
6	1772	100.0	1503	6	AX464230 Sequence
7	1766	99.7	1507	6	AX354366 Sequence
8	1766	99.7	1507	6	AX354369 Sequence
9	1759	99.3	1454	9	AF183423 Homo sapi
10	1645	92.8	1421	10	BC025602 Mus muscu
11	1596	90.1	1414	10	BC005487 Mus muscu
12	944	53.3	1454	9	BC010120 Homo sapi
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us-09-768-840-1.p2n.rge

Tue May 20 14:43:25 2003

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ORGANISM			
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BANDMAN, O., Hillman, J. L., Lal, P., Corley, N. C. and Shah, P.			
AUTHORS			
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Patent: US 5976801-A 2 02-NOV-1999;			
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[illegible]

[illegible]

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AUTHORS	Strausberg, R.		
TITLE	Direct Submission		
JOURNAL	Submitted (06-MAR-2002) National Institutes of Health, Mammalian		
	Gene Collection (MGC), Cancer Genomics Office, National Cancer		
	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,		
	USA		
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov		
COMMENT	Contact: MGC help desk		
	Email: cgapbs-remail.nih.gov		
	Tissue Procurement: Lohar Hennighausen Ph.D., Robin Humphreys		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
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	Sequencing Center (NISC),		
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	Web site: http://www.nisc.nih.gov/		
	Contact: nisc_mgc@nih.gov		
	Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,		
	Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,		
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	Maduro, Q. L., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,		
	McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,		
	Tsurgou, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,		
	Young, A., Zhang, L.-H. and Green, E.D.		

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK plate: 56 Row: B Column: 12
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, genomeScan gene prediction, Similarity but not identity to protein.

FEATURES

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Gaps:	0

US-09-768-840-1 (1-328) x BC025602 (1-1421)

[illegible]

QY	281	GlulaAsnHisLeuLeuHisGluSerAspThrAspLysAspGlyArgLeuSerLysAla	300
Db	916	GAGGCCAACCACTGCTGTCATGAGAGCGACACGGACNAGCATGGCGGCTGAGCAAGCT	975
QY	301	GluiLeuGluLysAsnTrpAsnMetPheValGlySerGlnAlaThrAsnTyrGlyGluAsp	320
Db	976	GAGATCTTGAGCACTGGGAACATGTTTGGGCACGCCACGGCACCACCACTACGCTGAGGAC	1035
QY	321	LeuThrArgHisHisAspGluLeu	328
Db	1036	CTGACAAGGCACCATGATGAGCTC	1059
RESULT 11	BC005487	1414 bp mRNA linear	ROD 07-AUG-2002
LOCUS	BC005487	IMAGE:3486146, mRNA, partial cds.	
DEFINITION	BC005487	Mus musculus, Similar to hypothetical protein LOC57333, clone	
ACCESSION	BC005487		
VERSION	BC005487.1	GI:13529538	
KEYWORDS			
SOURCE		house mouse.	
ORGANISM		Mus musculus	
REFERENCE		Eukaryota: Metazoa; Chordata; Cranial; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;	
TITLE		1 (bases 1 to 1414)	
JOURNAL		Strausberg, R.	
		Direct Submission	
		Submitted (27-MAR-2001) National Institutes of Health, Mammalian	
		Gene Collection (MGC), Cancer Genomics Office, National Cancer	
		Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,	
		USA	
REMARK		NIH-MGC Project URL: http://mgc.nci.nih.gov	
COMMENT		Contact: MGC help desk	
		Email: cgapbs-r@mail.nih.gov	
		Tissue Procurement: Lotzhar Hennighausen Ph.D., Robin Humphreys	
		CDNA Library Preparation: Life Technologies, Inc.	
		CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	
		Center, Stanford University School of Medicine, Stanford, CA 94305	
		Web site: http://www-shgc.stanford.edu	
		Contact: (Dickson, Mark) mcd@paxil.stanford.edu	
		Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,	
		R. M.	

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 7 Row: h Column: 5
 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

FEATURES source

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/map="C57BL/6J"
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old, gross tissue."
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CDS

BASE COUNT

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Db 901 GCCACCTACGCTGAGGACCTGACAAGCACCACCATGATGAGCTC 945
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RESULT 12
BC010120 1454 bp mRNA linear PRI 12-JUL-2001

LOCUS
DEFINITION
Homo sapiens, reticulocalbin 1, EF-hand calcium binding domain,
clone MGC:19541 IMAGE:3836263, mRNA, complete cds.

ACCESSION
BC010120
VERSION
BC010120.1 GI:14603329

KEYWORDS
MGC.

SOURCE
Homo sapiens.

ORGANISM
Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 1454)
Strausberg, R.
Direct Submission
Submitted (02-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: DCTD/DTp
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/nisc_mgc@nhgri.nih.gov
Contact: Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
Dietrich, N.D., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
Lim, M., Maduro, O.L., Mastello, C., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Snyder, B., Stantipop, S., Thomas, P.J.,
Tlonsong, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 27 Row: 1 Column: 8
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 5419788.

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BASE COUNT
ORIGIN
Alignment Scores: 8.93e-56 Length: 1454
Pred. No.: 1

ORIGIN
Alignment Scores: 1414
Pred. No.: 293
Score: 1596.00
Percent Similarity: 95.87%
Best Local Similarity: 93.02%
Query Match: 90.07%
DB: 10

US-09-768-840-1 (1-328) x BC005487 (1-1414)

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QY 34 ValHisGlnAlaAlaProLeuSerAspAlaProHisAspAlaHisGlyAsnPhcGln 53
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Db 61 GTCCATCATGGAACCCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
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QY 54 TyrAspHisGluAlaPheLeuGlyArgGluValAlaLysGluPheAspGlnLeuThrPro 73
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Db 121 TAGGACCATGAGCGCTTCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
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QY 74 GluGluSerGlnAlaArgLeuGlyArgLeuValAspArgMetAspArgAlaGlyAspGly 93
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Db 181 GAGGAAAGCCAGGCGGCTGGGCGGATCGTAGCCGATGATGATGATGATGATGATGAT 240
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QY 94 AspGlyTrpValSerLeuAlaGluLeuArgAlaTrpIleAlaHisThrGlnGlnArgHis 113
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QY 114 IleArgAspSerValSerAlaAlaTrpAspThrThrAspThrAspArgAspGlyArgVal 133
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QY 134 GlyTrpGluGluLeuArgAsnAlaThrTyrGlyHisTyrAlaProGlyGluGluPheHis 153
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Db 361 GGTGGGAGGAGTGGCAATGTCACCTATGCGCATATGATGCGCGGAGGAGGTTCAT 420
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QY 154 AspValGluAspAlaGluThrTyrLysMetLeuAlaArgAspGluArgPheArg 173
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QY 214 ArgAsnLysAspGlyTyrValGlnValGluGluTyrIleAlaAspLeuTyrSerAlaGlu 233
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QY 234 ProGlyGluGluGluProAlaTrpValGlnThrGluArgGlnGlnPheArgAspPheArg 253
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QY 314 AlaThrAsnTyrGlyGluAspLeuThrArgHisHisAspGluLeu 328
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QY 178 AspGlyAspSerMetAlaThrArgGluGluLeuThrAlaPheLeuHisProGluGluPhe 197
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QY 198 ProHisMetArgAspIleValIleAlaGluThrLeuGluAspLeuAspArgAsnLysAsp 217
Db 653 GAACATATGAGGAATGTTGGTTTGGAAACCTCGAGGACATCGACAAAGACGGGAT 712
QY 218 GlyTyrValGlnValGluGluTyrIleAlaAspLeuTyrSerAlaGluProGlyGluGlu 237
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QY 238 GluProAlaThrValGlnThrGluArgGlnPheArgAspPheArgAspLeuAsnLys 257
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Db 833 GACGGAAGTTAGACAAAGATGAGATTCGCCACTGGATCTCCTCAAGATTATGATCAC 892
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RESULT 14
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LOCUS Human mRNA for reticulocalbin, complete cds.
DEFINITION D42073
ACCESSION D42073
VERSION D42073.1 GI:1262328
KEYWORDS rcn; calcium binding protein; ER-hand protein; ER-resident protein;
reticulocalbin.
SOURCE Homo sapiens transitional carcinoma cell cell_line:BOY cDNA to
mRNA, clone:hr12 and hr19.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2104)
AUTHORS Ozawa,M.
TITLE Cloning of a human homologue of mouse reticulocalbin reveals
conservation of structural domains in the novel endoplasmic
reticulum resident Ca(2+)-binding protein with multiple EF-hand
motifs
J. Biochem. 117 (5), 1113-1119 (1995)
JOURNAL 96172582
MEDLINE 2 (bases 1 to 2104)
REFERENCE Ozawa,M.
AUTHORS Direct Submission
TITLE Submitted (10-NOV-1994) Masayuki Ozawa, Faculty of Medicine,
Kagoshima University, Department of Biochemistry; 8-35-1
Sakuragaoka, Kagoshima, Kagoshima 890, Japan (Tel:0992-75-5246,
Fax:0992-64-5618)
COMMENT On Apr 12, 1996 this sequence version replaced gi:575579.
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US-09-768-840-1 (1-328) x HUMRCN (1-2104)
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Db 98 CTGCTGCTGGCGTGGTGGTGGCGCCCGGTTCTGGCGCCCAAGCCCGGTCGCAAA 157
QY 24 -----ProAspAlaGlyProHisGlyGlnGlyArgValHisGlnAlaAla 38
Db 158 GAGCGCGTGGTGGCGCCGAC-----TCG 181
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QY 59 PheLeuGlyArgGluValAlaLysGluPheAspGlnLeuThrProGluGluSerGlnAla 78
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Db 413 GCCAAGTCTGGAAGGATTATGATAGGACAAAGATGATAAAATTCCTGGGAAGAATAC 472
QY 139 ArgAsnAlaThrTyrGlyHisTyrAlaProGly---GluGluPheHisAspValGluAsp 157
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 QY 238 GluProAlaTTPValGlnGluArgGlnPheArgAspPheArgAspLeuAsnLys 257
 Db 773 GAGCAGACTGGGTTTATACAGCGGAGCAGTTTAACGAATTCGCGGATCTGAACAAG 832
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 QY 318 GlyCluAspLeuThrArgHisHisAspGluLeu 328
 Db 1013 GGGGAGATCTCAAAAAATCATGAGCTT 1045

RESULT 15
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 ACCESSION D13003
 VERSION D13003.1
 KEYWORDS ER-resident protein; calcium-binding protein; endoplasmic reticulum protein; multiple EF hand motifs; reticulocalbin.
 SOURCE Mus musculus (strain:129/Sv) teratocarcinoma cell_line:OTT6050 cDNA to mRNA, clone:OI and M10.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Ozaawa.M. and Muramatsu.T.
 Reticulocalbin, a novel endoplasmic reticulum resident Ca(2+)-binding protein with multiple EF-hand motifs and a carboxyl-terminal HDEL sequence
 J. Biol. Chem. 268 (1), 699-705 (1993)
 93107083
 2 (bases 1 to 1998)
 Ozaawa.M.
 Direct Submission
 Submitted (23-AUG-1992) Masayuki Ozaawa, Faculty of Medicine, Kagoshima University, Department of Biochemistry; 8-35-1 Sakuragaoka, Kagoshima, Kagoshima 890, Japan (Tel:0992-75-5246, Fax:0992-64-5618)
 Location/Qualifiers
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 Query Match: 53.02% Indels: 16
 DB: 10 Gaps: 4

US-09-768-840-1 (1-328) x MUSRCAL (1-1998)

QY 16 HisGlyValaGlnGlyLysProSerProAspAlaGlyProHisGlyGlnGlyArg-ValH1 35
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 Db 253 GAGCAAGGAGAGGCTGGGAAATTTGGATCGAATTGAC-----AGTCATGGTGTGG 306
 QY 95 YTrpValSerLeuAlaGluLeuArgAlaTTPileAlaHisThrGlnGlnArgHisLea1 115
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us-09-768-840-1.p2n.rge

Tue May 20 14:43:25 2003

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Db 967 TACCAACTACGGGAAGACCTGACCAAAATCATGATGAACCTT 1009

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Job time : 3424 secs

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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 14, 2003, 10:40:07 ; Search time 103.883 Seconds
(without alignments)
650.575 Million cell updates/sec

Title: US-09-768-840-1
Perfect score: 1772
Sequence: 1 MMWRPSVLLLLLRHGAQG.....FVGSQATNYCEDLTRHDEL 328

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: sp_archaea:*
- 3: sp_bacteria:*
- 4: sp_fungi:*
- 5: sp_human:*
- 6: sp_invertebrate:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	1772	100.0	328	4 Q96D15	Q96d15 homo sapien
2	1759	99.3	328	4 Q9HB28	Q9hb28 homo sapien
3	1645	92.8	328	11 Q8R137	Q8r137 mus musculus
4	1596	90.1	315	11 Q99K35	Q99k35 mus musculus
5	1321	74.5	259	11 Q9CTD4	Q9ctd4 mus musculus
6	911	51.4	322	13 Q93434	Q93434 fugu rubrip
7	857.5	48.4	315	4 Q96RL3	Q96rl3 homo sapien
8	852	48.1	296	4 Q9NR43	Q9nr43 homo sapien
9	839.5	47.4	315	11 Q35783	Q35783 rattus norv
10	818	46.2	296	6 Q9MZ46	Q9mz46 sus scrofa
11	703.5	39.7	329	5 Q9SZK6	Q9szk6 drosophila
12	685	38.7	322	5 Q93136	Q93136 bombyx mori
13	639.5	36.1	314	5 Q23017	Q23017 caenorhabdi
14	481	27.1	98	11 Q63399	Q63399 rattus norv
15	457	25.8	342	5 Q9VMV2	Q9vmv2 drosophila
16	448.5	25.3	192	5 Q9W0H8	Q9w0h8 drosophila

17	444.5	25.1	321	11 Q70341	Q70341 mus musculu
18	442	24.9	193	5 Q96051	Q96051 drosophila
19	357	20.1	313	5 Q9TYS8	Q9tys8 caenorhabdi
20	230.5	13.0	259	4 Q96AA1	Q96aa1 homo sapien
21	224	12.6	348	4 Q9NZP7	Q9nzp7 homo sapien
22	214.5	12.1	345	10 Q9STP7	Q9stp7 arabidopsis
23	196.5	11.1	391	10 Q9FNN0	Q9fnn0 arabidopsis
24	195	11.0	343	5 Q9U460	Q9u460 plasmodium
25	188	10.6	343	5 Q25793	Q25793 plasmodium
26	175	9.9	320	5 Q18887	Q18887 caenorhabdi
27	145	8.2	571	10 Q48827	Q48827 caenorhabdi
28	140	7.9	194	16 Q8XUT1	Q8xut1 ralsstonia s
29	140	7.9	523	10 Q9FKW4	Q9fkW4 arabidopsis
30	137	7.7	487	5 Q24929	Q24929 elmeria ten
31	135.5	7.6	418	5 Q95T97	Q95t97 drosophila
32	133.5	7.5	564	10 Q9ZTU9	Q9ztu9 solanum tub
33	133	7.5	572	10 Q8W560	Q8w560 nicotiana t
34	132	7.4	529	10 Q48565	Q48565 fragaria an
35	131	7.4	541	10 Q38868	Q38868 arabidopsis
36	130	7.3	521	10 Q9C6P3	Q9c6p3 arabidopsis
37	130	7.3	2439	5 Q9VSM2	Q9vsm2 drosophila
38	129.5	7.3	261	5 Q9VDY9	Q9vdy9 drosophila
39	129.5	7.3	387	5 Q8SYN0	Q8syn0 drosophila
40	129.5	7.3	426	5 Q9NF73	Q9nf73 drosophila
41	129.5	7.3	534	10 Q9ZPM0	Q9zpm0 mesembryant
42	128	7.2	185	10 Q8R2B5	Q8r2b5 oryza sativ
43	128	7.2	414	5 Q24892	Q24892 elmeria max
44	127.5	7.2	271	4 Q96BK4	Q96bk4 homo sapien
45	125.5	7.1	271	11 Q8VHC5	Q8vhc5 mus musculu

ALIGNMENTS

RESULT 1

Q96D15 PRELIMINARY; PRT; 328 AA.
AC Q96D15
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical 37.5 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Strausberg R.;
EL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013436; AAH13436.1; -;
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000886; EF-hand.
DR Pfam; PF00036; ehand; 5
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
DR PROSITE; PS00014; EF_TARGET; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 328 AA; 37493 MW; B64EDB28B9610B8D CRC64;

Query Match 100.0%; Score 1772; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.4e-124;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWRPSVLLLLLRHGAQKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60
DB 1 MMWRPSVLLLLLRHGAQKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60
QY 61 GREVAKEFDQLPEESQARLGRIVDRMDRAGDGDGVSLAEALRAVIAHTQORHIRDSVSA 120
DB 61 GREVAKEFDQLPEESQARLGRIVDRMDRAGDGDGVSLAEALRAVIAHTQORHIRDSVSA 120
QY 121 AWDYTDTRDGRGVGWEELRNATYGHYAPCEEPHDVEDAETVKKMLARDERFRVADQGD 180

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|||||
Db 121 AWTYTDTRDGRGVGWEELRNATYGHVAPGEEFHDVEDAETKKMLARDERRFRVADQDGD 180
Qy 181 SMATREELTAFLHPEEPFPHMRDIVIAETLEDLDRNKDGVQVVEEYIADLYSAEPGEEPA 240
Db 181 SMATREELTAFLHPEEPFPHMRDIVIAETLEDLDRNKDGVQVVEEYIADLYSAEPGEEPA 240
Qy 241 WVQTERQOQFRDRLNKGDLGSEVGHVWVLPQAQDQPLVEANHLHESDTDKDGRLSKA 300
Db 241 WVQTERQOQFRDRLNKGDLGSEVGHVWVLPQAQDQPLVEANHLHESDTDKDGRLSKA 300
Qy 301 EILGNWNNFVGSQATNYGEDLTRHDEL 328
Db 301 EILGNWNNFVGSQATNYGEDLTRHDEL 328

RESULT 2
Q9HBZ8 PRELIMINARY; PRT; 328 AA.
AC Q9HBZ8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Reticulocabin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HYPOPHALAMUS;
RA Peng Y., Gu Y., Huang C., Xu S., Han Z., Fu G., Chen Z.;
RT "A novel gene expressed in human hypothalamus.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF183423; AAG09692.1;
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000886; EF-target.
DR Pfam; PF00036; ehand; 4.
DR SMART; SM00054; EFh; 3.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
DR PROSITE; PS00014; EF_TARGET; UNKNOWN_1.
SQ SEQUENCE 328 AA; 37424 MW; 9D23648795D3C670 CRC64;

Query Match 99.3%; Score 1759; DB 4; Length 328;
Best Local Similarity 99.4%; Pred. No. 1.3e-123;
Matches 326; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MMWRPSVLLLLLLRHGAQKPSDPAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60
Db 1 MMWRPSVLLLLLLRHGAQKPSDPAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60
Qy 61 GREVAKEFDLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWIAHTQQRHIDSYSVA 120
Db 61 GREVAKEFDLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWIAHTQQRHIDSYSVA 120
Qy 121 AWTYTDTRDGRGVGWEELRNATYGHVAPGEEFHDVEDAETKKMLARDERRFRVADQDGD 180
Db 121 AWTYTDTRDGRGVGWEELRNATYGHVAPGEEFHDVEDAETKKMLARDERRFRVADQDGD 180
Qy 181 SMATREELTAFLHPEEPFPHMRDIVIAETLEDLDRNKDGVQVVEEYIADLYSAEPGEEPA 240
Db 181 SMATREELTAFLHPEEPFPHMRDIVIAETLEDLDRNKDGVQVVEEYIADLYSAEPGEEPA 240
Qy 241 WVQTERQOQFRDRLNKGDLGSEVGHVWVLPQAQDQPLVEANHLHESDTDKDGRLSKA 300
Db 241 WVQTERQOQFRDRLNKGDLGSEVGHVWVLPQAQDQPLVEANHLHESDTDKDGRLSKA 300
Qy 301 EILGNWNNFVGSQATNYGEDLTRHDEL 328
Db 301 EILGNWNNFVGSQATNYGEDLTRHDEL 328

RESULT 3
Q9HBZ8 PRELIMINARY; PRT; 328 AA.
AC Q9HBZ8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to hypothetical protein LOC57333.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005487; AAH05487.1;
DR MGD; MGI:1915346; 6030455P07R1k.
DR InterPro; IPR000886; EF-hand.
DR InterPro; IPR00036; ehand; 4.
DR SMART; SM00054; EFh; 3.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
DR PROSITE; PS00014; EF_TARGET; UNKNOWN_1.
SQ SEQUENCE 328 AA; 37973 MW; 913F5C6F0F88B316 CRC64;

Query Match 92.8%; Score 1645; DB 11; Length 328;
Best Local Similarity 92.7%; Pred. No. 4.3e-115;
Matches 304; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

Qy 1 MMWRPSVLLLLLLRHGAQKPSDPAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60
Db 1 MMWRPSVLLLLLLRHGAQKPSDPAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFL 60
Qy 61 GREVAKEFDLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWIAHTQQRHIDSYSVA 120
Db 61 GREVAKEFDLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWIAHTQQRHIDSYSVA 120
Qy 121 AWTYTDTRDGRGVGWEELRNATYGHVAPGEEFHDVEDAETKKMLARDERRFRVADQDGD 180
Db 121 AWTYTDTRDGRGVGWEELRNATYGHVAPGEEFHDVEDAETKKMLARDERRFRVADQDGD 180
Qy 181 SMATREELTAFLHPEEPFPHMRDIVIAETLEDLDRNKDGVQVVEEYIADLYSAEPGEEPA 240
Db 181 SMATREELTAFLHPEEPFPHMRDIVIAETLEDLDRNKDGVQVVEEYIADLYSAEPGEEPA 240
Qy 241 WVQTERQOQFRDRLNKGDLGSEVGHVWVLPQAQDQPLVEANHLHESDTDKDGRLSKA 300
Db 241 WVQTERQOQFRDRLNKGDLGSEVGHVWVLPQAQDQPLVEANHLHESDTDKDGRLSKA 300
Qy 301 EILGNWNNFVGSQATNYGEDLTRHDEL 328
Db 301 EILGNWNNFVGSQATNYGEDLTRHDEL 328

RESULT 4
Q99K35 PRELIMINARY; PRT; 315 AA.
AC Q99K35;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to hypothetical protein LOC57333 (Fragment).
GN 6030455P07R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005487; AAH05487.1;
DR MGD; MGI:1915346; 6030455P07R1k.
DR InterPro; IPR000886; EF-hand.
DR InterPro; IPR00036; ehand; 4.
DR SMART; SM00054; EFh; 3.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
DR PROSITE; PS00014; EF_TARGET; UNKNOWN_1.
SQ SEQUENCE 315 AA; 37973 MW; 913F5C6F0F88B316 CRC64;
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KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 315 AA; 36269 MW; CECE4DAEE54D24E4 CRC64;

Query Match
Best Local Similarity 90.1%; Score 1596; DB 11; Length 315;
Matches 293; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 14 LRHGAGKPSDAGPHGQGRVHOAAPLSDAPHDDAHGAFQYDHEAFLGREVAKEFDQLTP 73
Db 1 LRHWLGKPSDAGPHGQGRVHHGTPLSAPHDDAHGAFQYDHEAFLGRDVAKEFDKLSP 60

QY 74 EESQARLGRIVDRMDRAGDGGWVSLAELRAWIAHTQQRHIRDSVSAAWDYTDGRGV 133
Db 61 EESQARLGRIVDRMDRAGDGGWVSLAELRAWIAHTQQRHIRDSVSAAWHYTDGRGV 120

QY 134 GWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQDGDGSMATREELT 193
Db 121 GWEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQDGDGSMATREELT 180

QY 194 PEEFPHMRDIVVAETLEDLRNKGQYVOVEEYIADLYSAEPGEEPAWVQTERQOQFDR 253
Db 181 PEEFPHMRDIVVAETLEDLRNKGQYVOVEEYIADLYSAEPGEEPAWVQTERQOQFDR 240

QY 254 DLNKGHLGDSGVGHVWLPAPQDQPLVEANHLHSDTDKGRLSKAEILGNMNFVGSQ 313
Db 241 DLNKGHLGDSGVGHVWLPAPQDQPLVEANHLHSDTDKGRLSKAEILGNMNFVGSQ 300

QY 314 ATNYGEDI TRHDEL 328
Db 301 ATNYGEDI TRHDEL 315

RESULT 5
Q9CTD4 PRELIMINARY; PRT; 259 AA.
AC Q9CTD4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 6030455P07Rik protein (Fragment).
GN 6030455P07RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Frieschmann W., Gaasterland T., Gliss C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaudo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guscinclach S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Nombarts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Suzuki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK003918; BAB23076.1;
DR MGD; MGI:1915346; 6030455P07Rik.
DR InterPro; IPR002048; EF-hand.

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DR InterPro; IPR000886; ER-target.
DR Pfam; PF00036; EF-hand; 4.
DR SMART; SM00054; EFh; 3.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 259 AA; 30163 MW; 7910A9F0476260A1 CRC64;

Query Match
Best Local Similarity 74.5%; Score 1321; DB 11; Length 259;
Matches 244; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 70 QLTPESQARLGRIVDRMDRAGDGGWVSLAELRAWIAHTQQRHIRDSVSAANDYTDTR 129
Db 1 KLSPEESQARLGRIVDRMDRAGDGGWVSLAELRAWIAHTQQRHIRDSVSAARHYTDTR 60

QY 130 DGRVGHHEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQDGDGSMATREELT 189
Db 61 DGRVGHHEELRNATYGHYAPGEEFHDVEDAETKKMLARDERRFRVADQDGDGSMATREELT 120

QY 190 AFLHPEEFPHMRDIVVAETLEDLRNKGQYVOVEEYIADLYSAEPGEEPAWVQTERQOQF 249
Db 121 AFLHPEEFPHMRDIVVAETLEDLRNKGQYVOVEEYIADLYSAEPGEEPAWVQTERQOQF 180

QY 250 RFRDLNKGHLGDSGVGHVWLPAPQDQPLVEANHLHSDTDKGRLSKAEILGNMNF 309
Db 181 RFRDLNKGHLGDSGVGHVWLPAPQDQPLVEANHLHSDTDKGRLSKAEILGNMNF 240

QY 310 VGSQATNYGEDI TRHDEL 328
Db 241 VGSQATNYGEDI TRHDEL 259

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RESULT 6
O93434 PRELIMINARY; PRT; 322 AA.
AC O93434;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Reticulocalbin.
GN RCN1.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
ON NCBI_TaxID=31033;
RP SEQUENCE FROM N.A.
RX MEDLINE=99007268; PubMed=9789042;
RA Miles C., Elgar G., Coles E., Kleinjan D.J., Van Heyningen V.,
RA Hastie N.;
RT "Complete sequencing of the Fugu WAGR region from WT1 to PAX6:
RT Dramatic compaction and conservation of synteny with human chromosome
RT 11p13."
RL Proc. Natl. Acad. Sci. U.S.A. 95:13068-13072(1998).
DR EMBL; AL021531; CAA16492.1; -.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000886; ER-target.
DR Pfam; PF00036; EF-hand; 6.
DR SMART; SM00054; EFh; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 322 AA; 38207 MW; 85F99C053AC34C5C CRC64;

Query Match
Best Local Similarity 51.4%; Score 911; DB 13; Length 322;
Matches 167; Conservative 50; Mismatches 69; Indels 4; Gaps 3;

QY 40 LSDAPHDDAHGAFQYDHEAFLGREVAKEFDQLTPESQARLGRIVDRMDRAGDGGWVSL 99
Db 36 LQOATNED-NNSFOYDHEVFLGKESTFDQLSPESKDRLSKIVDRID--GDGNSYITT 92

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Q9NR43: 01-OCT-2000 (Tremblrel. 15, Created)
01-OCT-2000 (Tremblrel. 15, Last sequence update)
01-JUN-2002 (Tremblrel. 21, Last annotation update)
Crocalbin-like protein (Fragment).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE-BRAIN;
MEDLINE=99192326; PubMed=10094503;
Hsu M.J., Yen C.H., Tzeng M.C.;
"Crocalbin: a new calcium-binding protein that is also a binding
protein for crotoxin, a neurotoxic phospholipase A2.";
FEBS Lett. 445:440-444(1999).
[2]
SEQUENCE FROM N.A.
TISSUE-BRAIN;
Hsu M.J., Tzeng M.C.;
Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
EMBL; AF257659; AAF76141.1; -
InterPro; IPR002048; EF-hand.
Pfam; PF00036; ehand; 6.
SMART; SM00054; EFh; 3.
PROSITE; PS00018; EF_HAND; UNKNOWN_4.
NON_TER 1
SEQUENCE 296 AA; 34990 MW; D011D029ADE2A02E CRC64;
Query Match 48.1%; Score 852; DB 4; Length 296;
Best Local Similarity 52.7%; Pred. No. 6.8e-56;
Matches 155; Conservative 58; Mismatches 75; Indels 6; Gaps 3;
QY 33 RVHQAPLSDPHDHAHGNFYDHEAFGLGREVAKEFDQLTPEESQARLGRIVDRMDRAGD 92
Db 8 RVHEPQLSDKVHNDQ-SFYDHDFAFLGAEAKTFDQLTPEESKERLGMIVDKID--AD 64
QY 93 GDGVSLAEALRAWTAHTQQRHSDVSAAWDYTDDBDGRVGVWEELRNATYGHVAPGEF 152
Db 65 KDGFTGELKSWIKHAQKYYIDVNDVQDFMDNODGLISWDYRNVTYGYL---DD 121
QY 153 HDVEDAETKMLARDERRFRVADODGDSMATREELTAFLHPEEPHMRDIVIAETLEDL 212
Db 122 PPDGNGNYKMMYRDERFRKMDKDGDLATKEEFTAFHPEEYDKDIVVQETMEDI 181
QY 213 DRNKDGVVVEEYIADLYSAEPGEEPAWVQTERQQRDFRDLNKGDLGDSGVGHVWLP 272
Db 182 DKNADGFTDLEEYICDMYSHDNTDEPEWVKTEREQEVRDRNRDGMKDEETKDWLP 241
QY 273 PAQDQPLVEANHLHESDTKDGRLSKAEILGNMNFVGSQATNYGDLTRHHD 326
Db 242 SDYDHAEAEARHLVYESQNDKDKLTKEEIVDKYDLFVGSQATDFGEALVRHDE 295
RESULT 9
ID O35783 PRELIMINARY; PRT; 315 AA.
AC O35783;
DT 01-JAN-1998 (Tremblrel. 05, Created)
01-JAN-1998 (Tremblrel. 05, Last sequence update)
01-MAR-2002 (Tremblrel. 20, Last annotation update)
CBP-50 protein.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A.
STRAIN=SPRAGUE-DAWLEY; TISSUE-BRAIN;
Hsu M.J.;
Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
[2]

QY 100 AELRAWTAHTQQRHSDVSAAWDYTDDBDGRVGVWEELRNATYGHVAPG-BEFDHVEDA 158
Db 93 DELKAWTKRVQKRYVENVVKKWADYDLNKNKISWEEYKQATYGYLSPPEFDETTQD 152
QY 159 ETKKMLARDERRFRVADQDSMATREELTAFLHPEEPHMRDIVIAETLEDLDRNKG 218
Db 153 FSKKMLPRDERFRKADLDGDSAAANREFTSLHPEEFHMDIVVLETLEDIKNSDG 212
QY 219 YVQVEEYIADLYSAEPGEEPAWVQTERQQRDFRDLNKGDLGDSGVGHVWLPQAQDP 278
Db 213 HVDEDEYIADFAHEDRGPPEWVKTEREQFSDFRDLNKGDKMDLDIRHWIMPQYDHA 272
QY 279 LVEANHLHESDTKDGRLSKAEILGNMNFVGSQATNYGDLTRHDEL 328
Db 273 QAEARHLVYESDKDKQDLKKEILNWNMFVGSQATNYGDLTRHDEL 322
RESULT 7
ID O96RL3 PRELIMINARY; PRT; 315 AA.
AC O96RL3;
DT 01-DEC-2001 (Tremblrel. 19, Created)
01-DEC-2001 (Tremblrel. 19, Last sequence update)
01-MAR-2002 (Tremblrel. 20, Last annotation update)
Calumenin.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
Peterson R.E. Jr., Watson D.K.;
"Novel splice variant of human calumenin.";
Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
EMBL; AF345637; AAK72908.1; -
InterPro; IPR002048; EF-hand.
Pfam; PF00036; ehand; 6.
PROSITE; PS00018; EF_HAND; UNKNOWN_4.
SEQUENCE 315 AA; 37135 MW; E1BF415B25076676 CRC64;
Query Match 48.4%; Score 857.5; DB 4; Length 315;
Best Local Similarity 50.5%; Pred. No. 2.9e-56;
Matches 161; Conservative 62; Mismatches 85; Indels 11; Gaps 4;
QY 8 LLLLLLHGAQKSPDAGPHGQGRVHQAPLSDPHDHAHGNFYDHEAFGLGREVAKE 67
Db 7 LMCLSLCTAFALSKPT-----EKKDRVHEPQLSDKVHNDQ-SFYDHDFAFLGAEAKT 60
QY 68 FDLTPESQARLGRIVDRMDRAGDGVSLAEALRAWTAHTQQRHSDVSAAWDYTD 127
Db 61 FDLTPESKERLGMIVDKID--ADKDGFTGELKSWIKHAQKYYIDVNDVQDFMD 118
QY 128 DRDGRVGVWEELRNATYGHVAPGEFHDVEDAETKMLARDERRFRVADODGDSMATREE 187
Db 119 NQDGLISDWEYRNVYGYL---DDPPDNGNYKMMYRDERFRKMDKDGDLATKEE 175
QY 188 LTAFLHPEEPHMRDIVIAETLEDLDRNKGQYVQVEEYIADLYSAEPGEEPAWVQTERQ 247
Db 176 FTAFLHPEEYDKDIVVQETMEDIKDNADGFTDLEEYICDMYSHDNTDEPEWVKTERE 235
QY 248 QFRDRLNKGDLGDSGVGHVWLPQAQDQPLVEANHLHESDTKDGRLSKAEILGNWN 307
Db 236 QFVEFRDKNRDKMDEETKDWLPISDYDHAEAEARHLVYESQNDKDKLTKEEIVDKYD 295
QY 308 MFVGSQATNYGDLTRHHD 326
Db 296 LFVGSQATDFGEALVRHDE 314
RESULT 8
ID O9NR43 PRELIMINARY; PRT; 296 AA.
Q9NR43

[illegible]

RESULT	10
Q9MZ46	
ID	Q9MZ46
AC	PRELIMINARY; PRT; 296 AA.
DC	Q9MZ46;
DT	01-OCT-2000 (TRMBLrel. 15, Created)
DT	01-OCT-2000 (TRMBLrel. 15; Last sequence update)
DT	01-MAR-2002 (TRMBLrel. 20, Last annotation update)
DE	Crocalbin-like protein (Fragment).
OS	Sus scrofa (pig).
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutharia; Cetartiodactyla; Suina; Suidae; Sus.
OX	NCBI_TaxID=9823;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=BRAIN;
EC	MEDLINE=99192326; PubMed=10094503;
RA	Hseu M.J., Yen C.H., Tzeng M.C.;
RR	*Crocalbin: a new calcium-binding protein that is also a binding
RT	protein for crotoxin; a neurotoxic phospholipase A2.";
RL	FEBS Lett. 445:440-444(1999).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=BRAIN;
RR	Hseu M.J., Tzeng M.C.;
RL	Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR	EMBL: AF257660; AAF76142.1;
DR	InterPro: IPR002048; EF-hand.
DR	Pfam: PF00036; efnhd; 6.
DR	SMART: SM00054; EFN; 2.

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DR PROSITE; PS00018; EF_HAND; UNKNOWN_3.
FT NON_TER 1
FT NON_TER 296
SQ SEQUENCE 296 AA; 34896 MW; 7C01BB38C6275914 CRC64;

Query Match
Best Local Similarity 46.28; Score 818; DB 6; Length 296;
Matches 152; Conservative 59; Mismatches 77; Indels 6; Gaps 3;

QY 33 RVHQAPISDAPHDDAHGCFYDHEAFGLGREVAKEFDQLTPESQARLGRIVDRMDRAG 92
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
8 RVHHEPQLSDKVKHNDQAQ-SFYDHDALFGLAAEAKTFDQLTPESKERLGMIVDKID--AD 64
QY 93 GDGWYSLAEALRAWIAHTQORHIRDSVSAANDTYDTRDGRVGEELRNATYGHYAPGEFF 152
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
65 KDGFEVTEGLSKWIKHAKKYIVDNVENQOEEDMNOGDLIPWDEYRVNYTGYL---DD 121
QY 153 HDVEDAEYTKKLLARDERRFRVADQDGDSMATREELTAFELHPPEEPHMRDVIETLEDL 212
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
122 PDPDGFNYKQMVYDRERRFKMADKQGLIATKEELTAFELHREEYDYKKDIVQETWEEL 181
QY 213 DRNKDGYVVEEYIADLYSAPEEGEPANVQTERQOFDRDLNKDGLDGSSEGVHWLP 272
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
182 DKNADGFIDEEYIGWYSHDGNADPEWVKTERQGFVFRKDKRDKMDKEETKDFFLP 241
QY 273 PAQDQVLEANHLHSHSDTKDGRLSKABELGNWNHNVGSOATNYGEDLRHHD 326
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
242 SDIDHAEAEARHLVYSDNQKGLTKEIVDKYDFVGSQVDFGEALVAHDE 295

RESULT 11
Q8SZK6
ID Q8SZK6 PRELIMINARY; PRT; 329 AA.
AC Q8SZK6;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE RH25118p.

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RESULT 11
Q8SZK6
ID Q8SZK6 PRELIMINARY; PRT; 329 AA.
AC Q8SZK6;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE RH251189.
GN SCF.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID:7227;
RN [1]
RP SEQUENCE FROM N. A.
RC STRAIN=BERKELEY.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guatin H., Konniller B., Li P., Liao G.,
RA Miranda A., Mungali C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celinder S.
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RD EMBL: AV070689; AAL48160.1.
SQ SEQUENCE 329 AA; 37992 MW; 486769E828B755A9 CRC64;

Query Match
Best Local Similarity 39.7%; Score 703.5; DB 5; Length 329;
Matches 146; Conservative 58; Mismatches 115; Indels 15; Gaps
6;

QY 2 MWKPSVLLLLLLR-----HGAQKQSPDAGPHCGRVHQAAPLSDAPHDHAGNFQYDH 56
Db 1 MARIQIMLLLVALTAVISGASSTPEELPHNP---LEHDLPHRPHRDGGHEHNAQFDH 57
QY 57 EAFGLREVAKEFDQLTPEESCARLGRITVDMRAGDGDGWVSLAEALRWIAHTQORHIRD 116
Db 58 EAFGLPDSKEKFDLSLTPEESRRRLGVITVRIDR--NRKGSVTLAEKKNWIAVQRYTEE 115
QY 117 SVSAANDYTDTRDGRGVGWEELRNATYG----HYAPGEEFHDVEDAETVKMLARDERRR 173
Db 116 DVGVRWKOHNPDNNETTSWDSYMQTVGVGEMDLSLPEKQEE-ENGVSVSKLLKRDYRWS 174

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DE 174 VADQDGSMTARELTAFLLHPEEPHMRDIVIAETLEDLRNKGQVQVEEYIADLYSAE 233
GN M03F4.7.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OC NCBI_TaxID=6239;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=BRISTOL N2;
RC STRAIN=BRISTOL N2;
RA Yabe D.;
RT "Caenorhabditis elegans homolog of mouse calumenin.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=BRISTOL N2;
RC STRAIN=BRISTOL N2;
RA Fulton L.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF228528; AAF34189.1; ...
DR EMBL; U64601; AAB04578.1; ...
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 5.
DR SMART; SM00054; EFh; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_5.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_5.
SQ SEQUENCE 314 AA; 36077 MW; 0350F2CBDA3AA62 CRC64;

Query Match 36.1%; Score 639.5; DB 5; Length 314;
Best Local Similarity 40.0%; Pred. No. 5.6e-40;
Matches 132; Conservative 63; Mismatches 100; Indels 35; Gaps 8;

QY 7 VLLLLLLRHGA-----QKPSPDAGPHGQGRVHQAPLSDAPHDDAHGNGFOYDHEAFILG 61
DB 3 VLLFVGLLATAALASHSSDPSKD-GEHPKGEHDK-----KYDHEQFLG 46
QY 62 REVAKEDQTLTPESQARLGRIVDRMDRAGDGGVWSLAELRAWTAHTQOHRIRDSVNA 121
DB 62 REVAKEDQTLTPESQARLGRIVDRMDRAGDGGVWSLAELRAWTAHTQOHRIRDSVNA 121
QY 47 KDTAAEFDELTPESKREKELAKLPKMD--ADSGFTEENELKDHINFMQRYVNNVDRT 104
DB 47 KDTAAEFDELTPESKREKELAKLPKMD--ADSGFTEENELKDHINFMQRYVNNVDRT 104
QY 122 WDTYDTR--DGRVGEELRNATYGHY-APGEFHDVEDEATYKKMLARDERRFRVADQD 178
DB 122 WDTYDTR--DGRVGEELRNATYGHY-APGEFHDVEDEATYKKMLARDERRFRVADQD 178
QY 105 WKYKAELIVDGKIKWEDYREMYVGSADGAGQEL-----SPEYAKMIARDEKQWAVADYD 159
DB 105 WKYKAELIVDGKIKWEDYREMYVGSADGAGQEL-----SPEYAKMIARDEKQWAVADYD 159
QY 179 GDSMATREELTAFLLHPEEPHMRDIVIAETLEDLRNKGQVQVEEYIADLYSAEPGEE- 237
DB 179 GDSMATREELTAFLLHPEEPHMRDIVIAETLEDLRNKGQVQVEEYIADLYSAEPGEE- 237
QY 160 SNGALDRTEYCGFMPECDCHMRDQVVAETVDDIDKKNKGSDVLDYIGDMYRPDPPEL 219
DB 160 SNGALDRTEYCGFMPECDCHMRDQVVAETVDDIDKKNKGSDVLDYIGDMYRPDPPEL 219
QY 238 ---EPAWQTERQOQFRDRLNKGHLDSGVGHVWLPAPADQQLVPEANHLHESDTPDKD 294
DB 238 ---EPAWQTERQOQFRDRLNKGHLDSGVGHVWLPAPADQQLVPEANHLHESDTPDKD 294
QY 220 NGKEPDWQVQSEREMFKEHRDKDGGKLNQEEWRDIMPVGFDAEAEARHLVGIADNDKD 279
DB 220 NGKEPDWQVQSEREMFKEHRDKDGGKLNQEEWRDIMPVGFDAEAEARHLVGIADNDKD 279
QY 295 GLSKAEILGNMNMVFGSOATNYGEDLTRH 324
DB 295 GLSKAEILGNMNMVFGSOATNYGEDLTRH 324
QY 280 GKLNLDEIVAHYDTFVGSQATDYGEOLOKH 309
DB 280 GKLNLDEIVAHYDTFVGSQATDYGEOLOKH 309

RESULT 14
Q63399 PRELIMINARY; PRT; 98 AA.
ID Q63399;
AC Q63399;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE (clone REM1) ORF (fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=HOLZMAN;
RC STRAIN=HOLZMAN;
RX MEDLINE=9623155; PubMed=8642059;
RA Asakura K., Pogulis R.J., Pease L.R., Rodriguez M.;
RT "A monoclonal antibody which promotes central nervous system
remyelination is highly polyreactive to multiple known and novel

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RESULT 12

Q93136 PRELIMINARY; PRT; 322 AA.

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ID Q93136;
AC Q93136;
DT 01-FEB-1997 (Tremblrel. 02, Created)
DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE DNA supercoiling factor.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Bombycoidea; Bombycidae; Bombyx.
OC NCBI_TaxID=7091;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=POSTERIOR SILK GLAND;
RC MEDLINE=95318140; PubMed=7797553;
RA Ohta T., Kobayashi M., Hirose S.;
RT "Cloning of a cDNA for DNA supercoiling factor reveals a distinctive
Ca-binding protein."
RL J. Biol. Chem. 270:15571-15575 (1995).
DR EMBL; D49948; BAA08704.1; ...
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 3.
DR SMART; SM00054; EFh; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
SQ SEQUENCE 322 AA; 37894 MW; DFB25C5E37F84E7 CRC64;

Query Match 38.7%; Score 685; DB 5; Length 322;
Best Local Similarity 45.5%; Pred. No. 2.3e-43;
Matches 136; Conservative 52; Mismatches 91; Indels 20; Gaps 5;

QY 40 LSDAPH-DDAHGNGFYDHEALFGRVAKFQTLTPESQARLGRIVDRMDRAGDGGVWS 98
DB 40 LSDAPH-DDAHGNGFYDHEALFGRVAKFQTLTPESQARLGRIVDRMDRAGDGGVWS 98
QY 31 LSDAEHYRNEHKKQFDHDAFLGEOAKTFDQLSPESKRLGELADKID--SDQGFIT 88
DB 31 LSDAEHYRNEHKKQFDHDAFLGEOAKTFDQLSPESKRLGELADKID--SDQGFIT 88
QY 99 LAELRAWIAHTOORHIRDSVSAADTYDTRDGRVGEELRNATYGHYAPGEEFHDVEDA 158
DB 99 LAELRAWIAHTOORHIRDSVSAADTYDTRDGRVGEELRNATYGHYAPGEEFHDVEDA 158
QY 89 LVELKDWIRYTKRYIDEDVERHWRQNPNEEFVTWEAYRKNVGF-----MDDMDK 142
DB 89 LVELKDWIRYTKRYIDEDVERHWRQNPNEEFVTWEAYRKNVGF-----MDDMDK 142
QY 159 E-----TYKKMLARDERRFRVADQDGSMTARELTAFLLHPEEPHMRDIVIAETL 209
DB 159 E-----TYKKMLARDERRFRVADQDGSMTARELTAFLLHPEEPHMRDIVIAETL 209
QY 143 ELKAPNSEGTYNLOKDRRWRTYADADQNDALNRTFAELHPEEDHSSMRDVVVLETL 202
DB 143 ELKAPNSEGTYNLOKDRRWRTYADADQNDALNRTFAELHPEEDHSSMRDVVVLETL 202
QY 210 EDLDRNKGQVQVEEYIADLYSAEPG--EPEAWQTERQOQFRDRLNKGHLDSGVG 267
DB 210 EDLDRNKGQVQVEEYIADLYSAEPG--EPEAWQTERQOQFRDRLNKGHLDSGVG 267
QY 203 EDIDKQDQGVSLDEYIGDMYNAGDGEDEEPPDWKQREQFTGYRDTNKGDFMDEHVK 262
DB 203 EDIDKQDQGVSLDEYIGDMYNAGDGEDEEPPDWKQREQFTGYRDTNKGDFMDEHVK 262
QY 268 HWLPPAPQDQPLVEANHLHESDTPDKDGLSKAEILGNMNMVFGSOATNYGEDLTRHHD 326
DB 268 HWLPPAPQDQPLVEANHLHESDTPDKDGLSKAEILGNMNMVFGSOATNYGEDLTRHHD 326
QY 263 DWIAPPEFDHAEAEARHLVFEADADEKLTAKAEIIDKYDLFVGSQATDFGGALARHDE 321
DB 263 DWIAPPEFDHAEAEARHLVFEADADEKLTAKAEIIDKYDLFVGSQATDFGGALARHDE 321

RESULT 13
Q23017 PRELIMINARY; PRT; 314 AA.
ID Q23017;
AC Q23017;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)

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RT antigens.*;
RL J. Neuroimmunol. 65:11-19(1996).
DR EMBL; L41683; AAB05841.1; -.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
FT NON_TER 1
FT TER 98
SQ SEQUENCE 98 AA; 11277 MW; FOA3D6D9EF624CE1 CRC64;

Query Match      27.1%; Score 481; DB 11; Length 98;
Best Local Similarity 93.7%; Pred. No. 7.7e-29;
Matches 89; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 62 REVAKFQDQTPESQARLGRIVDRMDRAGDGGWLSLAELRAWIAHTQOIRHDSVSA 121
Db 2 IDVAKEFDQTPESQARLGRIVDRMDRAGDGGWLSLAELRAWIAHTQOIRHDSVSA 61

OY 122 WDVTYDTRDGRVGEELRNATYCHYAPGEEFHDE 156
Db 1 IDVAKEFDQTPESQARLGRIVDRMDRAGDGGWLSLAELRAWIAHTQOIRHDSVSA 61

OY 62 WHYDTRDGRVGEELRNATYCHYAPGEEFHDE 96
Db 1 IDVAKEFDQTPESQARLGRIVDRMDRAGDGGWLSLAELRAWIAHTQOIRHDSVSA 61

RESULT 15
Q9VMV2
ID Q9VMV2 PRELIMINARY; PRT; 342 AA.
AC Q9VMV2;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE CG9112 protein (LD34388P).
GN CG9112.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_taxid=7227;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazei R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Baau A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flesler C., Gabrielian A.C., Garg N.S., Gelbart W.M., Glasser K.,
RA Glöck A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reibert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kimms I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner E., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,

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RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guerin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacle J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celnik S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003608; AAF52207.1; -.
DR EMBL; AY061412; AAL28960.1; -.
DR HSSP; P02593; 1CDM.
DR FlyBase; FBgn0031673; CG9112.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00036; ehand; 6.
DR SMART; SM00054; EFh; 3.
DR PROSITE; PS00018; EF_HAND; 4.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Calcium-binding.
SQ SEQUENCE 342 AA; 39453 MW; C3C0D0F75ADC8286 CRC64;

Query Match      25.8%; Score 457; DB 5; Length 342;
Best Local Similarity 33.7%; Pred. No. 2.7e-26;
Matches 118; Conservative 59; Mismatches 131; Indels 42; Gaps 13;

OY 5 PSVLLLLLRHGAQKPSDAGPHGQGRVHQA-----APLSDAPH--DDAAG 50
Db 9 PLTICAVALL---AAGPMPAHGAVANSHKHEKLSKERVVDGIYAP-RDAHHGDEGH 64

OY 51 NFQYDHEAFGLGR-EVAKFEDQTPESQARLGRIVDRMDRAGDGGWLSLAELRAWIAHT 109
Db 65 NYEFDHEAIIIGTKAEQFDSLSPDESKRRLLILIKMMDL--NKDEFIDRHLKAWILRS 122

OY 110 QQRHIRDSVSAWDYTDTRDGRVGEELRNATYCHYAPGEEH---DVEDAETTKML 165
Db 123 FKKLSEEAADRFEEIDODADERITWKEYLQDTYA--MEDEFKKTIDYDSYDEQKMI 180

OY 166 ARDERRRFVADQDGDGMATREELTAFLHPBEFPHMRDIVIAETLEDLRNKGQVVOVEEY 225
Db 181 KQDKEMFNAADTNKDGVLTLTEEFVLFQNPBEHPQMLPILLEHTMQDKADHDGKINQOE 240

OY 226 IADLYSAEPGEEEPANVQTERQOFDRFDLNKQDGLDGEVGHVLP-----AQDQPLVE 281
Db 241 VGDAAS----HDKEWLITKEKFDKDHDSNGDGVLTGDEVLSWIYSPNTAAND----E 292

OY 282 ANHLLHSDTKDGRGSKABEILGNWNVGSAQNTYGEDLTR--HH--DEL 328
Db 293 VDHLFVSTDHDDHRLSYLEILNNYDTEVGSSEATDYGDLHNLQNLHLSDEL 342

Search completed: May 14, 2003, 10:45:29
Job time : 107.983 secs

```

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 14, 2003, 10:34:22 ; Search time 27.8944 Seconds
 (without alignments)
 487.704 Million cell updates/sec

Title: US-09-768-840-1
 Perfect score: 1772
 Sequence: 1 MMWRPSVLLLLLLLRHGAQ.....FVGSQATNYGEDLIRHDEL 328

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	944	53.3	331	1 RCN1_HUMAN	Q15293 homo sapien
2	938	52.9	325	1 RCN1_MOUSE	Q05186 mus musculus
3	845.5	47.7	315	1 CALU_MOUSE	Q35887 mus musculus
4	842.5	47.5	315	1 CALU_HUMAN	Q43852 homo sapien
5	476	26.9	318	1 RCN2_RAT	Q62703 rattus norv
6	456.5	25.8	317	1 RCN2_HUMAN	Q14257 homo sapien
7	269.5	15.2	362	1 CB45_HUMAN	Q9brk5 homo sapien
8	261.5	14.8	361	1 CB45_MOUSE	Q91zsz3 rattus norv
9	260.5	14.7	361	1 CB45_MOUSE	Q61112 mus musculus
10	138.5	7.8	344	1 TCH3_ARATH	P25071 arabidopsis
11	134.5	7.6	169	1 CAF1_DICDI	P54670 dictyosteli
12	129.5	7.3	276	1 SEG1_HUMAN	O76038 homo sapien
13	129.5	7.3	275	1 CAB1_HUMAN	P57796 homo sapien
14	129	7.3	321	1 LPSA_LYPTI	P38505 entamoeba h
15	128	7.2	134	1 CABP_ENTHI	P38485 lytechinus
16	127.5	7.2	271	1 CABP_ENTHI	P22676 homo sapien
17	127	7.2	271	1 CLB2_MOUSE	Q08331 mus musculus
18	127	7.2	271	1 CLB2_MOUSE	P47728 rattus norv
19	126.5	7.1	215	1 CAB2_MOUSE	Q0790 gallus gall
20	126	7.1	269	1 CLB2_CHICK	Q03975 lytechinus
21	125.5	7.1	243	1 LPSB_LYPTI	Q9jmb3 mus musculus
22	124.5	7.0	148	1 CLM4_MOUSE	P81660 anguilla an
23	124.5	7.0	160	1 TPCS_ANGAN	Q9nzt1 homo sapien
24	124	7.0	146	1 CLSP_HUMAN	Q9n1q9 bos taurus
25	123	6.9	162	1 CAB2_BOVIN	P49101 zea mays (m
26	119.5	6.7	513	1 CDP2_MALZE	P10246 meleagris g
27	118.5	6.7	162	1 TPCS_MELGA	Q9npb3 homo sapien
28	118.5	6.7	219	1 CAB2_HUMAN	P53683 oryza sativ
29	118	6.7	533	1 CDP2_ORYSA	Q07167 schistosoma
30	117.5	6.6	143	1 SM16_SCHMA	P02589 rana esculie
31	117.5	6.6	162	1 TPCS_RANES	Q06850 arabidopsis
32	116.5	6.6	610	1 CDPI_ARATH	P02588 gallus gall
33	115.5	6.5	162	1 TPCS_CHICK	

34 114.5 6.5 150 1 SP15_HEMPU
 35 114.5 6.5 175 1 CALC_RAT
 36 114.5 6.5 189 1 NCS1_YEAST
 37 113 6.4 149 1 CABO_LOLPE
 38 112.5 6.3 178 1 CALC_MOUSE
 39 112 6.3 165 1 POC2_JUNOX
 40 111 6.3 152 1 SPIA_STRPU
 41 111 6.3 163 1 TPC_BRALA
 42 111 6.3 176 1 CATR_GIALA
 43 110 6.2 149 1 CALM_WHEAT
 44 109.5 6.2 148 1 CALM_METSE
 45 109.5 6.2 148 1 CALM_PATSP

ALIGNMENTS

RESULT 1

RCN1_HUMAN STANDARD; PRT; 331 AA.

ID RCN1_HUMAN
 AC Q15293;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 13-JUN-2002 (Rel. 41, Last annotation update)
 DE Reticulocalbin 1 precursor.
 GN RCN1 OR RCN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96172582; PubMed=8586628;
 RA Ozawa M.;
 RT "Cloning of a human homologue of mouse reticulocalbin reveals
 conservation of structural domains in the novel endoplasmic reticulum
 resident Ca(2+)-binding protein with multiple EF-hand motifs.";
 RL J. Biochem. 117:1113-1119(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Coville G.;
 RT Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 RL -1- FUNCTION: MAY REGULATE CALCIUM-DEPENDENT ACTIVITIES IN THE
 CC ENDOPLASMIC RETICULUM LUMEN OR POST-ER COMPARTMENT.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
 CC SITES; POTENTIAL SITES II AND VI HAVE LOST AFFINITY FOR CALCIUM
 CC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CREC FAMILY.
 CC -1- SIMILARITY: CONTAINS 6 EF-HAND CALCIUM-BINDING DOMAINS.
 CC
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 CC EMBL; D42073; BAA07670.1; -;
 CC EMBL; AL078612; CAB53067.1; -;
 CC Genew; HGNC:9934; RCN1.
 CC MIM; 602735; -;
 CC InterPro; IPR002048; EF-hand.
 CC InterPro; IPR000886; EF_target.
 CC Pfam; PF00036; ehand; 6.
 CC SMART; SM00034; EFh; 3.
 CC PROSITE; PS00014; ER_TARGET; 1.
 CC PROSITE; PS00018; EF_HAND; 4.
 CC Calcium-binding; Endoplasmic reticulum; Signal; Glycoprotein; Repeat;
 CC Polymorphism.
 FT SIGNAL 1 29
 FT CHAIN 30 331
 FT RETICULOCALBIN 1.

QY 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLRNKGYYVOVEYIADLYSABPGEPEA 240
 DB 178 LTATREELTAFLHPEEPHMRDIVIAETLEDLRNKGYYVOVEYIADLYSABPGEPEA 237
 QY 241 WYOTERQOFRDLNKGDLGSEVGHVWLPQAQDPLVEANHLHESDTRKGRLSKA 300
 DB 238 WYLSERQOFRDLNKGDLGSEVGHVWLPQAQDPLVEANHLHESDTRKGRLSKA 297
 QY 301 EILGNWNVFSGQATNGEDLTRHDEL 328
 DB 298 EILGNWNVFSGQATNGEDLTRHDEL 325

RESULT 3

ID CALU_MOUSE STANDARD; PRT; 315 AA.
 AC O35887;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Calumenin precursor.
 GN CALU.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

SEQUENCE FROM N.A., AND CHARACTERIZATION.

RC STRAIN-ICR; TISSUE-Heart;
 RX MEDLINE=97364750; PubMed=9218460;
 RA Yabe D., Nakamura T., Kanazawa N., Tashiro K., Honjo T.;
 RT "Calumenin, a Ca2+-binding protein retained in the endoplasmic
 reticulum with a novel carboxyl-terminal sequence, HDEF";
 RL J. Biol. Chem. 272:18232-18239(1997).
 CC - FUNCTION: NOT KNOWN, BINDS 7 CALCIUM IONS WITH A LOW AFFINITY (BY
 similarity).
 CC - SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC - SIMILARITY: BELONGS TO THE CREC FAMILY.
 CC - SIMILARITY: CONTAINS 6 EF-HAND CALCIUM-BINDING DOMAINS.
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EMBL: U81829; AAC3316.1; -
 MGD; MGI:1097158; Calu.
 InterPro: IPR002048; EF-hand.
 Pfam: PF00036; ehand; 6.
 SMART: SM00054; EFh; 2.
 DR PROSITE: PS00018; EF_HAND; 4.
 KW Calcium-binding; Endoplasmic reticulum; Signal; Repeat.
 FT SIGNAL 1 19
 FT CHAIN 20 315
 FT CA_BIND 81 92
 FT CA_BIND 117 128
 FT CA_BIND 164 175
 FT CA_BIND 201 212
 FT CA_BIND 242 253
 FT CA_BIND 278 289
 FT CARBOHYD 131 131
 FT SITE 312 315
 FT SEQUENCE 315 AA; 37063 MW; 742361814171E273 CRC64;

Query Match 47.78; Score 845.5; DB 1; Length 315;
 Best Local Similarity 50.58; Pred. No. 4.3e-52;
 Matches 161; Conservative 59; Mismatches 88; Indels 11; Gaps 4;

QY 8 LLLLLLHGHAGGKSPDAGPHGQGRVHQAPLSDAPHDHAGNFQYDHEAFLGREVAKE 67.

DB 7 LMCLSLCTAFALSAPT-----EKKDRVHHPQLSDKVHNDQA-NFYDHDHDFLGAEAKS 60
 QY 68 FDQLTPESQARLGRIVDNRMDRAGDGGWVSLAELRAWIAHTOORHRSVSAAWDYDT 127
 DB 61 FDQLTPESQARLGRIVSKID--DDKGFVTVDELKGVKFAQKRWIHEDVERQWKGHD 118
 QY 128 DRGRVWEEELRNATYGHYAPGEEFHDVEDAETTKKLARDERRFRVADQDGSNATREE 187
 DB 119 NEDGLVSWEYKNTATGYVL---DDPDDGFGYKQMYRDERFRKADKDGDLATREE 175
 QY 188 LTAFLEHPEEPHMRDIVIAETLEDLRNKGYYVOVEYIADLYSABPGEPEAWQTERQ 247
 DB 176 FTAFLEHPEEYDKMDIVVQETMEDIDKNAGDFIDLEEYIGDMYSHDGNADENPVKTERE 235
 QY 248 QFRDRLNKGDLGSEVGHVWLPQAQDPLVEANHLHESDTRKGRLSKAELGNWN 307
 DB 236 QFYEFDRDKNRDGMKDEETKDWILPSDYDHAENAEARHLVYESDQNKDKGLTKKEIVDKYD 295
 QY 308 MFVGSQATNGEDLTRHHD 326
 DB 296 LFVGSQATNGEDLTRHHD 314

RESULT 4

ID CALU_HUMAN STANDARD; PRT; 315 AA.
 AC O43852; O60456;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calumenin precursor (IEF SSP 9302).
 GN CALU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CALCIUM-BINDING DATA.
 RC TISSUE-Keratinocytes;
 RX PubMed=9675259;
 RA Vorum H., Liu X., Madsen P., Rasmussen H.H., Honore B.;
 RT "Molecular cloning of a cDNA encoding human calumenin, expression in
 Escherichia coli and analysis of its Ca2+-binding activity";
 RL Biochim. Biophys. Acta 1386:121-131(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98260687; PubMed=9598325;
 RA Yabe D., Tanigaki M., Nakamura T., Kanazawa N., Tashiro K., Honjo T.;
 RT "Human calumenin gene (CALU): cDNA isolation and chromosomal mapping
 to 7q32";
 RL Genomics 49:331-333(1998).
 RN [3]
 RP SUBCELLULAR LOCATION.
 RX PubMed=10222138;
 RA Vorum H., Hager H., Christensen B.M., Nielsen S., Honore B.;
 RT "Human calumenin localizes to the secretory pathway and is secreted to
 the medium";
 RL Exp. Cell Res. 248:473-481(1999).
 CC - FUNCTION: NOT KNOWN, BINDS 7 CALCIUM IONS WITH A LOW AFFINITY.
 CC - SUBCELLULAR LOCATION: Endoplasmic reticulum lumen and secreted.
 CC - TISSUE SPECIFICITY: Ubiquitously expressed. Expressed at high
 levels in heart, placenta and skeletal muscle, at lower levels in
 lung, kidney and pancreas and at very low levels in brain and
 liver.
 CC - SIMILARITY: BELONGS TO THE CREC FAMILY.
 CC - SIMILARITY: CONTAINS 7 EF-HAND CALCIUM-BINDING DOMAINS.
 CC

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Tue May 20 14:43:28 2003

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CC CC EMBL; U67280; AAB97725.1; -.
CC CC EMBL; AF013759; AAC17216.1; -.
CC CC Genew; HGNC:1458; CALU.
CC DR MIM; 603420; -.
CC DR InterPro; IPR002048; EF-hand.
CC DR SMART; SM00054; EFh; 2.
CC DR PROSITE; PS00018; EF-HAND; 4.
CC DR Calcium-binding; Endoplasmic reticulum; Signal; Repeat.
KW SIGNAL 1 19 CALUMENIN
FT CHAIN 20 315
FT CA_BIND 81 92 EF-HAND 1 (POTENTIAL).
FT CA_BIND 117 128 EF-HAND 2 (POTENTIAL).
FT CA_BIND 164 175 EF-HAND 3 (POSSIBLY ANCESTRAL).
FT CA_BIND 201 212 EF-HAND 4 (POTENTIAL).
FT CA_BIND 242 253 EF-HAND 5 (POTENTIAL).
FT CA_BIND 278 289 EF-HAND 6 (POTENTIAL).
FT CA_BIND 131 131 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 131 131 PREVENT SECRETION FROM ER (BY
FT SITE 315 SIMILARITY).
FT F -> L (IN REF. 1).
FT CONFLICT 207
FT SEQUENCE 315 AA; 37107 MW; 25BAE5A99B527375 CRC64;
Query Match 47.5%; Score 842.5; DB 1; Length 315;
Best Local Similarity 50.5%; Pred. No. 6.9e-52;
Matches 101; Conservative 60; Mismatches 87; Indels 11; Gaps 4;
QY 8 LLLLLLHGAQCKSPDAGPHGQGRVHQAAPLSDAPHDHAGNFQYDHEAFLGREVAKE 67
DB 7 LMLSLCTAFALSKPT-----EKKDRVHPEQLSKDVHNDQAQ-SFDYDHAFLGAEAAKT 60
QY 68 FDLTPESQARIGRIVDRMDRAGDGGWVSLAELRAWTAAHTQQRHIRDSVSAADTDT 127
DB 61 FDLTPESQARIGRIVDRMDRAGDGGWVSLAELRAWTAAHTQQRHIRDSVSAADTDT 118
QY 128 DRGRVGEWELRNATYGHVAPGEEHVDVDAETKYKMLARDERRFRVADODGDSMATREE 187
DB 119 NEDGLVSEWYKNTATGYVL---DDPPDDGDFNYKQWVDRDRFRKMAKDGDLIATKEE 175
QY 188 LTAFLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPAWVQTERQ 247
DB 176 FTAFLHPEEYDKMDIVVQETMEDIDKADGDFIDLEEYIGDMYSHDGDTEPEWVKTERE 235
QY 248 QFRDRLNKGDLGSEVGHVWLPAPADQPLVEANHLHESDTDKDGLSLKAEILGNW 307
DB 236 QVEFRDKNRDKGDKKEETKDWLLPSDYDHAEEARHLVYESQNKDKGLTKEEIVDKYD 295
QY 308 MFVGSQATNYGEDLTRHHD 326
DB 296 LFVGSQATDFGEALVRHDE 314
RESULT 5
RCN2_RAT RCN2_HUMAN
ID RCN2_RAT ID RCN2_HUMAN STANDARD; PRT; 318 AA.
AC Q62703; AC Q14257;
DT 01-NOV-1997 (Rel. 35, Created) DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update) DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Reticulocalbin 2 precursor (Calcium-binding protein ERC-55) (Taipoxin-
DE associated calcium-binding protein-49) (TCBP-49).
DE RCN2 OR ERC55.
GN Rattus norvegicus (Rat).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RC STRAIN-Sprague-Dawley;
RX MEDLINE=95239201; PubMed=7722520;

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RA Dodds D., Schlimmen A.K., Lu S.Y., Perin M.S.;
RT "Novel reticular calcium binding protein is purified on taipoxin
RL columns.";
RL J. Neurochem. 64:2339-2344(1995).
CC -1- FUNCTION: NOT KNOWN, BINDS CALCIUM.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- TISSUE SPECIFICITY: UBIQUITOUS.
CC -1- SIMILARITY: BELONGS TO THE CREC FAMILY.
CC -1- SIMILARITY: CONTAINS 6 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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EMBL; U15734; AAA80197.1; -
InterPro; IPR002048; EF-hand.
Pfam; PF00036; efhand; 5.
SMART; SM00054; EFh; 3.
PROSITE; PS00018; EF-HAND; 5.
PROSITE; PS00014; ER_TARGET; 1.
Calcium-binding; Endoplasmic reticulum; Signal; Repeat.
KW SIGNAL 1 23
FT CHAIN 24 318 RETICULOCALBIN 2.
FT CA_BIND 75 86 EF-HAND 1 (POTENTIAL).
FT CA_BIND 111 122 EF-HAND 2 (POTENTIAL).
FT CA_BIND 163 174 EF-HAND 3 (POSSIBLY ANCESTRAL).
FT CA_BIND 200 211 EF-HAND 4 (POTENTIAL).
FT CA_BIND 241 252 EF-HAND 5 (POTENTIAL).
FT CA_BIND 277 288 EF-HAND 6 (POTENTIAL).
FT SITE 315 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 318 AA; 37176 MW; 57B50F45FC09CEFF CRC64;
Query Match 26.9%; Score 476; DB 1; Length 318;
Best Local Similarity 35.2%; Pred. No. 2.3e-26;
Matches 117; Conservative 58; Mismatches 131; Indels 26; Gaps 8;
QY 4 RPSVLLLLLRHGAQCKSPDAGPHGQGRVHQAAPLSDAPHDHAGNFQYDHEAFLG-R 62
DB 6 RPAVLGLLLLYAAVAGASKAEELHYPGGE-HRA-----DYDREALLGQV 49
QY 63 EVAKFEDLTPEEQARIGRIVDRMDRAGDGGWVSLAELRAWTAAHTQQRHIRDSVSAAW 122
DB 50 EDVDEYVLGHEEQRRQLSIKKID--SDSDGFLTENELSQWISQMSFKHYAMQEAQKF 107
QY 123 DTYDTRDGRVGEWELRNATYGHVAPGEEHVDVDAETKYKMLARDERRFRVADODGD 180
DB 108 VEYDKNSDGTVTWDEYNVOMYDRVIDFDENTALDDTEESFQLHLKDKKRFKANKDQG 167
QY 181 SMATREELTAFLHPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEP-GEEP 239
DB 168 PGLNLEEFATFEPHEPEVDYMTFVIOEALAEHDKNGDGVSLFEFLGD-YRDRPTANEDP 226
QY 240 AWVQTERQFRDRLNKGDLGSEVGHVWLPAPADQPLVEANHLHESDTDKDGLSLK 299
DB 227 EWILVEKFRVNDYDKSDGRLDQPELLSWVYVNNQGTAEALHLIDEMLNSDKLSE 286
QY 300 AEILGNWFMVGSQATNYGEDLTR---HHDEL 328
DB 287 EEILENQDLFLTSEATIDYGRQLHDDYFYHDEL 318
RESULT 6
RCN2_HUMAN RCN2_HUMAN STANDARD; PRT; 317 AA.
ID RCN2_HUMAN ID RCN2_HUMAN
AC Q14257; AC Q14257;
DT 01-NOV-1997 (Rel. 35, Created) DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update) DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)


```


DE Reticocalbin 2 precursor (Calcium-binding protein ERC-55) (E6-
DE binding protein) (E6BP).
GN RCN2 OR ERC55.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Cranial; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN NCBI_TaxID=9606;
 RN 111

SEQUENCE FROM N.A.
MEDLINE=94308182; PubMed=8034671;
Weis K., Griffiths G., Lamond A. T.

RT The endoplasmic reticulum calcium-binding protein of 55 kDa is a
RT novel EF-hand protein retained in the endoplasmic reticulum by a
RT carboxyl-terminal His-Asp-Glu-Leu motif".

J. Biol. Chem. 269:19142-19150(1994).
 - FUNCTION: NOT KNOWN, BINDS CALCIUM.
 - SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 - TISSUE SPECIFICITY: Liver.

CC - TISSUE SPECIFICITY: UBIQUITOUS.
CC - SIMILARITY: BELONGS TO THE CREC FAMILY.
CC - SIMILARITY: CONTAINS 6 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----

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DR EMBL; X78659; CAA55343.1; -.
DR Genew; HGNC:9935; PCW2

```

MIN; 602584; -
InterPro; IPR003048; EF-hand.
InterPro; IPR00886; ER_target.

```

PFAM; PF00036; efhand; 5.
SMART; SM00054; EfH; 2.
PROSITE; PS00014; ER_TARGET; 1.
PROSITE; PS00018; ER_TARGET; 1.

NAME	CHAIN	SIGNAL	Calcium-binding; Endoplasmic reticulum; Signal; Repeat.
PROS1; PS000018; EF_HAND; 5.	23	1	POTENTIAL.
PROS1; PS000018; EF_HAND; 5.	317	22	POTENTIAL.

Sample	Concentration	Protein	Concentration	Protein
CA-BIND	74	EF-HAND 1 (POTENTIAL)	85	RETICULOCALBIN 2.
CA-BIND	110	EF-HAND 2 (POTENTIAL)	121	
CA-BIND	162	EF-HAND 3 (POTENTIAL)	173	

T	210	EF-HAND 3 (POSSIBLY ANCESTRAL).
CA_BIND	199	EF-HAND 4 (POTENTIAL).
T	240	EF-HAND 5 (POTENTIAL).
CA_BIND	276	EF-HAND 6 (POTENTIAL).
T	287	
SITE	314	

Query Match

317 AA: 36876 MW; E7C0A4211DBF04AB CRC64; .

317 PREVENT SECRETION FROM ER (POTENTIAL).

Best Local Similarity 25.8%; Score 456.5; DB 1; Length 317;
Matches 116; Conservative 60; Mismatches 128; Indels 29; Gaps

4 RPSVLLLLLLLRRHGAQGPSPDAGPHGQGRVHQAA-APLSDAPHDDAHGNFOYDHEAFGLG-6
| : | | | | |
6 RTAALGLLLLC-----AAAAGAKAEELHYPLGERRSD-----YDREALICV4

```

62 REVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWSLAELRAWIAHTQQRHDSVSA
  : | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
48 QEDVDEYVRLGHEEOOKRIGCALITKTDYVPCGQVETVETVETVETVETVETVETVET
  : | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

122 WDTYDTRDRGRVGEELRNATYGHYAPGEFFHVEDA--ETVKKMLARDERRFRVADQDG 17

106 FFEYDKNSDDTVTWDEYNQIMYDRVIDFDENTALDDAAEESFRKHLKDKRFEKANQDS 16
180 DSMATREELTAFLHPEEFPHMRDIVIAETLEDLRNKDGVVQVEEYIADLYSAPD-CSEP 23

166 GPGLSLEEFIAFEHPPEVDYMTFVQIALEEHDKNGDGFVSLEEF LGD-YRWDPTANED 22

239 PAWVQTERQOFRERDRLNKDCHYDCGKMGVATL 22

225 PEWILVEKDFRVNDYDKDNGRLDPOQLLPWVVPVNNQGTAEAEALHLIDEMDLNGDKKLS 28

```

Qy 299 KAEILGNWNFVGSQATNYGDELTR--HHDEL 328
      :||| |::| :||| | :|||
Db 285 EEETILENPDLFTSATDYGROLHDDYFVHDET 317

```

RESULT 7	
CB45_HUMAN	
ID CB45_HUMAN	PRT: 162 AA
STANDARD:	

AC	Q9BRK5;
DT	15-JUN-2002 (Rel. 41, Created)
DT	15-JUN-2002 (Rel. 41, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)
45 kDa calcium-binding protein precursor (Cab45) (Stromal cell-derived factor 4) (SDF-4).
SDF4 OR CAB45

Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.

Medline-97396029; PubMed-9254016;
Koivu T., Laitinen S., Riento K., Olkkonen V.M.;
"Sequence of a human cDNA encoding Cab45, a Ca2+-binding protein with
six EF-hand motifs".

SEQUENCE FROM N.A.

Yue P., Yu L., Zhao S.Y.; "Cloning of a new human cDNA homologous to Mus musculus calcium-binding protein Cap45b.";

Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
TISSUE=Brain, Pancreas and

Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

- 1- ENDOPLASMIC RETICULUM LUMEN OR POST-ER COMPARTMENT.
- 1- SUBCELLULAR LOCATION: Golgi lumen (By similarity).
- 1- TISSUE SPECIFICITY: Ubiquitous.
- 1- STANTON, J. (1994)

-1- SIMILARITY: BELONGS TO THE CREC FAMILY.
-1- SIMILARITY: CONTAINS 6 EF-HAND CALCIUM-BINDING DOMAINS.

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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announcement/> or send an email to license@isb-sib.ch).

EMBL: L79912; AAL40084.1; -
EMBL: AF132749; AAL75950.1; -
EMBL: BC006211; AAF06211.1; -

EMBL: BC008211.1; -
EMBL: BC007625; AAH07625.1; -
EMBL: BC008917; AAH08917.1; -
EMBL: BC011244; AAH11244.1; -

EMBL; BC022375; AAH22375.1; -.
InterPro: IPR002048; EF-hand.
Pfam: PF00036; ehand; 5.
SMART: SM00024; ehand; 5.

SMART; SM00054; Eph; 5.
 PROSITE; PS00018; EF_HAND; 5.
 Calcium-binding; Golgi stack; Signal; Glycoprotein; Repeat.
 SIGNAL 1 36

CHAIN	36	POTENTIAL.
CA_BIND	37	45 KDA CALCIUM-BINDING PROTEIN.
CA_BIND	111	EF-HAND 1 (POTENTIAL).
CA_BIND	150	EF-HAND 2 (POTENTIAL).

CA_BIND	209	EF-HAND 2 (POTENTIAL)
CA_BIND	220	EF-HAND 3 (POTENTIAL)
CA_BIND	246	EF-HAND 4 (POTENTIAL)
CA_BIND	257	EF-HAND 5 (POTENTIAL)
CA_BIND	291	EF-HAND 2 (POTENTIAL)
CA_BIND	292	EF-HAND 3 (POTENTIAL)
CA_BIND	302	EF-HAND 4 (POTENTIAL)
CA_BIND	303	EF-HAND 5 (POTENTIAL)

CA_BIND	327	338	EF-HAND 6 (POTENTIAL).	(POTENTIAL).
---------	-----	-----	------------------------	--------------

FT CARBOHYD 40 40 N-LINKED (GLCNAC... (POTENTIAL).
FT CONFLICT 70 78 DGLNRGPH -> ERALSGFGQ (IN REF. 2).
FT CONFLICT 86 97 DLGGFDEDAEPR -> NLVALINGAP (IN REF. 2).
FT CONFLICT 150 150 D -> G (IN REF. 2).
FT CONFLICT 281 282 DR -> KK (IN REF. 2).
FT CONFLICT 286 286 F -> L (IN REF. 2).
FT CONFLICT 322 325 MAV -> IRL (IN REF. 2).
FT CONFLICT 356 356 R -> S (IN REF. 2).
FT CONFLICT 362 362 R -> S (IN REF. 2).
SQ SEQUENCE 362 AA; 41807 MW; 440C6990149AE2C CRC64;
Query Match 15.28; Score 269.5; DB 1; Length 362;
Best Local Similarity 25.18; Pred. No. 6.3e-12;
Matches 75; Conservative 63; Mismatches 136; Indels 25; Gaps 8;
QY 47 DAHGNFYDHEAFLEAGREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGVWYSLAEFLRAWI 106
Db 70 DGLNRGPHQEVFLGKDLGGFDEDAEPRSRKRLMVFISKVD--VNTDRKISAKEMORWI 127
QY 107 AHTQQRHINDSVAA---WDYTDTRDGRVGVWEELR---NATYGHYAPGEFHDV----- 155
Db 128 MEKTAHFQEAEMESKTHFRVAVDPDGDGVHSDVEYKVKFLASKGH--SEKEVADAIRLNE 185
QY 156 ---EDAEYTKMLARDERRFRVADQDGDGMATREELTAFLHPEEPHMRDIVIAETLEDL 212
Db 186 ELKVDEETQEVLENLDRWYQADSPADLLITTEEFSLFSLHPEHSGRLMFWKVEIVRDL 245
QY 213 DRNKDGVQVVEVIA---DLYSAEPCEE--EPAAWVOTERQDFRDLNKGDLHLDSEGVGH 268
Db 246 DQDQKQLSPFISLPVGTVENQOQDIDNNWVKRKKFEFLIDNSHNDGIVTAEELLES 305
QY 269 WVLPPADQDQVLEANEHLHSDTDKRLSKAEILGNWNNMFGVSOATNYGEDLTRHDE 327
Db 306 YMDPMNEYNALNEAKOMIAVDENQNHLEPEELVLYSEFFTGSKLVYARSV---HEE 361
RESULT 8
CB45_RAT STANDARD; PRT; 361 AA.
ID CB45_RAT 091233;
AC 091233;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 45 kDa calcium-binding protein precursor (Cab45) (Stromal cell-derived factor 4) (SDF-4).
DE SDF4 OR CAB45.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=BDIX;
RC Zhu Y., Wang M., Lin H., Luo J.;
RA "A calcium binding protein Cab45, identified in rat and up-regulated by alcohol."
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RL -!- FUNCTION: MAY REGULATE CALCIUM-DEPENDENT ACTIVITIES IN THE ENDOPLASMIC RETICULUM LUMEN OR POST-ER COMPARTMENT.
CC -!- SUBCELLULAR LOCATION: Golgi lumen (By similarity).
CC -!- SIMILARITY: BELONGS TO THE CREC FAMILY.
CC -!- SIMILARITY: CONTAINS 6 EF-HAND CALCIUM-BINDING DOMAINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC EMBL: AF405545; AAL01370.1;
CC InterPro: IPR002048; EF-hand.
DR

DR PFAM: PF00036; ehand; 5.
DR PROSITE: PS00018; EF_HAND; 5. Signal; Glycoprotein; Repeat.
KW Calcium-binding; Golgi stack; POTENTIAL.
FT SIGNAL 1 35
FT CHAIN 36 361
FT CA_BIND 110 121 EF-HAND 1 (POTENTIAL).
FT CA_BIND 149 160 EF-HAND 2 (POTENTIAL).
FT CA_BIND 208 219 EF-HAND 3 (POTENTIAL).
FT CA_BIND 245 256 EF-HAND 4 (POTENTIAL).
FT CA_BIND 290 301 EF-HAND 5 (POTENTIAL).
FT CA_BIND 326 337 EF-HAND 6 (POTENTIAL).
FT CARBOHYD 39 N-LINKED (GLCNAC... (POTENTIAL).
SQ SEQUENCE 361 AA; 42075 MW; 1BF74F014B033FC5 CRC64;
Query Match 14.88; Score 261.5; DB 1; Length 361;
Best Local Similarity 25.38; Pred. No. 2.3e-11;
Matches 75; Conservative 66; Mismatches 135; Indels 21; Gaps 8;
QY 47 DAHGNFYDHEAFLEAGREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGVWYSLAEFLRAWI 106
Db 69 DGLNRGPHQEVFLGKDLGGFDEDAEPRSRKRLMVFISKVD--VNTDRKISAKEMORWI 126
QY 107 AHTQQRHINDSV---SAAWDTYDTRDGRVGVWEELR---NATYGH---YAPGEFHDV-- 154
Db 127 MEKTAHFQEAEMESKTHFRVAVDPDGDGVHSDVEYKVKFLASKGHNERIAIDAKNHEEL 186
QY 155 VEDAETTKMLARDERRFRVADQDGDGMATREELTAFLHPEEPHMRDIVIAETLEDLDR 214
Db 187 KVDEETQEVLENLDRWYQADSPADLLITTEEFSLFSLHPEHSGRLMFWKVEIVRDLQ 246
QY 215 NKDGVQVVEVIA---DLYSAEPCEE--EPAAWVOTERQDFRDLNKGDLHLDSEGVGHV 270
Db 247 DQDQKQLSPFISLPVGTVENQOQDIDNNWVKRKKFEFLIDNSHNDGIVTAEELLENM 306
QY 271 LPPADQDQVLEANEHLHSDTDKRLSKAEILGNWNNMFGVSOATNYGEDLTRHDE 327
Db 307 YMDPMNEYNALNEAKOMIAVDENQNHLEPEELVLYSEFFTGSKLVYARSV---HEE 360
RESULT 9
CB45_MOUSE STANDARD; PRT; 361 AA.
ID CB45_MOUSE 061112;
AC 061112; Q61113;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 45 kDa calcium-binding protein precursor (Cab45) (Stromal cell-derived factor 4) (SDF-4).
DE SDF4 OR CAB45.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=96195270; PubMed=8609160;
RA Scherer P.E., Lederkremer G.Z., Williams S., Fogliano M., Baldini G., Lodish H.F.;
RT "Cab45, a novel (Ca2+)-binding protein localized to the Golgi lumen." J. Cell Biol. 133:257-268(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=97092876; PubMed=8938438;
RA Shirozu M., Tada H., Tashiro K., Nakamura T., Lopez N.D., Nazarea M., Hamada T., Sato T., Nakano T., Honjo T.;
RT "Characterization of novel secreted and membrane proteins isolated by the signal sequence trap method." Genomics 37:273-280(1996).
RL -!- FUNCTION: MAY REGULATE CALCIUM-DEPENDENT ACTIVITIES IN THE ENDOPLASMIC RETICULUM LUMEN OR POST-ER COMPARTMENT.
CC -!- SUBCELLULAR LOCATION: Golgi lumen.
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- SIMILARITY: BELONGS TO THE CREC FAMILY.

[illegible]

RESULT 15	CABP_ENTHI	STANDARD;	PRT;	134 AA.
ID	CABP_ENTHI			
P38505;				
01-OCT-1994 (Rel. 30, Created)				
01-OCT-1994 (Rel. 30, Last sequence update)				
16-OCT-2001 (Rel. 40, Last annotation update)				
Calcium-binding protein (CABP).				
Entamoeba histolytica.				
Eukaryota; Entamoebidae; Entamoeba.				
NCBI_TaxID=5759;				
11				

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 14, 2003, 10:40:47 ; Search time 50.9795 Seconds
(without alignments)
618.525 Million cell updates/sec

Title: US-09-768-840-1
Perfect score: 1772
Sequence: 1 MMWRFSVLLLLLLRHGAQG.....FVGSQATNYGEDLTRHDEL 328

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:.*
1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	944	53.3	331	2 JC4173	reticulocalbin pre
2	938	52.9	325	2 A45337	reticulocalbin pre
3	692	39.1	322	2 A57516	DNA supercoiling f
4	639.5	36.1	314	2 T25842	hypothetical prote
5	476	26.9	318	2 I56519	talpoxin-associate
6	466.5	26.3	319	2 JCS402	vitamin D receptor
7	456.5	25.8	317	2 I37371	ER calcium-binding
8	357	20.1	313	2 T33849	hypothetical prote
9	214.5	12.1	345	2 T09018	probable calcium-b
10	188	10.6	374	2 A42264	membrane-associate
11	175	9.9	320	2 T15849	hypothetical prote
12	145	8.2	371	2 T00835	calcium-dependent
13	138.5	7.8	324	2 T02109	calmodulin-like pr
14	130	7.3	521	2 G96543	calcium-dependent
15	129	7.3	317	1 A31797	Spec-related prote
16	127.5	7.2	271	1 A0253	calretinin - human
17	127	7.2	271	1 S25006	calretinin - rat
18	126.5	7.1	243	2 A40394	spec-related prote
19	126	7.1	269	1 A27067	calretinin - chick
20	124	7.0	154	2 G85041	probable calmoduli
21	123.5	7.0	166	2 T07949	calcium binding pr
22	122.5	6.9	163	2 J00062	fast skeletal trop
23	122.5	6.9	536	2 T05500	calcium-dependent
24	121.5	6.9	544	2 D84550	probable calmoduli
25	120	6.8	167	2 J00065	fast skeletal trop
26	119.5	6.7	163	2 J00063	fast skeletal trop
27	119.5	6.7	513	1 T02259	calcium-dependent
28	118.5	6.7	162	1 A40803	troponin C, skelet
29	118.5	6.7	531	1 T02993	calcium-dependent

calmodulin 8 [impo
calcium-dependent
troponin C, skelet
calcium-dependent
calcium-dependent
probable calcium-d
troponin C, skelet
15K calcium-bindin
calcineurin regula
hypothetical prote
hypothetical prote
calcium-binding pr
hypothetical prote
hypothetical prote
calcium-dependent

30. 118 6.7 151 2 A71409
31 118 6.7 533 1 S56652
32 117.5 6.6 162 1 TPFGCS
33 116.5 6.6 484 2 T05650
34 116.5 6.6 610 1 A49082
35 116 6.5 582 2 E84721
36 115.5 6.5 163 1 TPCHCS
37 114.5 6.5 150 2 JS0024
38 114.5 6.5 176 2 JQ1232
39 114.5 6.5 190 2 S61168
40 113.5 6.4 166 2 A86447
41 113 6.4 149 2 A33353
42 113 6.4 150 2 H86194
43 113 6.4 246 2 T05308
44 113 6.4 246 2 H85387
45 113 6.4 540 1 T01989

ALIGNMENTS

RESULT 1
JC4173
reticulocalbin precursor - human
C:Species: Homo sapiens (man)
C>Date: 27-Aug-1995 #sequence_revision 27-Oct-1995 #text_change 02-Aug-2002
C:Accession: JC4173
R:Ozawa, M.
J. Biochem. 117, 1113-1119, 1995
A:Title: Cloning of a human homologue of mouse reticulocalbin reveals conservation of
A:Reference number: JC4173; MUID:96172582; PMID:8586628
A:Accession: JC4173
A:Molecule type: mRNA
A:Residues: 1-331 <OZA>
A:Cross-references: DDBJ:D42073; MID:g1262328; PIDN:BAA07670.1; PID:d1008252; PID:g1
C:Comment: This protein is a luminal protein of the endoplasmic reticulum, and is a c
a signal for its retention in the endoplasmic reticulum of cells.
C:Genetics:
A:Gene: GDB:RCN; Rcal
A:Cross-references: GDB:6383031
A:Map position: lrp13-1lp13
C:Superfamily: reticulocalbin; calmodulin repeat homology
C:Keywords: calcium binding; calmodulin binding; EF hand; endoplasmic reticulum
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-331/Product: reticulocalbin homolog #status predicted <MAT>
F:79-111/Domain: calmodulin repeat homology <EF1>
F:113-145/Domain: calmodulin repeat homology <EF2>
F:166-198/Domain: calmodulin repeat homology <EF3>
F:203-235/Domain: calmodulin repeat homology <EF4>
F:244-276/Domain: calmodulin repeat homology <EF5>
F:280-312/Domain: calmodulin repeat homology <EF6>
F:328-331/Region: endoplasmic reticulum retention signal

Query Match 53.3%; Score 944; DB 2; Length 331;
Best Local Similarity 54.7%; Pred. No. 1e-59;
Matches 181; Conservative 51; Mismatches 75; Indels 24; Gaps 5;

QY 7 VLLLLLLRHGAQGKPS-----PDAGPHGQGRVHQAPLSDAPHDDAHGNGFYDHEA 58
Db 16 LLLALLAPRVLRKPTVRKVRWPD-----SELGERPPD-NQSFQYDHEA 62
QY 59 FLGFEVAKFEEDOLTPEESQALRGRIVDRMDRAGDGDGWVSLAEIRAWTAHTQQRHDSV 118
Db 63 FLGKEDSKTFDQLTPEDESKERLGRIVDRID--NDGDGFTVTEELKTKWIKRVKRYIFDNV 120
QY 119 SAAWDTYDTRDGRVGEWELRNATYGHYAPG--EEFHDVEDAEYTKMLARDERFRVADQ 177
Db 121 AKWMDYDRDKDKISWEYKQATYGYLGNPAEFHSDSHHTTKMLPDRERFKAADL 180
QY 178 GDGSDNATREELTAFALHPEFFPHMDIVTAETPLDLDNRKQGVQVEEYIADLYSAEPGEE 237
Db 181 NGDLTATREETAFALHPEFFPHMKIEIVVLETLEDIKNGDGFVDQDDYIADMSHEENGP 240

A57516
DNA supercoiling factor - silkworm
C:Species: Bombyx mori (silkworm)
C>Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 02-Aug-2002
C:Accession: A57516
R:Ohta, T.; Kobayashi, M.; Hirose, S.
J. Biol. Chem. 270, 15571-15575, 1995
A:Title: Cloning of a cDNA for DNA supercoiling factor reveals a distinctive Ca(2+)-b
A:Reference number: A57516; MUID:95318140; PMID:7797553
A:Accession: A57516
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-322 <OHT>
A:Cross-references: GB:D49948
C:Superfamily: reticulocalbin; calmodulin repeat homology
C:Keywords: calcium binding; EF hand
F:67-99/Domain: calmodulin repeat homology <EF1>
F:156-188/Domain: calmodulin repeat homology <EF2>
F:193-225/Domain: calmodulin repeat homology <EF3>
F:236-268/Domain: calmodulin repeat homology <EF4>
Query Match 39.1%; Score 692; DB 2; Length 322;
Best Local Similarity 45.8%; Pred. No. 7.5e-42;
Matches 137; Conservative 52; Mismatches 90; Indels 20; Gaps 5;
5;
QY 40 LSDAPH-DDAHGNFYDHEAFGLREVAKFFDOLTPEESQARLGRIVDRMDRAGDGDGWVS 98
DB 31 LSDAEHYRNEHHNKOFDHDFAFLGDEOAKTFDQLSPSESKRRRLGEIADKID--SQDQGFIT 88
QY 99 LAELRAWIAHTQORHTRDSVSAADWTYDTRDRGRVGEELRNATYGHVAPGEEFHDEDA 158
DB 89 LVELKDWIRYTKRYTDEIDVERHWRQONNEEFVTWEAYRKNVYGF-----MDDMDEK 142
QY 159 E-----TYKKMLARDERFRVADQDQDSMATFEELTAFLHPPEFPHMRDVIATL 209
DB 143 ELKAPNSEGTYNLQKRRRTYADADONDAINLRTFAAFLHPDHSSMRDVVLETL 202
QY 210 EDLDKNGGVVVEEYIADLYSAEPG--EEPAWVOTERQOFRDRLNKGDLGSEV 267
DB 203 EDIDKQDQGVSLDEYIGDMYNAGDGEDEEPEPMWQOEREQFTGYRDTNKGDFMDEHV 262
QY 268 HWLPPAQDQPLVEANILLHESDTDKGRSLKAEILGNMNMVFGSOATNYGDELTRHHD 326
DB 263 DWIAPPEFDHAEARHLVFEADADADEKLTAKKIDKYLDFVGSQATDGEALARRHE 321
RESULT 4
T25842
hypothetical protein M03F4.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Aug-2002
C:Accession: T25842
R:Fulton, L.
submitted to the EMBL Data Library, July 1996
A:Description: The sequence of C. elegans cosmid M03F4.
A:Reference number: Z20097
A:Accession: T25842
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-314 <FUL>
A:Cross-references: EMBL:U64601; PIDN:AAB04578.1; GSPDB:GN00028; CESP:M03F4.7
A:Experimental source: strain Bristol N2; clone M03F4
C:Genetics:
A:Gene: CESP:M03F4.7
A:Map position: X
A:Introns: 31/3; 66/2; 248/3
C:Superfamily: reticulocalbin; calmodulin repeat homology
C:Keywords: EF hand
Query Match 36.1%; Score 639.5; DB 2; Length 314;
Best Local Similarity 40.0%; Pred. No. 3.9e-38;
Matches 132; Conservative 63; Mismatches 100; Indels 35; Gaps 8;
8;
A55337
reticulocalbin precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 02-Aug-2002
C:Accession: A45337; I55203
R:Ozawa, M.; Muramatsu, T.
J. Biol. Chem. 268, 699-705, 1993
A:Title: Reticulocalbin, a novel endoplasmic reticulum resident Ca(2+)-binding protein
A:Reference number: A45337; MUID:93107083; PMID:8416973
A:Contents: teratocarcinoma OMT6050
A:Accession: A45337
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-325 <OZA>
A:Cross-references: GB:DL3003; NID:g220581; PIDN:BA002366.1; PID:dl1002865; PID:g220582
A:Note: sequence extracted from NCBI backbone (NCBIP:121512)
R:Ozawa, M. 118, 154-160, 1995
A:Title: Structure of the gene encoding mouse reticulocalbin, a novel endoplasmic reticu
A:Reference number: I55203; MUID:96015163; PMID:8537305
A:Accession: I55203
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-325 <RES>
A:Cross-references: GB:D43956; NID:g2190295; PIDN:BA007896.1; PID:g968894
C:Genetics: 79/2; 144/1; 203/3; 224/1; 290/3
C:Superfamily: reticulocalbin; calmodulin repeat homology
C:Keywords: EF hand
F:1-23/Domain: signal sequence #status predicted <SIG>
F:32-325/Region: endoplasmic reticulum retention signal
Query Match 52.9%; Score 938; DB 2; Length 325;
Best Local Similarity 55.2%; Pred. No. 2.7e-59;
Matches 181; Conservative 47; Mismatches 76; Indels 24; Gaps 5;
5;
QY 10 LLLLLRHGAQKPS-----PDAGPHGQGRVHQAPLSADPHDAGHGNFYDHEAFGL 61
DB 13 LLLALVLALRAKPTVRKRVVRPD-----SELGERPPD-NOSFYDHEAFGL 59
QY 62 REVAKEDOLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQORHIRDSVSA 121
DB 60 KEDSKTFDQSPDESKEKLGKIVDRID--SDGGLVTEELKWLKRVKRYIDNVAKV 117
QY 122 WDTYDTRDGRGVGEELRNATYGHYAPG-BEFHVDDEATYKMLARDERFRVADQDGD 180
DB 118 WKDYDRDKDKISWEYKQATGYGLNPAEFHDSDDHHTFKMLPRDERFRKASLDLGD 177
QY 191 SMATREELTAFLHPPEFPHMRDIVIAETLEDLRNKGQVYQVEEYIADLYSAEPGEEPA 240
DB 178 LTATREETAFLHPPEEHEMKKEIVVLETLIDKNGDGFVDQDEYIADMFSHEDNGPEPD 237
QY 241 WYQTERQOFRDLNKGDLGSEVGHVWLPPAQDQPLVEANILLHESDTDKGRLSKA 300
DB 238 WYLSEREQFNDRDLNKGDKLKDKEIRHWILPQDYDHAQAEARHLVYESDKNDKMLTKE 297
QY 301 EILGNMNMVFGSOATNYGDELTRHDEL 328
DB 298 EILDNNMFMVGSQATNYGDELTKNHDEL 325
RESULT 3


```

QY 7 VLLVLLLLRHGA-----QKPSDPAGPHGQGRVHQAPLSDAPHDDAHGNFYQDHEAFGL 61
Db 3 VLLVGLLAATAASHSSDSKQ-GEHFGKEHDK-----KYDHEQFLG 46
QY 62 REVAKFQDLTPERSQARGLRIVDRMDRAGDGGVSLAEALRAWIAHTQORHTRDSVSA 121
Db 47 KDTAAEFDELTPERSKELAKLVPKMD-ADSDGFTEENELKHOFNFMQKRVNNDVDR 104
QY 122 WDTYDTR--DGRVGEELRNATYGHV-APGEFHVDVEDAETKMLARDERRFRVADQ 178
Db 105 WKNYKAERKIVDGKIKWEDYRMYGVSADGAGQEL-----SPEYAKMIARDEKRWAVADY 159
QY 179 GDSMATRELTAFUHPPEFPHMRDIVIAETLEDLRNKGQYQVVEYIADLYSAEPGE- 237
Db 160 SNGALDRTEYCEFMHPCDCHMRDVVVAETVDDIDKANKGVSVDLBYIGDMYRPDPYEL 219
QY 238 ---EPANVQTERQFRDLNKGDLGSEVGHVLPAPQDQPLVEANHLHESDTRK 294
Db 220 NGREPQVQSEREMFKEHRDKDGGKLNQEMRDMTPVGFDAEAEARHLVGIDDKND 279
QY 295 GRLSKAEILGNWFMVGSQATNYGEDLTR 324
Db 280 GKLNLDIYVAHYDTEFGVSQATDYGEOLKH 309

RESULT 5
I56519
taipoxin-associated calcium binding protein-49 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 02-Aug-2002
C:Accession: I56519
R:Dodds, D.; Schlimgen, A.K.; Lu, S.Y.; Perin, M.S.
J. Neurochem. 64, 2339-2344, 1995
A:Title: Novel reticular calcium binding protein is purified on taipoxin columns.
A:Reference number: I56519; MUID:95239201; PMID:7722520
A:Accession: I56519
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-318 <RES>
A:Cross-references: EMBL:U15734; NID:g606967; PID:AA80197.1; PID:g606968
C:Superfamily: reticulocalbin; calmodulin repeat homology
C:Keywords: calcium binding; EF hand
F:62-94/Domain: calmodulin repeat homology <EF1>
F:120-152/Domain: calmodulin repeat homology <EF2>
F:187-219/Domain: calmodulin repeat homology <EF3>
F:228-260/Domain: calmodulin repeat homology <EF4>
F:264-296/Domain: calmodulin repeat homology <EF5>

Query Match 26.9%; Score 476; DB 2; Length 318;
Best Local Similarity 35.2%; Pred. No. 1.6e-26;
Matches 117; Conservative 58; Mismatches 131; Indels 26; Gaps 8;
QY 4 RPSVLLLLLRHGAQKPSDPAGPHGQGRVHQAPLSDAPHDDAHGNFYQDHEAFGL-R 62
Db 6 RPAVLGLLLLYAAVAGAKAEELHYQGE-HRA-----DYDREALLGQV 49
QY 63 EVAKFQDLTPERSQARGLRIVDRMDRAGDGGVSLAEALRAWIAHTQORHTRDSVSA 122
Db 50 EDVDEYVKLGHEQQRRLQSIKKID--SDSGFLTENELSQLQMSFKHYAQEAQKQF 107
QY 123 DTYDTRDGRVGEELRNATYGHVAPGEFHVEDA--ETKMLARDERRFRVADQGD 180
Db 108 VEYDKNSDGTWDEYNQYDRVIDFNTALDDTEESFRQLHDKKRFKANKQDSG 167
QY 181 SMATRELTAFUHPPEFPHMRDIVIAETLEDLRNKGQYQVVEYIADLYSAEP-GE 239
Db 168 PGLNLEETAFEPHEPEVDYMTFVIOEALEHDKNGDGFVSLFELG-DYRDDPTANEDP 226
QY 240 ANVQTERQFRDLNKGDLGSEVGHVLPAPQDQPLVEANHLHESDTRK 299
Db 227 EMILVEKDFRNDYDKSDGRLDQELLSWVVPNNQIGIAQEAALHLDMDLNSDKKLS 286
QY 300 AEILGNWFMVGSQATNYGEDLTR---HHDEL 328

Query Match 26.9%; Score 466.5; DB 2; Length 319;
Best Local Similarity 34.6%; Pred. No. 7.4e-26;
Matches 115; Conservative 58; Mismatches 134; Indels 25; Gaps 7;
QY 4 RPSVLLLLLRHGAQKPSDPAGPHGQGRVHQAPLSDAPHDDAHGNFYQDHEAFGL-R 62
Db 6 RPAVLGLLLLYAAVAGAKAEELHYQGE-HRA-----DYDREALLGQV 50
QY 63 EVAKFQDLTPERSQARGLRIVDRMDRAGDGGVSLAEALRAWIAHTQORHTRDSVSA 122
Db 51 EDVDEYVKLGHEQQRRLQSIKKID--SDSGFLTENELSQLQMSFKHYAQEAQKQF 108
QY 123 DTYDTRDGRVGEELRNATYGHVAPGEFHVEDAE--TYKMLARDERRFRVADQGD 180
Db 109 VEYDKNSDGTWDEYNQYDRVIDFNTALDDTEESFRQLHDKKRFKANKQDSG 168
QY 181 SMATRELTAFUHPPEFPHMRDIVIAETLEDLRNKGQYQVVEYIADLYSAEP-GE 239
Db 169 PGLSLEEFIAPEHPEELDYMTFVIOEALEQDKNGDGFVSLFELG-DYRDDPTANEDP 227
QY 240 ANVQTERQFRDLNKGDLGSEVGHVLPAPQDQPLVEANHLHESDTRK 299
Db 228 EMILVEKDFRNDYDKNDGRDLDPQELLSWVVPNNQIGIAQEAALHLDMDLNSDKKLS 287
QY 300 AEILGNWFMVGSQATNYGEDLTR---HHDEL 328
Db 288 EEILENODLFLTSEATDYGRQLHDDYFYHDEL 319

RESULT 7
I37371
ER calcium-binding protein ERC-55 precursor - human
C:Species: Homo sapiens (man)
C>Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 02-Aug-2002
C:Accession: I37371; S43194
R:Wels, K.; Griffiths, G.; Lamond, A.I.
J. Biol. Chem. 269, 19142-19150, 1994
A:Title: The endoplasmic reticulum calcium-binding protein of 55 kDa is a novel EF-ha
A:Reference number: A54873; MUID:94308182; PMID:8034671
A:Accession: I37371
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-317 <RES>
A:Cross-references: EMBL:X78669; NID:g459884; PIDN:CAAS5343.1; PID:g459885
C:Genetics:

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Db 287 EEILENODLFLTSEATDYGRQLHDDYFYHDEL 318

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RESULT 6

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JC5402
vitamin D receptor associated factor 1 - mouse
N:Alternate names: ERC-55 protein
C:Species: Mus musculus (house mouse)
C>Date: 07-Jul-1997 #sequence_revision 18-Jul-1997 #text_change 02-Aug-2002
C:Accession: JC5402
R:Imai, T.; Matsuda, K.; Shimajima, T.; Hashimoto, T.; Masuhiro, Y.; Kitamoto, T.; S.
Biochem. Biophys. Res. Commun. 233, 765-769, 1997
A:Title: ERC-55, a binding protein for the papilloma virus E6 oncoprotein, specific
A:Reference number: JC5402; MUID:97312489; PMID:9168930
A:Accession: JC5402
A:Molecule type: mRNA
A:Residues: 1-319 <IMA>
C:Comment: This protein acts as a vitamin D receptor-specific cofactor modulating 1
C:Superfamily: reticulocalbin; calmodulin repeat homology
C:Keywords: EF hand
F:63-95/Domain: calmodulin repeat homology <EF1>
F:99-131/Domain: calmodulin repeat homology <EF2>
F:151-183/Domain: calmodulin repeat homology <EF3>
F:188-220/Domain: calmodulin repeat homology <EF4>
F:229-261/Domain: calmodulin repeat homology <EF5>
F:265-297/Domain: calmodulin repeat homology <EF6>

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Query Match

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26.3%; Score 466.5; DB 2; Length 319;
Best Local Similarity 34.6%; Pred. No. 7.4e-26;
Matches 115; Conservative 58; Mismatches 134; Indels 25; Gaps 7;

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QY 4 RPSVLLLLLRHGAQKPSDPAGPHGQGRVHQAPLSDAPHDDAHGNFYQDHEAFGL-R 62

```

```

Db 6 RPAVLGLLLLYAAVAGAKAEELHYQGE-HRA-----DYDREALLGQV 50

```

```

QY 63 EVAKFQDLTPERSQARGLRIVDRMDRAGDGGVSLAEALRAWIAHTQORHTRDSVSA 122

```

```

Db 51 EDVDEYVKLGHEQQRRLQSIKKID--SDSGFLTENELSQLQMSFKHYAQEAQKQF 108

```

```

QY 123 DTYDTRDGRVGEELRNATYGHVAPGEFHVEDAE--TYKMLARDERRFRVADQGD 180

```

```

Db 109 VEYDKNSDGTWDEYNQYDRVIDFNTALDDTEESFRQLHDKKRFKANKQDSG 168

```

```

QY 181 SMATRELTAFUHPPEFPHMRDIVIAETLEDLRNKGQYQVVEYIADLYSAEP-GE 239

```

```

Db 169 PGLSLEEFIAPEHPEELDYMTFVIOEALEQDKNGDGFVSLFELG-DYRDDPTANEDP 227

```

```

QY 240 ANVQTERQFRDLNKGDLGSEVGHVLPAPQDQPLVEANHLHESDTRK 299

```

```

Db 228 EMILVEKDFRNDYDKNDGRDLDPQELLSWVVPNNQIGIAQEAALHLDMDLNSDKKLS 287

```

```

QY 300 AEILGNWFMVGSQATNYGEDLTR---HHDEL 328

```

```

Db 288 EEILENODLFLTSEATDYGRQLHDDYFYHDEL 319

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RESULT 7

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I37371

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ER calcium-binding protein ERC-55 precursor - human

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C:Species: Homo sapiens (man)

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```

C>Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 02-Aug-2002

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C:Accession: I37371; S43194

```

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R:Wels, K.; Griffiths, G.; Lamond, A.I.

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```

J. Biol. Chem. 269, 19142-19150, 1994

```

```

A:Title: The endoplasmic reticulum calcium-binding protein of 55 kDa is a novel EF-ha

```

```

A:Reference number: A54873; MUID:94308182; PMID:8034671

```

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A:Accession: I37371

```

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A>Status: preliminary

```

```

A:Molecule type: mRNA

```

```

A:Residues: 1-317 <RES>

```

```

A:Cross-references: EMBL:X78669; NID:g459884; PIDN:CAAS5343.1; PID:g459885

```

```

C:Genetics:

```

A:Gene: ERC-55
C:Superfamily: reticulocalbin; calmodulin repeat homology
C:Keywords: calcium binding; EF hand; endoplasmic reticulum
F:1-22/Domain: signal sequence #status predicted <SIG>
F:61-93/Domain: calmodulin repeat homology <EF1>
F:97-129/Domain: calmodulin repeat homology <EF2>
F:186-218/Domain: calmodulin repeat homology <EF3>
F:227-259/Domain: calmodulin repeat homology <EF4>
F:263-295/Domain: calmodulin repeat homology <EF5>
F:314-317/Region: endoplasmic reticulum retention signal

Query Match 25.88; Score 456.5; DB 2; Length 317;
Best Local Similarity 34.88; Pred. No. 3.8e-25;
Matches 116; Conservative 60; Mismatches 128; Indels 29; Gaps 9;

QY 4 RPSVLLLLHLLRHGAQKPSDAGPHGQGRVHQ-APLSDAPDDAHNGFYDHEAFLG- 61
DB 6 RFAALGLLLLC-----AAAGAGAAELHYPLGRRSD-----YDREALLV 47
QY 62 REVAKFEDLTPESQARLGRIVDRMDRAGDGVSWLAELRAWIAHQRRHDSVSAA 121
DB 48 QEDVDYKVLGHEEQKRLQAIKKIDL--DSGFLTESELSSWQMSFRHYAQEAQKQ 105
QY 122 WQYDTRDRGRVGEELRNATYGHYAPGEFHVEDA--EYKKMLARDERFRVADQG 179
DB 106 FVEYDKNSDDTVWDEYNIQMVDRIEDFDENTALDDAEESFRKLHLKRRFEKANQDS 165
QY 180 DSMATREELTAFLHPEEFPHMRDIVIAETLEDLRNKGQYVQVEEYIADLYSAEP- 238
DB 166 GPGLSLEEFIAFHEPEVDYMTFVIOEALAEHDKNGDGVSLSEFLGD-YRWDPANED 224
QY 239 PAWQVQROQFRDLNKGDLGSEVGHVWVLPAPADQPLVEANHLHESDTRKDGRLS 298
DB 225 PEWLVKORFVNDYDKNDGRLLDQELLPPVWVNNQGTAAQEALHLIDEMDLNGDKKLS 284

QY 299 KAETLGNWNVFVGSQATNYGEDLTR---HDEL 328
DB 285 EEEILENPDILFTSEATDYGRQLHDDYFYHDEL 317

RESULT 8
T33849
hypothetical protein F08B6.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 16-Aug-2002
R:Le. T.T.; Scheet, P.; Kemp, K.
submitted to the EMBL Data Library, November 1998
A:Description: The sequence of C. elegans cosmid F08B6.
A:Reference number: 221423
A:Accession: T33849
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-313 <LET>
A:Cross-references: EMBL:AF106590; PIDN:AAC78237.1; GSPDB:GN00019; CESP:F08B6.3
A:Experimental source: strain Bristol N2; clone F08B6
C:Genetics:
A:Gene: CESP:F08B6.3
A:Map position: 1
A:Introns: 78/1; 112/3; 127/3; 161/1; 231/2
C:Superfamily: reticulocalbin; calmodulin repeat homology

Query Match 20.1%; Score 357; DB 2; Length 313;
Best Local Similarity 31.6%; Pred. No. 4.3e-18;
Matches 86; Conservative 51; Mismatches 101; Indels 34; Gaps 7;

QY 74 EESQARLGRIVDRMDRAGDGVSWLAELRAWIAHQRRHDSVSAAWDTYDTRDG-- 131
DB 59 QESVERFAKALDT-----NNDGFVKSEILAWVSEYQKTVDRRAVERISELDENADGFL 113
QY 132 -----RVGWEELRNATYGHYAPGEFHVEDAETYYKKMLARDERFRVADQD 178
DB 114 YFNTLFLSLVDRKHVSWEEYLDSP-----PDEELHNKEE-----ESLIAQDKMYFKQADE 165

QY 179 GDSMATREELTAFLHPEEFPHMRDIVIAETLEDLRNKGQYVQVEEYIADLYSAEPGEE 238
DB 166 NDGKLNLEELASFLNPEHPHMPVLIAVTLLEKQDQNGDAIEKEFLGEL-DEQRGSE- 223
QY 239 PAWQVQROQFRDLNKGDLGSEVGHVWVLPAPADQPLVEANHLHESDTRKDGRLS 298
DB 224 --WKVVEVERFTYVDKNDKGLAGDELTDWLLVDGTTAGSYEAESLLTNSDDDKDQGLS 281
QY 299 KAETLGNWNVFVGSQATNYGEDLTRH--HDEL 328
DB 282 VEEIVKHAFKTAQAQADHHLHPYSHDEL 313

RESULT 9
T09018
probable calcium-binding protein T27E11.30 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 02-Aug-2002
C:Accession: T09018
R:Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Ban-
submitted to the Protein Sequence Database, June 1999
A:Reference number: Z16533
A:Accession: T09018
A:Molecule type: DNA
A:Residues: 1-345 <BEV>
A:Cross-references: EMBL:AL078579; GSPDB:GN00062; ATSP:T27E11.30
A:Experimental source: cultivar Columbia; BAC clone T27E11
C:Genetics:
A:Gene: ATSP:T27E11.30
A:Map position: 4
A:Introns: 163/1; 197/2; 219/2; 304/3
C:Superfamily: reticulocalbin; calmodulin repeat homology
C:Keywords: EF hand

Query Match 12.1%; Score 214.5; DB 2; Length 345;
Best Local Similarity 27.4%; Pred. No. 6.3e-08;
Matches 82; Conservative 53; Mismatches 125; Indels 39; Gaps 12;

QY 56 HEAFGLR---EVAKE-----FDQLTPEE---SQARLGRIVDRMDRAGDGVSWLAELR 103
DB 60 HEKEAGTKTVEAAKEEKDMFEYFAOERLNTNRILKFLPLLD-ASPRDGFVSLKELQ 118
QY 104 AWIAHQRRHDSVSAAWDTYDTRDRGRVGEELRNATYGHYAPGEFHVEDAETYYK 163
DB 119 TWMMQOTEDNVYRTAKLEQLDKDKGVITFE-----YLPQFSKODIEKNEKGHG 170
QY 164 MLARDERFRVADQDGSMAETRELTAFLEHPEEPH--MRDIVIAETLEDLRNKGQYVQ 221
DB 171 EAGWMEQFKNSDFDHNGSLDIEEFNLFHEDSRNGDTQWVWKERTGMTGDTNGDKLE 230
QY 222 VEEYIADLYS-----AEPGEPEPAWQVQROQFRDLNKGDLGSE---VGHVWVLP 273
DB 231 YKEFVNAYEMKFEAKFEKEEDENVPTQLFAEM-DRDKRDLVLADELPILOYLPQG 289
QY 274 ADOQPLVEANHLHESDTRKDGRLSKAELLGNWNVFVGSQATNYGEDLTRH----HDEL 328
DB 290 EMSYAKFYSTFLCHEADKDKGLSLEELHHEVDVY--KAVHH-EDLDDDEDYFDHDEL 345

RESULT 10
A42264
membrane-associated calcium-binding protein pfs40 - malaria parasite (Plasmodium fa-
C:Species: Plasmodium falciparum
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jun-2000
C:Accession: A42264
R:Rawlings, D.J.; Kaslow, D.C.
J. Biol. Chem. 267, 3976-3982, 1992
A:Title: A novel 40-kDa membrane-associated EF-hand calcium-binding protein in Plasmo-
A:Reference number: A42264; M01D:92156141; PMID:1740445
A:Accession: A42264
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid; protein

120modulin-like protein At2g41100 [imported] - Arabidopsis thaliana
 alternate names: calmodulin-related protein T3K9.13
 species: Arabidopsis thaliana (mouse-ear cress)
 date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 16-Feb-1999
 accession: T02109; G84837
 counsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Br
 submitted to the EMBL Data Library, February 1999
 description: Arabidopsis thaliana chromosome II BAC T3K9 genomic s
 reference number: Z14570
 accession: T02109
 status: translated from GB/EMBL/DBJ
 molecule type: DNA

